

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 25, 2006, 21:43:01 ; Search time 6217.24 Seconds  
(without alignments)  
4242.296 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403  
Sequence: 1 MSFLEGENSSWSPAVTSS.....LSDIQLVLSPAGIDALGA 464

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlp  
-O=/cgn2\_1/USPTO\_spool\_p/US10070794/runat\_24012006\_164415\_8786/app\_query.fasta\_1.1102  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOPCCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10070794 @CGN 1.1 7830 @runat\_24012006\_164415\_8786 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*  
1: gb.ba.\*  
2: gb.in.\*  
3: gb.env.\*  
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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
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11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
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15: gb.pl.\*

ALIGNMENTS

RESULT 1  
AX814738  
LOCUS AX814738 1470 bp DNA linear PAT 05-DEC-2003  
DEFINITION Sequence 1 from Patent WO03063586.  
ACCESSION AX814738  
VERSION AX814738.1 GI:39103937  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1  
AUTHORS Andersson, L. and Marklund, S.  
TITLE Transgenic animals expressing prkag3  
JOURNAL Patent: WO 03063586-A 1 07-AUG-2003;  
Arexis AB (SE)  
FEATURES  
source Location/Qualifiers  
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/note="unnamed protein product"

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2403	100.0	1470	6	AX814738 Sequence
2	2403	100.0	2115	6	AX099802 Sequence
3	2403	100.0	2115	8	AF214519 Homo sapi

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## ORIGIN

Alignment Scores:  
Pred. No.: 1,41e-135 Length: 1470  
Score: 2403.00 Matches: 464  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-070-794A-30 (1-464) x AX814738 (1-1470)

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Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
Db GTGGAGGAGGAGGAGCCACAGGTGAGGGGAGAGGTCCCGGTCCAGGCCAATGCTGAG 255  
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
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Qy 241 GlnHisLysLileGluThrTrpArgGluLileTyArgGlnGlyCysPheLysProLeuVal 260  
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AX099802  
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DEFINITION AX099802  
ACCESSION AX099802.1 GI:13538836  
VERSION  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Andersson, L., Looft, C., Kalm, P., Milan, D., Robic, A.,  
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and  
Chardon, P.  
TITLE Variants of the gamma chain of ampk, dna sequences encoding the  
same, and uses thereof  
JOURNAL Patent: WO 0120003-A 29 22-MAR-2001;  
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;  
Andersson, Looft, Christian (DE) ; Kalm, Ernst (DE)  
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CDS

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## ORIGIN

## Alignment Scores:

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Pred. No.: 2,13e-135 Length: 2115
Score: 2403.00 Matches: 464
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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US-10-070-794A-30 (1-464) x AX099802 (1-2115)

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DB 61 TCAGAAAGATCCGTGGGAACGAGAGGCCCAAGCCTTGAGTGGACAGCAGAGTGC 120
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DB 121 GTGAGGAGAGGGAGCCACAGGTCAGGGGAGGTCCTCCCGTCCAGGCCAATGCTGAG 180
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
DB 181 TCCACCGGGTGGAGGCCACATATCCCAAGACCAACACCTTGGCTCAAGCTGATCTCGCC 240
QY 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
DB 241 GGGGTGGGCACTCCACCAACAGGGTGGGACTGCTCCCTCCCTCTGACTGTACAGCTCAGCT 300
QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
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DB 361 GAGTGTGAGTGAAGGCCCTGCTGGAAGAGAGGCGCTGCTGTGCTGCTCCCGCAGGCC 420
QY 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyMet 160
DB 421 CCATTTCCCAAGCTGGGCTGGATGACGAACTGGGAAACCCGGCGCCCAAGTCTCATG 480
QY 161 ArgPheMetGlnGluHisThrCysTyAspAlaMetAlaThrSerSerLysLeuValIle 180
DB 481 CGCTTTCATGAGGAGCACACTGTACGATGCCATGCAACTAGTCTCAAGTAGTCATC 540
QY 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
DB 541 TTCACACCACTGCTGGAGATCAAGAGGCCCTCTTTGCTCTGTGGTGGCCAAACGGTGTGCGG 600
QY 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
DB 601 GCAGCCCTCTATGGGACGACGAGACAGAGCTTTTGGGGATGCTGACCATCCTGAC 660
QY 221 PheIleLeuValLeuHisArgTyTrpArgSerProLeuValGlnIleTyGluIleGlu 240
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DB 1261 AGATGTCTCGGAGCAGGTACACAGGCTGGTGTAGTGACGAGACCCAGCATCTCTTG 1320
QY 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
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## RESULT 3

## AF214519

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

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## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

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**JOURNAL** Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24, Sweden

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## ORIGIN

Alignment Scores:	
Pred. No.:	2.13e-135
Score:	2403.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	8
Length:	2115
Matches:	464
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-070-794A-30 (1-464) X AF214519 (1-2115)

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ACCESSION BC098102
VERSION   BC098102.1   GI:66990059
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AUTHORS   Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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CONSRMT
TITLE    Mammalian Gene Collection Program Team
JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED   12477932
REFERENCE 2 (bases 1 to 1599)
AUTHORS   NIH MGC Project
          Direct Submission
          Submitted (03-JUN-2005) National Institutes of Health, Mammalian
          Gene Collection (MGC), Bethesda, MD 20892-2590, USA
          NIH-MGC Project URL: http://mgc.nci.nih.gov
          Contact: MGC help desk
          Email: cgapbs-x@mail.nih.gov
          Tissue Procurement: Baylor Human Genome Sequencing Center
          cDNA Library Preparation: Baylor Human Genome Sequencing Center
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: National Institutes of Health Intramural
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          Web site: http://www.nisc.nih.gov/
          Contact: nisc_mgc@hgrl.nih.gov
          Akhter, N., Ayèle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
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Clone distribution: MGC clone distribution information can be found
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DEFINITION Sequence 5 from Patent WO0177305.  
ACCESSION AX281582  
VERSION AX281582.1 GI:16608833  
KEYWORDS  
SOURCE Homo sapiens (human)  
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Andersson, L., Luthman, H. and Marklund, S.  
Variants of the human amp-activated protein kinase gamma 3 subunit  
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Arexis AB (SE)  
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Alignment Scores:  
Pred. No.: 3,21e-135 Length: 1647  
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VERSION AX099776.1 GI:13538810  
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REFERENCE

1. Anderson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,  
Rogel-Gallard, C., Iannuccelli, N., Gellin, J., le Roy, P. and  
Chardon, P.

AUTHORS

Variants of the gamma chain of ampk, dna sequences encoding the  
same, and uses thereof  
Patent: WO 0120003-A 3 22-MAR-2001;  
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;  
Anderson, Loeff, Christian (DE) ; Kalm, Ernst (DE)

TITLE

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JOURNAL

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FEATURES

source  
CDS

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## ORIGIN

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Pred. No.: 7,39e-135 Length: 2109  
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 Qy 243 LysIleGluThrTrpArgGluIleTyLeuGlnGlyCysPheLysProLeuValSerIle 262  
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 Qy 263 SerProAsnAspSerLeuPheGluAlaValTyThrLeuIleLysAsnArgIleHisArg 282  
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 Qy 283 LeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArgLeu 302  
 Db 841 CTGGCTGTTCTTGACCGGTGTGAGCAAGTACTCCATCTCTCACACAAACGCGCTG 900

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 Qy 383 GlnThrTyRhenHisLeuAspMetSerValGlyAlaLeuArgGlnArgThrLeuCys 402  
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 Qy 403 LeuGluGlyValLeuSerCysGlnProHisSerLeuGlyGluValIleAspArgIle 422  
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 Qy 423 AlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeuGlyVal 442  
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 Db 1381 GGGGCC 1386

RESULT 8  
 BC098255  
 LOCUS  
 DEFINITION Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit, mRNA (cdna clone MGC:119343 IMAGE:40005883), complete cds.  
 ACCESSION BC098255  
 VERSION BC098255.1 GI:67514300  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1597)  
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Mammalian Gene Collection Program Team  
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 JOURNAL  
 PUBMED 12477932

REFERENCE	2	(bases 1 to 1597)	
AUTHORS	NIH MGC Project		
CONSTRM	Direct Submission		
TITLE	Submitted (10-JUN-2005) National Institutes of Health, Mammalian		
JOURNAL	Gene Collection (MGC), Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: Baylor Human Genome Sequencing Center cDNA Library Preparation: Baylor Human Genome Sequencing Center cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:nisc_mgc@hgrl.nih.gov">nisc_mgc@hgrl.nih.gov</a> Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, J.-H. and Green, E.D.		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAM Plate: 4 Row: e Column: 2. Location/Qualifiers		
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Alignment Scores:			
Pred. No.:	9,39e-135	Length:	1597
Score:	2390.00	Matches:	462
Percent Similarity:	99.57%	Conservative:	0
Best Local Similarity:	99.57%	Mismatches:	2
Query Match:	99.46%	Indels:	0
DB:	8	Gaps:	0
US-10-070-794A-30 (1-464) x BC098255 (1-1597)			

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 Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460  
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## RESULT 9

BC098306 1597 bp mRNA linear PRI 02-JUL-2005  
 DEFINITION Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic  
 subunit, mRNA (CDNA clone MGC:119345 IMAGE:40005888), complete cds.  
 ACCESSION BC098306  
 VERSION BC098306.1 GI:67514235  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

## REFERENCE

1 (bases 1 to 1597)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
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 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Mammalian Gene Collection Program Team  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences

## CONSTRM

TITLE Mammalian Gene Collection Program Team  
 human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 PUBMED 12477932

## REFERENCE

2 (bases 1 to 1597)  
 NIH MGC Project  
 Direct Submission  
 Submitted (10-JUN-2005) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

## REMARK

Tissue Procurement: Baylor Human Genome Sequencing Center  
 cDNA Library Preparation: Baylor Human Genome Sequencing Center  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc\\_mgc@hgrl.nih.gov](mailto:nisc_mgc@hgrl.nih.gov)  
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
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 Young, A., Zhang, L., H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
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 Series: IRAM Plate: 4 Row: f Column: 2.

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## ORIGIN

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 Pred. No.: 9,39e-135 Length: 1597  
 Score: 2390.00 Matches: 462  
 Percent Similarity: 99.57% Conservative: 0  
 Best Local Similarity: 99.57% Mismatches: 2  
 Query Match: 99.46% Indels: 0  
 DB: 8 Gaps: 0

US-10-070-794A-30 (1-464) x BC098306 (1-1597)

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 VERSION AJ249977.1 GI:6698200  
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 Homiidae; Homo.  
 1.  
 REFERENCE 1  
 AUTHORS Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D.  
 TITLE Characterization of AMP-activated protein kinase gamma-subunit  
 isoforms and their role in AMP binding  
 JOURNAL Biochem. J. 345 Pt 3, 659-669 (2000)  
 PUBMED 10698692  
 REFERENCE 2 (bases 1 to 2290)  
 AUTHORS Carling, D.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC  
 Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,  
 London, W12 0NN, UNITED KINGDOM  
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 REFERENCE  
 AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.  
 TITLE Novel p-kag3 alleles and use of the same as genetic markers for  
 JOURNAL reproductive and meat quality traits  
 Patent: WO 0220850-A 3 14-MAR-2002;  
 Iowa State University Research Foundation, Inc. (US)  
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 REFERENCE  
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 AUTHORS  
 Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,  
 Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and  
 Chardon, P.  
 TITLE  
 Variants of the gamma chain of ampk, dna sequences encoding the  
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 JOURNAL  
 Patent: WO 0120003-A 27 22-MAR-2001;  
 INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;  
 Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)  
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 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 Sus.  
 REFERENCE 1  
 AUTHORS Rothschild, M.F., Giobanu, D.C., Malek, M. and Plastow, G.  
 TITLE Novel prkag3 alleles and use of the same as genetic markers for  
 reproductivity and meat quality traits  
 JOURNAL Patent: WO 0220850-A 1 14-MAR-2002;  
 Iowa State University Research Foundation, Inc. (US)  
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1
AUTHORS Anderson, L., Looft, C., Kalm, B., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
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Best Local Similarity: 86.02% Mismatches: 44
Query Match: 83.69% Indels: 2
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REFERENCE  
1 (bases 1 to 2023)  
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,  
Rogel-Gallard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,  
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.  
and Andersson,L.  
A mutation in PRKAG3 associated with excess glycogen content in pig  
skeletal muscle  
Science 288 (5469), 1248-1251 (2000)  
10818001  
PUBMED  
2 (bases 1 to 2023)  
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,  
Rogel-Gallard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,  
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.  
Direct Submission  
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish  
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,  
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3 (bases 1 to 2023)  
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,  
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Best Local Similarity: 86.02% Mismatches: 44  
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US-10-070-794A-30 (1-464) x AF214520 (1-2023)

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GenCore version 5.1.6  
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-NO MMAP -LARGEOURY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hcc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2281	94.9	1470	11	DQ030935 Homo sapi
2	2055	85.5	1470	11	DQ030936 Pan trogl
3	2010	83.6	2256	4	AK036585 Mus muscu
c	4	1239	51.6	754	6 CD628194
c	5	1177	49.0	796	6 CD628192
	6	1154	48.0	799	6 CD628195
	7	1121.5	46.7	805	6 CD628193
					56028544H
					56028562J
					56028554J

8	1113	46.3	2839	4	AK032238	AK032238 Mus muscu
9	1097	45.7	1990	4	CR861174	CR861174 Pongo pyg
10	1094	45.5	2058	4	BC079017	BC079017 Rattus no
11	1043.5	43.4	824	8	CK313244	CK313244 JGI X2T90
12	1017	42.3	1136	5	BX403964	BX403964 BX403964
13	1017	42.3	1144	5	EX421925	EX421925 BX421925
14	1017	42.3	1561	4	CR604823	CR604823 full-leng
15	1017	42.3	1577	4	CR608916	CR608916 full-leng
16	1017	42.3	1584	4	CR613967	CR613967 full-leng
17	1017	42.3	1600	4	CR596899	CR596899 full-leng
18	1017	42.3	1610	4	CR612109	CR612109 full-leng
19	1017	42.3	1648	4	CR620523	CR620523 full-leng
20	1016.5	42.3	1006	1	AL513784	AL513784 AL513784
21	1006	41.9	1015	3	BM907915	BM907915 AGENCOURT
22	1004	41.8	900	10	AY420782	AY420782 Mus muscu
23	1004	41.8	978	1	AL533446	AL533446 AL533446
24	1003	41.7	900	10	AY420780	AY420780 Homo sapi
25	991.5	41.3	1912	4	CNSUGLSJ	CR724269 Tetradon
26	989	41.2	1623	4	CR611774	CR611774 full-leng
27	982	40.9	1081	1	AL554278	AL554278 AL554278
28	977	40.7	1096	5	EX424876	EX424876 BX424876
29	972.5	40.5	1023	1	AL555228	AL555228 AL555228
30	964	40.1	1062	1	AL524822	AL524822 AL524822
31	960	40.0	929	1	AL548987	AL548987 AL548987
32	955	39.7	1085	3	BM548053	BM548053 AGENCOURT
33	946	39.4	857	8	DR866220	DR866220 JGI_CABG8
34	941	39.2	944	5	BQ954908	BQ954908 AGENCOURT
35	928	38.6	1033	5	BX382758	BX382758 BX382758
36	924	38.5	937	5	BM845992	BM845992 BX845992
37	915.5	38.1	1070	3	BQ224866	BQ224866 AGENCOURT
38	913	38.0	845	8	DN067954	DN067954 JGI_CABD4
39	913	38.0	850	8	DR880606	DR880606 JGI_CABU1
40	910	37.9	1134	3	BM922418	BM922418 AGENCOURT
41	909	37.8	922	6	CA982776	CA982776 AGENCOURT
42	909	37.8	1314	8	DN731086	DN731086 CNB56-E11
43	909	37.8	809	7	CV561269	CV561269 UI-M-HU0
44	908	37.8	937	1	AL552459	AL552459 AL552459
45	906	37.7	937	1	AL552459	AL552459 AL552459

ALIGNMENTS

RESULT 1

DQ030935

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

DQ030935 Homo sapiens PRKAG3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

DQ030935 GI:66882139

GSS.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1470)

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees

(er) PLOS Biol. 3 (6), E170 (2005)

2 (bases 1 to 1470)

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Direct Submission

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

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FEATURES
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ORIGIN
Alignment Scores:
Pred. No.:            8.27e-196      Length:      1470
Score:                2281.00        Matches:    443
Percent Similarity:   95.47%         Conservative: 0
Best Local Similarity: 95.47%         Mismatches: 21
Query Match:         94.92%         Indels:    0
DB:                  11              Gaps:      0

US-10-070-794A-30 (1-464) x DQ030935 (1-1470)
Qy      1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20
Db      76 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAAGC 135
Qy      21 SerGluArgIleArgGlyArgAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 40
Db      136 TCAGAAAGAAATCCGTGGGAAACGAGGCGCAAGGCTTGAGATGGACAAAGCTG 195
Qy      41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db      196 GTGAGGAGGAGGAGCCACAGGTCAGGGGAGAGGTCCCCGGTCCAGGCCAGCTGCTGAG 255
Qy      61 SerThrGlyLeuGluAlaThrPheProIlyThrThrProLeuAlaGlnAlaAspProAla 80
Db      256 TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACCACACCCCTTGGCTCAAGCTGATCTGCC 315
Qy      81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
Db      316 GGGGTGGGCACTCCACCAACAGGGTGGGACTGCCCTCCCTCTGACTGTACAGCCCTCAGCT 375
Qy      101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db      376 CGAGCTCCAGCAGCAGATGATGTGAGCTGGCCAGCGAGTTCACGACGACAGAGGCTGG 435
Qy      121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db      436 GAGTGTGAGCTAGAAAGGCTGCTGGAAGAGAGGCTGCGCTGTGCTGTGCCCGCAGGCC 495
Qy      141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyMet 160
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Qy      161 ArgPheMetGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuValIle 180
Db      556 CGCTTCATGCAGGACACACCTGCTACGATGCCATGGCACTAGCTCCAGCTAGTCAATC 615
Qy      181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db      616 TTCGACACCATGCTGGAGATCAAGAAGCGCTCTTTTGTCTGTGGTGGCCAAACGGTGGGG 675
Qy      201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db      676 GCAGCCCTCTATGGGACGACGAAGACAGAGCTTTGTGGGGATGCTGACCATCACTGAC 735
Qy      221 PheIleLeuValLeuHisArgTyTrpArgSerProLeuValGlnIleTyGluIleGlu 240
Db      736 TTCATCTTGGTGTGCTGATCGCTACTACAGTCCCCCTGGTCCAGATCTATGAGATTGAA 795
Qy      241 GlnHisLysIleGluThrTrpArgGluIleTyLeuGlnGlyCysPheLysProLeuVal 260
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261 SerIleSerProAsnAspSerLeuPheGluAlaValTyThrLeuIleLysAsnArgIle 280
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Qy      281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
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Qy      301 ArgLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTy 320
Db      976 CGCTGTCTCAAGTTCTTCGACATCTTTGGTTCCCTGCTGCCCGCGCTCTCTCTCTAC 1035
Qy      321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db      1036 CGACTATCCAGATTTGGGCATCGGCACATTCGAGACTTGGCTGTGGTCTGGAGACA 1095
Qy      341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
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Qy      381 AlaGlnGlnThrTyraAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
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Qy      401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp 420
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Qy      441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
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Qy      461 AlaLeuGlyAla 464
Db      1456 GCCCTCGGGGCC 1467

RESULT 2
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LOCUS
DEFINITION
    Pan troglodytes PRKAG3 gene, VIRTUAL TRANSCRIPT, partial sequence,
    genomic survey sequence.
ACCESSION
    DQ030936
VERSION
    DQ030936.1
KEYWORDS
    GSS.
SOURCE
    Pan troglodytes (chimpanzee)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Pan.
REFERENCE
    1 (bases 1 to 1470)
    Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
    Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D.,
    White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
    A Scan for Positively Selected Genes in the Genomes of Humans and
    Chimpanzees
    (er) Eos Biol. 3 (6), E170 (2005)
JOURNAL
    PUBMED
REFERENCE
    2 (bases 1 to 1470)
    Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
    Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D.,
    White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
    Direct Submission
    Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
    Rockville, MD 20850, USA
    This sequence was made by sequencing genomic exons and ordering

```

them based on alignment. Translation starts at the beginning of alignment.

## FEATURES

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/db_xref="taxon:9598"
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locus_tag="HC66"

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gene

## ORIGIN

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Percent Similarity:	87.72%	Conservative:	2
Best Local Similarity:	87.28%	Mismatches:	57
Query Match:	85.52%	Indels:	0
DB:	11	Gaps:	0

US-10-070-794A-30 (1-464) x D0030936 (1-1470)

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	Qy	21	SerGluAArgIleArgGlyLeuArgArgAlaLysAlaLeuArgTTPThrArgGlnLysSer	40
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	Qy	41	ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgP-oThrAlaGlu	60
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	Qy	101	AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp	120
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	Qy	121	GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLysSerProGlnAla	140
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	Qy	181	PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg	200
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	Qy	201	AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp	220
	Db	676	GCAGGCCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGATGTCGACCATCATCTGAC	735
	Qy	221	PheIleLeuValLeuHisArgTyrrArgSerProLeuValGlnIleTyrrGluIleGlu	240
	Db	736	TTCACTCTGGTGTGCATCGCTACTACAGGTCCTCCCNNNNNCCAGCATCTATGAGATTGAA	795
	Qy	241	GlnHisLysIleGluThrTrpArgGluIleTyrrLeuGlnGlyCysPheLysProLeuVal	260
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Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
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Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
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Qy 440 LeuGlyValValSerLeuSerAspIleGlnAlaLeuValLeuSerProAlaGlyIle 459
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RESULT 4
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ACCESSION
VERSION CD628194.1 GI:40276460
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
PUBMED 1 (bases 1 to 754)
COMMENT Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
15203218
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1. 754
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FEATURES
source
CD628192/c
LOCUS
DEFINITION 56028554H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD628192
VERSION CD628192.1 GI:40276458
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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## ORIGIN

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Alignment Scores:
Pred. No.: 9.52e-102 Length: 754
Score: 1239.00 Matches: 245
Percent Similarity: 97.61% Conservative: 0
Best Local Similarity: 97.61% Mismatches: 4
Query Match: 51.56% Indels: 2
DB: 6 Gaps: 0

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US-10-070-794a-30 (1-464) x CD628194 (1-754)

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Qy 198 lYValArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrI 218
Db 510 GTGTGGCGGAGCGCCCTCTATGGGACAGCAAGAGAGAGCTTTGTGGGAGATGTGACCA 451
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Qy 238 luIleGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysP 258
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Qy 338 euGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaL 358
Db 90 TGGGGACAGACACCCATCTGACTGCACTGGACATCTTTGTGGACCGGCGGTGTCTGCAC 31
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Db 30 TGCCTGTGGTCAACGAATGTGGTCAAGGTC 2

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 796)  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)  
PUBMED 15203218

COMMENT Contact: Fu GK

Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102

Email: gfu@incyte.com.

FEATURES Location/Qualifiers

source

1..796

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/clone\_lib="FLP"

/note="Vector: pDrive Cloning Vector"

ORIGIN

Alignment Scores:

Pred. No.: 4,33e-96 Length: 796  
Score: 1177.00 Matches: 248  
Percent Similarity: 93.94% Conservativeness: 0  
Best Local Similarity: 93.94% Mismatches: 9  
Query Match: 48.98% Indels: 8  
DB: 6 Gaps: 2

US-10-070-794A-30 (1-464) x CD628192 (1-796)

QY 111 AlaThrGluPheProAlaThrGluAlaTrpGluCysGluLeuGluGlyLeuLeuGlu-Gl 130  
DB 782 GCCACGGAGTTCCTCCACACAGAGCC-TGGAGTGTGAGCTAGAGGCTCTGGTAAGA 724  
QY 130 uArgProAlaLeuCysLeuSer-ProGlnAlaPro---PheProLysLeuGlyTrp-Asp 148  
DB 723 GAGGCTGCCCTGTGCTGTCCCGCAGGGGCCATGTTCCGCCAAGCTTGGGCTGGGGAT 664  
QY 149 AspGlu---LeuArgLysProGlyAlaGlnIle-TyrMetArgPheMetGlnGluHisTh 167  
DB 663 GACGAAACTTGGGAAACCTGGCGCCAGATTCTACATGGCTTCATGCGAGGACAC 604  
QY 167 rCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePheAspThrMetLeuGluIl 187  
DB 603 CTGCTACGATGCCATGGCACTAGCTCCAGCTAGTCATCTCGACACCATGCTGGAGAT 544  
QY 187 eLysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAlaAlaProLeuTrpAspSe 207  
DB 543 CAAGAAGGCTTCTTTGTCTGTGGTGGCAACGGTGTGGGGCAGCCCTCTATGGGACAG 484  
QY 207 r-LysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisA 227  
DB 483 CAAGAAGCAGAGCTTGTGGGGATGCTGACCATCACTGACTTCATCTGCTGGTGGCATC 424  
QY 227 rGlyTyrArgSerProLeuValGlnIleTyrGluIleGluGlnHisLysIleGluThrT 247  
DB 423 GCTACTACAGTTCCTCCCTGGTCCAGATCTATGAGATTGACCAACATTAAGATTGAGACT 364  
QY 247 rPArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIleSerProAsnAspS 267  
DB 363 CGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGCTCTCCATCTCTCTTAATGATA 304  
QY 267 eLLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuA 287  
DB 303 GCCTGTGTGAAGCTGTCTACACCTCATCAAGACCGGATCATCGCTCGCTGTCTGTG 244  
QY 287 spProValSerGlyAsnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuH 307  
DB 243 ACCCGGTGTGAGCAACGCTACTCCCATCTCCACACACAAACGCTGCTCAAGTTCTCTGC 184

QY 307 isIlePheGlySerLeuLeuProArgProSerPheLeuTyrArgThrIleGlnAspLeuG 327  
DB 183 ACATCTTTGGTTCCTGCTGCCCGCCCTCTCTCTTACCGCACTATCCAGATTGG 124  
QY 327 lyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAlaProIleLeuThrAla 347  
DB 123 GCATCGGCACATTCGAGACTTGGCTGTGGTGTGGAGACAGACCCATCTGACTGCAC 64  
QY 347 euAspIlePheValAspArgValSerAlaLeuProValValAsnGluCysGlyGlnV 367  
DB 63 TGGACATCTTTGTGGACCGCGTGTGTCTGCACTGCTGTGGTCAACGAATGTGGTCAG 4  
QY 367 al 367  
DB 3 TC 2  
RESULT 6  
LOCUS CD628195 799 bp mRNA linear EST 12-JAN-2004  
DEFINITION 5602856201 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD628195  
VERSION CD628195.1 GI:40276461  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 799)  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
PUBMED 15203218  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.  
FEATURES Location/Qualifiers  
source 1..799  
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Score: 1154.00 Matches: 223  
Percent Similarity: 96.98% Conservativeness: 2  
Best Local Similarity: 96.12% Mismatches: 7  
Query Match: 48.02% Indels: 1  
DB: 6 Gaps: 0  
US-10-070-794A-30 (1-464) x CD628195 (1-799)  
QY 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
DB 104 ATGAGCTTCCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC 163  
QY 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTTPThrArgGlnLysSer 40  
DB 164 TCAGAAAGAAATCCGTGGGAAACGGAGGGCCAAAGCCTTTGATGTGACAAAGGCAGAGTCG 223  
QY 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
DB 224 GTGGGGGAAGGGAGCCACAGGTTCAGGGGAGAGTCCCGGTCAGGCCAGCTGCTGAG 283  
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
DB 284 TCCACCGGGCTGGAGGCCACATTCGCCAAGACCAACCCCTTGGCTCAAGCTGATCCTGCC 343

Qy	81	GlyValGlyThrProProThrGlyTyrTrpAspCysLeuProSerAspCysThrAlaSerAla	100
Db	344	GGGGTGGGCATCTCCACCAAGGGTGGGACTGCCCTCTGACTGTACAGCCTCAGCT	403
Qy	101	AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp	120
Db	404	GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGAGGTGCCAGCCACAGAGCGCTGG	463
Qy	121	GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla	140
Db	464	GAGTGTGAGCTGAAGGCGCTGCTGGAGAGAGGCGTGCCTGTGCTGTCCCGCAGGCC	523
Qy	141	ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyValaGlnIleTyrMet	160
Db	524	CCATTTCCAAGCTGGGCTGGGATGACGAACTGCGGAAACCGCGCGCCAGATCTACATG	583
Qy	161	ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle	180
Db	584	CGCTTCATGCAGAGGACACACTGCTACGATGGCATGGCAACTAGCTCCAGCTAGTCACT	643
Qy	181	PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg	200
Db	644	TTCCGATACCATGCTGGAGATCAAGAAGGTCCTCTTTGCTCTGTTGGTGGCCAAACGGTGTGGCG	703
Qy	201	AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp	220
Db	704	GCAGGCGCTCTATGGGACGACGAGACGAGAGCTTTGTGGGGATGCTGACATCACTCA	762
Qy	221	PheIleLeuValLeuHisArgTyrTyrArgSerPro	232
Db	763	TTTCATCTGGTGGCTGCATCTGTTACTTACCAAGCGTCCGC	798

RESULT 7			
CD628193			
LOCUS	CD628193	805 bp	mRNA linear
DEFINITION	S6028554J1 FLP Homo sapiens cDNA, mRNA sequence.		EST 12-JAN-2004

ACCESSION	CD628193
VERSION	CD628193.1
KEYWORDS	GI:40276459
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 805)
AUTHORS	Fu, G.K., Wang J.T., Yang J., Au-Young, J. and Stuve, L.L.
TITLE	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL	Genomics 84 (1), 205-210 (2004)

```

PUBMED
COMMENT
15203218
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
source
Location/Qualifiers
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/clone_lib="PLP"
/note="Vector: pDrive Cloning Vector"
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Alignment Scores:
Pred. No.: 4.76e-91
Score: 1121.50
Percent Similarity: 96.22%
Best Local Similarity: 95.80%
Query Match: 46.67%
DB: 6
Matches: 228
Conservative: 1
Indels: 6
Gaps: 1

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US-10-070-794A-30 (1-464) x CD628193 (1-805)

Qy	1	MetSerPheLeuGluGlnGluAAsnSerSerSerTrpProSerProAlaValThrSerSer	20
Db	103	ATGAGCTTCCTAGAGCAAGAAAAACAGCAGCTCATGGCCATCACCCAGCTGTGACCCAGCAGC	162
Qy	21	SerClnuArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer	40
Db	163	TCAGAAAGAAATCCGTGGGAAACGAGAGGCCAAAGCCTTGAGATGGACAAAGCAGAAAGTCG	222
Qy	41	ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu	60
Db	223	GTGGAGAGAGGGAGCCACAGGTCAGGGGAAGGTCCCGGTCCAGGCCAGCTGCTCGAG	282
Qy	61	SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla	80
Db	283	TCCACCGGGCTGGAGGCCACATTCCCCAAGACACACCCCTGGCTCAAGCTGATCCTGCC	342
Qy	81	GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla	100
Db	343	GGGGTGGGCATCCACCACAGGGGTGGACTGCTCCCTCTGACTGTACAGCCCTCAGCT	402
Qy	101	AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp	120
Db	403	GCAGGCTCCAGCACAGATGATGGAGCTGGCCACGGAGTTCCACAGCCACAGAGGCCTGG	462
Qy	121	GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla	140
Db	463	GAGTGTGAGCTAGNAGGCTCTGGAAAGAGAGGCTGCTGTCCTGTCCCTCCGAGGCC	522
Qy	141	ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet	160
Db	523	CCATTTCCCAAGCTGGGCTGGGATGACGAACTCGGGAAACCCGCGCCCCAGATCTACATG	582
Qy	161	ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSer-LysLeuValIle	180
Db	583	CGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAAGCTAGTTCAT	642
Qy	180	ePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuVal-AlaAsnGlyVala	200
Db	643	CTTCGACACCATGCTGGAGATCAAGAAGGCTCTTTTGCTGTGGTTGGCCAACGGTGTGC	702
Qy	200	rgAlaAlaProLeuTrpAspSerLysLysGln-SerPheValGlyMetLeuThrIleThr	219
Db	703	GGGCAGC-CTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGATGCTGACA---TCA	758
Qy	220	AspPheIleLeu-ValLeuHisArgTyrTyrArgSerProLeuVal	234
Db	759	TGATTATCTCGGGTGTGATCGTTACTACAGGCTCCCGCTGGTC	804

RESULT	8
LOCUS	AK032238
DEFINITION	Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430509K05 product:similar to AMP ACTIVATED PROTEIN KINASE GAMMA 1 (FRAGMENT) [Mus musculus], full insert sequence.
ACCESSION	AK032238
VERSION	AK032238.1 GI:26328068
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning <i>Weth. Enzymol.</i> 303, 19-44 (1999) 10349636
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okasaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL	
PUBLISHED	
REFERENCE	2
AUTHORS	



TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
11042159

3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishire, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
11076861

4  
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2839)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Sano, H., Saito, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers  
1. .2839  
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400. .1731

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ORIGIN

Alignment Scores:  
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Percent Similarity: 67.23% Conservative: 83  
Best Local Similarity: 49.79% Mismatches: 111  
Query Match: 46.32% Indels: 45  
DB: 4 Gaps: 7

US-10-070-794a-30 (1-464) x AK032238 (1-2839)

Qy 13 ProSerProAlaValThrSerSerSerGluArgIleArgGlyLysArgAlaLysAla 32  
Db 321 CCTTCCCGCTGAGACTCACACTGGTTCGATATGTTTCCACCTGTCTACGTGCT 380  
Qy 33 --LeuArgTrpThrArgGlnLysSerValGluGluGlyGluProProGlyGlnGly 51  
Db 381 TCTGTGGCCACAGTACTATGAAGCGCTTTGGAAGTCTCAGGGGACCAAGAACCAA 440  
Qy 52 GlyProArgSerArgProThrAlaGluSerThrGlyLeuGluAlaThrPhe----- 68  
Db 441 GGACCAAAACCGAAGCACCACCGCGCGCCAGTCGACCCCATGCTTTTGGCTCCAG 500  
Qy 69 -----ProLysThrThrProLeuAlaGlnAlaSerPro----- 79  
Db 501 CGTCTCTCTTCTCCGTCACACACCCACCAAGTGACCAAGCAGCACCCATTTCCCTCGGA 560  
Qy 80 -----AlaGlyValGlyThrProThrGlyTrpAspCys----- 91  
Db 561 GTCCTACAGCAGAGGCTGAAACGCCAGAGAGCGCATCTATGCTTCTCGTCCCTCC 620  
Qy 92 -----LeuPro-----SerAspCysThrAlaSerAlaAlaGly-Se 103  
Db 621 AGACACTGGGCGCGCTTCTGCTGGCTTCAGAGCCAGCGGACCTCGCTGGCATC 680  
Qy 103 rSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrpGluCysG 123  
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Db 741 A---GCCGCGCATGCTGGAG----- 756  
Qy 143 oLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTrpMetArgPheMe 163  
Db 757 -AGCTGGAGTTCAGGAGGAAGCAGAGACTCAGAAAGTGGCGTTTATATGCGATTCAT 815  
Qy 163 tGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuValIlePheAspTh 183  
Db 816 GAGGTCAACAAGTGTATGACATGCTTCCAAACAGATTCAAAGCTGTGTGTTCTTCGACAC 875  
Qy 183 rMetLeuGluIleLysLysAlaPhePheAlaLeuAlaLeuGlyValAlaArgAlaAlaPr 203  
Db 876 TAGCTTGCAAGTCAAAAAGCGCTTCTTGGCTTGGTAGCAACCGAGTCCGTCGACGCC 935  
Qy 203 oLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIleLe 223



Db	697	TCGTCCTCCCGACAGGACAGAGGTTCTGCCGCTCTCCCTCCAGAGCCCGAC	756
Qy	98	AlaSerAlaAlaGlySerThr-----AspAspValGluLeuAlaThr	112
Db	757	AGGCCTCCACTGGCATCACCAACACATATGCTCCCTCCAAAGCGCGGCGCGCG	816
Qy	113	GluPheProAlaThrGluAlaTrpGluCysGluLeuGluGlyLeuLeuGluArgPro	132
Db	817	GCCCTGGGACCGCGGAAGCC-----GGCATGCTGGAG-----	849
Qy	133	AlaLeuCysLeuSerProGlnAlaProPheProLysLeuGlyTrpAspAspGluLeuArg	152
Db	850	-----AAGCTGGAGTTCGAGGACGAAGTAGAA	876
Qy	153	LysProGlyAlaGlnIleTyrMetArgPheMetGlnGlnHisThrCysTyrAspAlaMet	172
Db	877	GACTCAGAAAGTGGTGTACATCGGATTCATGAGTTCACACAAAGTGTATGACATCGTT	936
Qy	173	AlaThrSerSerLysLeuValIlePheAspThrMetLeuGluIleLysLysAlaPhePhe	192
Db	937	CCAAACCAAGTTCAAAGCTTGTTGCTTTGATACATACATACAAAGTATAAAAGCCCTCTTT	996
Qy	193	AlaLeuValAlaAsnGlyValArgAlaAlaProLeuTrpAspSerLysLysGlnSerPhe	212
Db	997	GCTTTGGTAGCAACGGGTCCGAGCAGCGCGCTGGGGAGATGAACAAAGATTTT	1056
Qy	213	ValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisArgTyrTyrArgSerPro	232
Db	1057	GTAGGAATGCTAACAAATTACAGATTTTCATAATATCTACATACATACATATAAATCACCT	1116
Qy	233	LeuValGlnIleTyrGluIleGluGlnHisLysIleGluThrTrpArgGluIleTyrLeu	252
Db	1117	ATGTGTACAGATTTATGAATTAGAGCAACATAAAATTGAACATGCGAGGAGCTTTATTTA	1176
Qy	253	GlnGlyCysPheLysProLeuValSerIleSerProAsnAspSerLeuPheGluAlaVal	272
Db	1177	CAAGAAACATTTAAGCCTTTAGTGAATATATCTCCAGATGCAGCCTCTCGATGCTGTA	1236
Qy	273	TyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuAspProValSerGlyAsn	292
Db	1237	TACTCTTGATCAAAATAAAATCCACAGATTCGCCGTTATTGACCCCTATCAGTGGGAAT	1296
Qy	293	ValLeuHisIleLeuThrHisLysArgLeuLysPheLeuHisIlePheGlySerLeu	312
Db	1297	GCGCTTTATATCTTACCACAAAAGATTCCTCAAGTTCCTCCAGCTTTTATGTCTGAT	1356
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Qy	353	ArgArgValSerAlaLeuProValValAsnGluCysGlyGlnValValGlyLeuTyrSer	372
Db	1477	AGACGAATATCAGCTCTGCTGCTGCTGATGAGTCAAGGAAAGTGTGATATTTATTTCC	1536
Qy	373	ArgPheAspValIleHisLeuAlaGlnGlnThrTyrAsnHisLeuAspMetSerVal	392
Db	1537	AAATTTGATGTAATTAATCTTCTGCTGAGAAAACATACATACCTAGATATCAGTG	1596
Qy	393	GlyGluAlaLeuArgGlnArgThrLeuCysLysLeuGluGlyValLeuSerCysGlnProHis	412
Db	1597	ACCCAGGCCCTTCAGCAGCGTTTACAGATATTTTGAAGGTGTTGTGAAGTCAATAAGCTG	1656
Qy	413	GluSerLeuGlyGluValIleAspArgIleAlaArgGluGlnValHisArgLeuValLeu	432
Db	1657	GAATATCTGGAGACCATTTGTGACAGAATAGTAAGAGCTGAGGTCATCGCTGGTGGTG	1716
Qy	433	ValAspGluThrGlnHisLeuLeuGlyValValSerLeuSerAspIleLeuGlnAlaLeu	452

1717 GCCAATGACGACATAGTATTGTGGGTATTATTTCCTGTGCAGACATTCTGCAGCCCTG 1776

453 ValLeuSerProAlaGly 458

1777 ATCTTCACACGACGAGT 1794

RESULT 10

BC079017

LOCUS

DEFINITION

BC079017

VERSION

KEYWORDS

SOURCE

ORGANISM

BC079017.1 GI:50927344

HTC.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Rattus.

1 (bases 1 to 2058)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uesdin, T.B., Toshiyuki, S., Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2058)

Director MGC Project.

Direct Submission

Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Howard Jacobs

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

cDNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAP Plate: 182 Row: m Column: 20

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein

This clone has the following problem: frame shifted.

Location/Qualifiers

1. .2058

/organism="Rattus norvegicus"

/mol\_type="mRNA"

FEATURES

source

```

/db_xref="taxon:10116"
/clone_image="7113709"
/tissue_type="Testis, rat (Brown Norway)"
/clone_lib="NIH MGC_237"
/lab_host="DH10B"
/notes="vector: pExpress1"

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## ORIGIN

## Alignment Scores:

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Pred. No.: 6,05e-88 Length: 2058
Score: 1094.00 Matches: 234
Percent Similarity: 65.00% Conservative: 91
Best Local Similarity: 46.80% Mismatches: 115
Query Match: 45.53% Indels: 60
DB: 4 Gaps: 10

```

US-10-070-794A-30 (1-464) x BC079017 (1-2058)

```

QY 4 LeuGluGlnAenSerSerTrpProSerProAlaValThrSerSerSerGluArg 23
DB 280 CTTCCAGAGGACTCTTCTCCAGGGGCCCCCGCCCGCCCTCCAGCCCTGTGTCTC 339
QY 24 IleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSerValGluGlu 43
DB 340 CTGTGAGGCCCAAGATGAGCCCTGCTCCCAAACTGTGTCCCGTCTCTTACCAGAA 399
QY 44 GlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAla-----Glu 60
DB 400 TCCCTCCA-----CGCTCTCCAGCCGGATGAGTTTCAGTGGGATCTTCCGC 447
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaA 80
DB 448 TCCTCATCCAAAGAGTCTTCG---CCCAACTCCAAACCG-----TCTACCTCTCCCGGG 498
QY 81 GlyValGlyThrProProThrGlyTipAspCysLeuProSerAspCysThrAlaSerAla 100
DB 499 GGCATCAGGTTCT-----TTCTCGCGGTCCAGAAAACCTCCAGCGTC 540
QY 101 AlaGlySerThrAspAspValGluLeuAlaThrGluPhePro---AlaThrGluAla 119
DB 541 TCCTCTCTCCATCAACACCCACCAGTACCAAGCAGCAGCCATTTCCCTTGAGTCC 600
QY 120 TrpGlyCysGluLeuGlyLeuLeuGluGluArg-----Glu 131
DB 601 TACAAGCAGGAGCGCTGAA---CGCTAGAAAGCGCGCATCTATGCTCTCTCCTCCACCG 657
QY 132 -----ProAlaLeuCysLeuSerProGlnAlaPro----- 141
DB 658 GACACCGCCAGCGCTCTGCTGGCTTCAGAGCCCGGTCCGGCTTCCTCTGGCATCT 717
QY 141 ----- 141
DB 718 CCCACACCATGCTCTCTTTGAGAACCGCGCGCTGGCGGCGCCCGGACCGCGAA 777
QY 142 -----PheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIle 158
DB 778 GCGCGCATGCTGGAGAGCTGGAGTTCAGGAGGAA---GAAAGACTCAGAGAGTGGCGTT 834
QY 159 TyrMetArgPheMetGlnGluHisThrCysTyAspAlaMetAlaThrSerSerLysLeu 178
DB 835 TATATGCGATTCAGAGGTACACAGTGTATGACATCTGTTCACACCGCTCAAGCTT 894
QY 179 ValIlePheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGly 198
DB 895 GTTGTCTTCGACACTAGCTTGCAGTTAAAGAGCTTCTTTGCTTTGGTAGCCACCGA 954
QY 199 ValArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIle 218
DB 955 GTCCGTGCGCGCGCTGTGGGAAAGTAAAGAGCAGAGCTTCGTAGGAATGCTCAAAAT 1014
QY 219 ThrAspPheIleLeuValLeuHisArgTyTrpArgSerProLeuValGlnIleTyTrpGlu 238
DB 1015 ACAGATTTCATAACATACATACAGATACTATAAATATCCCTCCATGGTACAGATTATGAA 1074

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QY 239 ILeGluGlnHisLysIleGluThrTrpArgGluIleTyTrpLeuGlnGlyCysPheLysPro 258
DB 1075 TTGGAGGAACATAAGATTGAACCTGGAGGAACTGTACTTACAAGAAACCTTCAAGCCT 1134
QY 259 LeuValSerIleSerProAsnAspSerLeuPheGluAlaValTyThrLeuIleLysAsn 278
DB 1135 TTGGTGAATATCTCTCCAGATGCGAGCCTCTTCGATGCTGTATATCTCGTTGATCAAAAT 1194
QY 279 ArgIleHisArgLeuProValLeuAspProValSerGlyAenValLeuHisIleLeuThr 298
DB 1195 AAATCCACAGATTGCGAGTTATTGACCTATCATGTTGGGATGACCTTTATATATCTTACC 1254
QY 299 HisLysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPhe 318
DB 1255 CACAAAGAAATCTCAAGTTCTCCAGCTTTTATGTTCTGACATGCCAAAGCCCGCTTC 1314
QY 319 LeuTyArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeu 338
DB 1315 ATGAAGCAGAACCTGGATGAGCTCGGAATAGGAACATATCACATATTGCTTCATTCCAC 1374
QY 339 GluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeu 358
DB 1375 CCGAATACCCCATCATCAAAAGCTTGAACATCTTTGTGGAGAGCGGATATCTCGCGTG 1434
QY 359 ProValValAenGluCysGlyGlnValValGlyLeuTyTrpSerArgPheAspValIleHis 378
DB 1435 CCTGTGTGTGATGAGTCAGGAAAGTTGTAGATATTACTTCCAAGTTTGTATTAAT 1494
QY 379 LeuAlaAlaGlnGlnThrTyAsnHisLeuAspMetSerValGlyGluAlaLeuArgGln 398
DB 1495 CTTGTCTGAGAAAACGTACAATAACCTAGACATCAGCGTGACCGCCCTCGACGAC 1554
QY 399 ArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluVal 418
DB 1555 CGTCACAGTATTGAGGTGTGTCAGTCAAGTCAAGCTGGAAACACTGGAGACCAATT 1614
QY 419 IleAspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHis 438
DB 1615 GTGGACAGATAGTAGAGCGGAGTCCATCGGTGGTGGTAGTGAAGCAGATAGT 1674
QY 439 LeuLeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 458
DB 1675 ATTGTGGTATTATCTCTCTGTGACATCTCTCAAGCCCTGTCTCTCACACGACGAGT 1734

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RESULT 11  
CX313244  
LOCUS  
DEFINITION  
IMAGE:7586968 5', mRNA sequence.  
ACCESSION  
CX313244  
VERSION  
CX313244.1 GI:57041698  
KEYWORDS  
EST.  
SOURCE  
Xenopus tropicalis (western clawed frog)  
ORGANISM  
Xenopus tropicalis  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
Xenopodinae; Xenopus; Silurana.  
1 (bases 1 to 824)  
Richardson, P., Lucas, S., Rokhsar, D., Dettter, J.C., Ng, D.C.,  
Brokstein, P. and Lindquist, E.A.  
DOE Joint Genome Institute  
Unpublished (2004)  
Other ESTs: JGI XZT9073.rev  
Contact: Lindquist, E.A., Richardson, P.  
DOE Joint Genome Institute  
2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
Tel: 925 296 5600  
Fax: 925 296 5710  
Email: cdna@jgi-psf.org  
Tissue Procurement: Richard M. Harland Laboratory, University of  
California, Berkeley: <http://tropicalis.berkeley.edu/home>  
cDNA Library Preparation: Richard M. Harland Laboratory, University

of California, Berkeley  
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>  
 Clone Distribution: I.M.A.G.E. Consortium/LLNL:  
<http://image.llnl.gov>  
 Naming Conventions: EST name is generated by the concatenation of  
 the JGI Clone id and the direction of sequencing. The suffix '.fwd'  
 indicates a forward sequencing read of the insert. It does not  
 necessarily reflect the orientation of the insert.  
 Plate: X2T 0093 row: a column: 14  
 High quality sequence stop: 775.

## FEATURES

Location/Qualifiers  
 1..824  
 /organism="Xenopus tropicalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8364"  
 /clone="IMAGE:7586968"  
 /tissue\_type="whole embryo"  
 /dev\_stage="tadpole (st. 36-41)"  
 /lab\_host="E. coli XL1-Blue derivative, Stratagene  
 Electroten-Blue"  
 /clone\_lib="NIH\_XGC tropTad5"  
 /note="vector: pCS108; Site 1: SalI; Site 2: NotI; Tadpole  
 library constructed by Russell B. Fletcher in R. Harland's  
 lab using poly A RNA and oligo dt primers (Invitrogen  
 SuperScript Plasmid System for cDNA Synthesis and  
 Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted  
 into vector pCS108  
 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html).  
 ."

## ORIGIN

## Alignment Scores:

Pred. No.: 5.83e-84 Length: 824  
 Score: 1043.50 Matches: 202  
 Percent Similarity: 84.29% Conservative: 34  
 Best Local Similarity: 72.14% Mismatches: 37  
 Query Match: 43.42% Indels: 7  
 DB: 8 Gaps: 1

US-10-070-794A-30 (1-464) x CX313244 (1-824)

```

Qy 143 ProlysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMetArgPhe 162
Db 2 CCAGATCTGGGGAGAT-----GCCGGCTTATCATGGAGTTC 40

Qy 163 MetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePheasp 182
Db 41 ATGATGAAGAACTGCTGTACAGCGCCATTCTTACCAGCTGCAAGTTGGTGGTTTGAC 100

Qy 183 ThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyValArgAlaLa 202
Db 101 ACCACCTGCGAGATAAAGAGCGTTCTGGCACTGGTGGCAATGGAGTACGGGCAGCC 160

Qy 203 ProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheile 222
Db 161 CCTCTATGGGACAGACAGCAGCTTTGTGGGAATGCTCACCATTCCAGCTTTCATC 220

Qy 223 LeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGlnHis 242
Db 221 AACATCTGCGACCGATACACAGCGCCCTGGTTCAGATATACGAAGTGGAGGAGCAT 280

Qy 243 LysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIle 262
Db 281 AAAATAGAGACATGAGAGAGTTTACCTGCAAAAGTTCTTTCAAGCCATTATATATC 340

Qy 263 SerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArg 282
Db 341 TCCCCAGCAGACAGCGCTTTCCACCGCTGTATATTCATTCATCAAGATAAGATCCACCG 400

Qy 283 LeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArgLeu 302
Db 401 CTGCAGGTAATGATCCCATATCCGGAAACATCTCTGCATATCTTACGCACAAACGTCTC 460

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Qy 303 LeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArgThr 322
Db 461 CTCAAAGTTCTCCACCTGTTGGAGACACTCTCCCAAGGCCACGGTCTTTCGAGAAGACC 520

Qy 323 IleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAlaPro 342
Db 521 ATCTGGAGTTGGGATCGGCACCTTTAGGATGTGGCAGTCTGTGAGGAGACTCTCTCTCT 580

Qy 343 IleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProValValAsn 362
Db 581 GTCTACAACGCACACTGTAATCTTTGTAGAGAGAGAGATTCTGCCCTCCCGGTGGTGAAT 640

Qy 363 GluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAlaAlaGln 382
Db 641 GAATCTGGCGCGGTGGTGGAGCTCTATTCCTGGTTTGATGATATACACCTTGGGCACAG 700

Qy 383 GlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeuCys 402
Db 701 AAGATCTATAACAACCTGGATATCAGCGTACGAGATGCCCTGGCTTCTCTGAGT 760

Qy 403 LeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArgIle 422
Db 761 ATTGAGGGGTCTCTCATGTGTACCCCATGAAAGTCTGGAGGTGGTCAATTGATCGAATT 820

```

## RESULT 12

BX403964 1136 bp mRNA linear EST 01-MAY-2004  
 LOCUS BX403964 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone  
 DEFINITION CL0BB007ZF11 5-PRIME, mRNA sequence.  
 ACCESSION BX403964  
 VERSION BX403964.2 GI:46925338  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1136)  
 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On May 13, 2003 this sequence version replaced gi:30635099.  
 COMMENT  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: [secre@genoscope.cns.fr](mailto:secre@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was not normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.  
 This sequence belongs to sequence cluster 6712.f  
 For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?s=CL0BB007ZF11RP1&c=6712.f>.

## FEATURES

## source

1..1136  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CL0BB007ZF11"  
 /tissue\_type="NEUROBLASTOMA"  
 /clone\_lib="Homo sapiens NEUROBLASTOMA"  
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
 with a NotI-oligo(dT) primer. Five prime end enriched,  
 double-strand cDNA was digested with Not I and cloned into  
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
 Library was not normalized."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.39e-81 Length: 1136  
 Score: 1017.00 Matches: 193  
 Percent Similarity: 82.55% Conservative: 53

EST. Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 1144)  
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.  
Unpublished (2001)  
On May 13, 2003 this sequence version replaced gi.30638442.  
Contact: Genoscope  
Genoscope - Centre National de Sequençage  
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with NotI and cloned  
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 6712.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?cs=CS0DH005DGI1Q1&c=6712.f.  
Location/Qualifiers  
1..1144  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DH005YN22"  
/tissue\_type="T CELLS (JURKAT CELL LINE)"  
/cell\_lines="JURKAT CELL LINE"  
/clone\_libs="Homo sapiens T CELLS (JURKAT CELL LINE)"  
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with NotI and cloned into  
the NotI and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

Alignment Scores:  
Pred. No.: 2,41e-81 Length: 1144  
Score: 1017.00 Matches: 193  
Percent Similarity: 82.55% Conservative: 53  
Best Local Similarity: 64.77% Mismatches: 52  
Query Match: 42.32% Indels: 0  
DB: 5 Gaps: 0

US-10-070-794A-30 (1-464) x BX421925 (1-1144)

QY 158 IletyMetArgPheMetGlnGluHisThrCystyrAspAlaMetAlaThrSerSerLys 177  
Db 73 GTGTATATCTCTTCATGAGTCTCATCGCTGCTATGACCTGCCAAGCTCCAAA 132  
QY 178 LeuValIlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAen 197  
Db 133 TTGGTTGTATTGATACGCTCCCTGCAGGTGAAGAAAGCTTTTTTGTGGCTGACTAAC 192  
QY 198 GlyValArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThr 217  
Db 193 GGTGTACGAGTGGCCCTTTATGGGATAGTAAAGCAAGCTTTTGTGGCATCTGTCACC 252  
QY 218 IletyMetArgPheLeuValLeuHisArgTyrTrpArgSerProLeuValGlnIleTyr 237  
Db 253 ATCACTGATTTCATCAATATCTCCAGCGCTACTATTAATCAGGCTTGGTACAGATCTAT 312  
QY 238 GluIleGluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLys 257  
Db 313 GAGCTAGAACACACAGATAGAACTTGGAGAGAGGTGATCTCCAGGACTCTTTAAA 372  
QY 258 ProLeuValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLys 277  
Db 373 CCGCTTGTCTGCATTTCTCTATATGCGAGCTTGTGTGCTCTCTTCATTAATTCGG 432  
QY 278 AsnArgIleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeu 297  
Db 433 AACAGATCCACAGGCTGCCAGTTATTGACCCAGAAATCAGGCAATCTTTGTACATCTTC 492  
QY 298 ThrHisLysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSer 317  
Db 493 ACCCACAGCGCATCTGAAGTTCTCAATGTTTTCATCAGTGTCCCAAGCAGAG 552  
QY 318 PheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaVal 337  
Db 553 TTATGTCGAAGTCTCTGGAGAGCTACAGTTGGCACTATGCCAATATGCTATGGTT 612  
QY 338 LeuGluThrAlaProLeuLeuThrAlaLeuAspIlePheValAspArgValSerAla 357  
Db 613 CGCACTACCAACCCCGTCTATGTGGCTCTGGGATTTTGTACAGCATCAGTCTCAGCC 672  
QY 358 LeuProValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle 377  
Db 673 CTGCCAGTGTGTGATGAGAGGGCGGTGTGGTGCATCTACTCCAAGTTGATGTATTC 732  
QY 378 HisLeuAlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArg 397  
Db 733 AATCTGGCAGCAGAAAGACCTCAACAACCTAGATGTATCTGTGACTAAGCCTTGCAA 792  
QY 398 GlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGlu 417  
Db 793 CATCGATCACAATTTTGAGGGTGTCTCAAGTGCTACCTGCATCAGACTCTGGAGACC 852  
QY 418 ValIleAspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGln 437  
Db 853 ATCATCAACAGGCTAGTGGAGCAGCAGGTTTCCAGCTTTGTAGTGTGGATGAAATGAT 912  
QY 438 HisLeuLeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455  
Db 913 GTGGTCAAGGAATTTGATCACTGTCTGACATCTCTGCAGGCCCTGTGTCTCACA 966

RESULT 13  
BX421925 1144 bp mRNA linear EST 01-MAY-2004  
LOCUS  
DEFINITION  
BX421925 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA  
clone CS0DH005YN22 5-PRIME, mRNA sequence.  
ACCESSION  
BX421925  
VERSION  
BX421925.2 GI:46925182

```

Qy 278 AsnArgIleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeu 297
Db 433 AACAAAGATCCACAGGCTGCAGATTATTGACCAAGATCCAGCAATACTTTGTACATCCTC 492

Qy 298 ThrHisIysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSer 317
Db 493 ACCACCAAGGCATCTCGAAGTTCCTCAATTTGTTATCACTGAGTTCCTCCCAAGCCAGAG 552

Qy 318 PheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValVal 337
Db 553 TTCATGTCCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGTGTATGTT 612

Qy 338 LeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAla 357
Db 613 CGCACTACCAACCCCGCTATGTGGCTCTGGGGATTTTGTACAGCATCGAGTCTCAGCC 672

Qy 358 LeuProValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle 377
Db 673 CTGCCAGTGGTGGATGAGAGGGCGGTGGTGACATCTACTCCAAGTTTGATGTTATC 732

Qy 378 HisLeuAlaLaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArg 397
Db 733 AATCTGGCAGCAGAAAGACCTACAAACCTAGATGTATCTGTGACTATAAGCCTTGCAA 792

Qy 398 GlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGlu 417
Db 793 CATCGATCACATTACTTTGAGGGTGTCTCAAGTGTCTACCTGCAATGAGACTCTGGAGACC 852

Qy 418 ValIleAspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGln 437
Db 853 ATCATCAACAGCTAGTGGAGACGAGGTTCCCGACTTGTAGTGGTGGATGAAATGAT 912

Qy 438 HisLeuLeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455
Db 913 GTGGTCAAGGGAATTGTATCATCTGTGACATCTCTGACGAGCCCTGGTGTCTCACA 966

RESULT 14
CR604823 1561 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DK007YB02 of HeLa cells Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR604823.1 GI:50485630
VERSION HTC; cNSLT_cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1. (bases 1 to 1561)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2. (bases 1 to 1561)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
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FEATURES
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US-10-070-794A-30 (1-464) x CR604823 (1-1561)

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              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominoidea; Homo.
REFERENCE    1 (bases 1 to 1577)
AUTHORS      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished
REMARK       Contact: Feng Liang Email: fliang@lifetech.com URL:
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Faraday Avenue
              2 (bases 1 to 1577)
              Genoscope.
REFERENCE    Direct Submission
TITLE        Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL      BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr
              - Web : www.genoscope.cns.fr)
COMMENT      1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life Technologies, a
              division of Invitrogen.
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Alignment Scores:
Pred. No.:      3.9e-81      Length:      1577
Score:          1017.00      Matches:    193
Percent Similarity: 82.55%      Conservative: 53
Best Local Similarity: 64.77%      Mismatches: 52
Query Match:     42.32%      Indels:     0
DB:              4          Gaps:         0

US-10-070-794A-30 (1-464) x CR608916 (1-1577)
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

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Run on: January 25, 2006, 21:59:11 ; Search time 238.939 Seconds  
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ALIGNMENTS

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; Sequence 3, Application US/09950022A  
; Patent No. 6919177

; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950,022A  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1

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; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1392)  
; OTHER INFORMATION:  
US-09-950-022A-3

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## RESULT 2

US-09-950-022A-1  
; Sequence 1, Application US/09950022A  
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; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: No. 6919177e1 PRKAG3 Alleles and Use fo the Same as Genetic Mark  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P0468U83  
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; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260, 239  
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; PRIOR APPLICATION NUMBER: 60/299, 111  
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; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
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; LENGTH: 1873  
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; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1392)  
; OTHER INFORMATION:  
US-09-950-022A-1

Alignment Scores:  
Pred. No.: 1.12e-191 Length: 1873  
Score: 2011.00 Matches: 400  
Percent Similarity: 90.11% Conservative: 19  
Best Local Similarity: 86.02% Mismatches: 44  
Query Match: 83.69% Indels: 2  
DB: 3 Gaps: 2

US-10-070-794A-30 (1-464) x US-09-950-022A-1 (1-1873)	
Qy	1 MetSerPheLeuGluGlnGluAAsnSerSerSerTrrProSerProAlaValThrSerSer 20
Db	1 ATGAGCTCTCTAGAGCAGGAGAGCGGTCATGGCCATCCCGAGCTGTAAACACGAGC 60
Qy	21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrrPthrArgGlnLysSer 40
Db	61 TCAGAAAGAGCCATGGGACCAAGGGGAAACAAGGCTCTAGATGACAAAGCAGGAGGAT 120
Qy	41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db	121 GTAGAGAAAGGGGGCTCTCGGGCCCGAGGAAGTCCCGAGTCCAGGCCAGGTGTGCTGAG 180
Qy	61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro 79
Db	181 TCCACCGGGCAGGAGGCCACATCCCAAGGCCACACCTTGGCCCAAGCGCTCCCTTG 240
Qy	80 AlaGlyValGlyThrProProThrGlyTrrAspCysLeuProSerAspCysThrAlaSer 99
Db	241 GCCGAGGTGACAAACCCCAACAGAGCGGACATCTCCCTCTGACTGTGACGCTCA 300
Qy	100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db	301 GCCTCCGACTCCAAACACAGACCACTCGGATCTGGGCATAGAGTCTCAGGCTCGGGCGG 360
Qy	120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db	361 TCGGGGGATGAGCTT---GGGTGGTGGAGAGAGAGCAGCCCGTGGCCATCCCGAG 417
Qy	140 AlaProPheProLysLeuGlyTrrAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db	418 GTGCTGTATCCAGCTGGGCTGGGATGATGAGCTGCAGAAAGCGGGGGCCAGGTCTAC 477
Qy	160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db	478 ATGCACCTTCATGACGAGGACACCTCTGATGCCATGCGACCACTCCAAACTGGTC 537
Qy	180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db	538 ATCTTCAGACCATGCTGGAGATCAAGAGCCCTCTTTCCTCTGGTGGCCACGGGCTC 597
Qy	200 ArgAlaAlaProLeuTrrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db	598 CGAGCGGCACCTTGTGGGACAGCAAGCAGAGCTTCGTGGGATGCTGACCATCACA 657
Qy	220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db	658 GACTTCATCTTGGTGTGCACCGCTATTACAGGTCCCGCTTGGTCCAGATCTACGAGATT 717
Qy	240 GluGlnHisLysIleGluThrTrrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db	718 GAAGAATAGATTGAGACTGGAGGAGATCTACCTTCAGGCTGCTTCAAGCCTCTG 777
Qy	260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db	778 GTCTCCATCTCTCCATGACAGCTGTTCGAGCTGTCTAGGCTCTCATCAAGACCGG 837
Qy	280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db	838 ATCCACCGCTCGCGGTCTGGACCCCTGTCTCGGGGCTGTGTCTCCACATCTCCACACAT 897
Qy	300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db	898 AGCGGGTCTTCAAGTCTCTGACATCTTTGGACCCCTGTGCTGCCCGGCTCTCTCTC 957
Qy	320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
Db	958 TACCGCACCATCCAAAGATTTGGGCATCGGCACATTCGAGACTTGGCGGTGGTGGAA 1017
Qy	340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359

Db	1018 ACGGCGCCCATCTCTGACCGCAGCTGGACATCTTCGTGGACCGGGGTGTGTCTGCGCTGCCT 1077
Qy	360 ValValAsnGluCysGlyGlnValValGlnValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db	1078 GTGGTCAACGAACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGTATCCACCTG 1137
Qy	380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db	1138 GCTGCCCAACAACATACACACCTGGACATGAATGTGGGAGAAGCCCTGAGGACGCG 1197
Qy	400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 419
Db	1198 AACTGTGTCTGAAGCGTCTTCTTCGACGCCCCAGAGACCTTGGGGGAAGTCATT 1257
Qy	420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db	1258 GACCGGATTTGTCGGGAACAGGTGCACCGCTGTGTCTCGTGGATGAGACCCAGCACCTT 1317
Qy	440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db	1318 CTGGGCGTGTGTCTCTCTGACATCTTTCAGGCTCTGTGTGTCTGAGCCCTGCTGGAATT 1377
Qy	460 AspAlaLeuGlyAla 464
Db	1378 GATGCCCCCTCGGGGCC 1392
RESULT 3	
US-09-950-022A-7	
; Sequence 7, Application US/09950022A	
; Patent No. 6919177	
; GENERAL INFORMATION:	
; APPLICANT: Rothschild, Max	
; APPLICANT: Ciobanu, Dan	
; APPLICANT: Malek, Massoud	
; APPLICANT: Plastow, Graham	
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark	
; TITLE OF INVENTION: Reproductive	
; TITLE OF INVENTION: and Meat Quality Traits	
; FILE REFERENCE: P04668US3	
; CURRENT APPLICATION NUMBER: US/09/950, 022A	
; PRIOR FILING DATE: 2001-09-10	
; PRIOR APPLICATION NUMBER: 60/231045	
; PRIOR FILING DATE: 2000-09-08	
; PRIOR APPLICATION NUMBER: 60/260,239	
; PRIOR FILING DATE: 2001-01-08	
; PRIOR APPLICATION NUMBER: 60/299,111	
; PRIOR FILING DATE: 2001-06-18	
; NUMBER OF SEQ ID NOS: 21	
; SOFTWARE: PatentIn version 3.1	
; SEQ ID NO 7	
; LENGTH: 1873	
; TYPE: DNA	
; ORGANISM: Sus scrofa	
; FEATURE:	
; NAME/KEY: CDS	
; LOCATION: (1)..(1392)	
; OTHER INFORMATION:	
US-09-950-022A-7	
Alignment Scores:	
Pred. No.:	1,41e-191
Score:	2010.00
Percent Similarity:	90.11%
Best Local Similarity:	85.81%
Query Match:	83.65%
DB:	3
US-10-070-794A-30 (1-464) x US-09-950-022A-7 (1-1873)	
Qy	1 MetSerPheLeuGluGlnGluAAsnSerSerSerTrrProSerProAlaValThrSerSer 20
Db	1 ATGAGCTCTCTAGAGCAGGAGAGCGGTCATGGCCATCCCGAGCTGTAAACACGAGC 60

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QY 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 61 TCAGAAAGAACCCATGGGACCCAGGGAAACAAGGCCTCTAGATGGACAAGCCAGGAGAT 120
QY 41 ValGluGluGlyGluProGlyGlnGlyProGlyArgSerArgProThrAlaGlu 60
Db 121 GTAGAGGAAGGGGGCTTCGGGGCCGAGGGAAGGTCCCGAGTCCAGGCCAGTGTCTGAG 180
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACCGGGAGGAGGCCACATTCCTCCCAAGSCCACACCTTGGCCCAAGCGCTCCCTTG 240
QY 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCGAGGTGGACAACCCCAACAGAGCGGGACATCCTCCCTCTGACTGTGCGAGCCTCA 300
QY 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCCAAACAGACATCTGGATCTGGGCATAGAGTTCTCAGCCTCGCGCGCG 360
QY 120 TrpGluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGGATGAGCTT---GGGCTGGTGAAGAGAGCCAGCCCGCTGCCCCATCCCCAGAG 417
QY 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTATTACCGAGCTGGGCTGGGATGATGATGCGAGAGCGGGGGCCAGGCTCTAC 477
QY 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCATCTATCGAGGAGCACACCTGTACATGCGCATGCGGACAGCTCCAACTGGTC 537
QY 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGGCCCTGGTGGCCCAACGGCATC 597
QY 200 ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGAAGCAGAGCTTCTGTTGGGATGCTCACCATCACA 657
QY 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCATCTTGGTGTGCTGACCGCTATTACAGTCCCGCTGGTCCAGATCTACGAGATT 717
QY 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGAACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777
QY 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCCAATGACAGCCTGTTTGAAGCTGTCTAGCCCTCATCAAGAACCGG 837
QY 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCTGCTCGGCTCTGGACCTGTCTCCGGGGCTGTGCTCCACATCTCACACAT 897
QY 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTTCTCAAGTTCCTGCACATCTTTGGCACCTGTCTGGCACCTGTCTCCCTCTC 957
QY 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
Db 958 TACCCACCATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCCGTGGTGTCTGGAA 1017
QY 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359
Db 1018 ACGGGGCCCATCTCTACCGCATCGACATCTTCGTGGACCGCGTGTCTCGCGTGCCT 1077
QY 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 1078 GTGGTCAACAACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGTGATCCACCTG 1137
QY 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
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Db 1138 GCTGCCCAACAACATACACCACTGGCATGATGTGGAGAGCCCTTGAGCGCGG 1197
QY 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 419
Db 1198 AACTGTGTCTGGAAGCGTCTTTCTCTGCAGCCCCCAGAGACCTTGGGGGAAGTCATT 1257
QY 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATTCCTCCGGGAACAGGTGCAACCGCTGTCTGTGGATGAGACCCAGACCTT 1317
QY 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGCGTGTGTCTCTCTGATCATCTTCAGGCTCTGGTCTCAGCCCTGCTGGTAATT 1377
QY 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 4
US-09-950-022A-9
; Sequence 9, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668U83
; CURRENT APPLICATION NUMBER: US/09/950,022A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-09-950-022A-9

Alignment Scores:
Pred. No.: 2,82e-191 Length: 1873
Score: 2007.00 Matches: 399
Percent Similarity: 90.11% Conservative: 20
Best Local Similarity: 85.81% Mismatches: 44
Query Match: 83.52% Indels: 2
DB: 3 Gaps: 2

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Db 1 ATGACTTCTCTAGAGCAAGAGAGCGTTCATGCGCCATCCCGAGCTGTATACCAACACAGC 60
QY 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 61 TCAGAAAGAACCCATGGGACCCAGGGAAACAAGGCCTCTAGATGGACAAGCCAGGAGAT 120
QY 41 ValGluGluGlyGluProGlyGlnGlyProGlyArgSerArgProThrAlaGlu 60
Db 121 GTAGAGGAAGGGGGCTTCGGGGCCGAGGGAAGGTCCCGAGTCCAGGCCAGTGTCTGAG 180
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Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79  
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Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99  
Db 241 GCCAGGTGGACAAACCCCAACAGAGCGGACATCCTCCCTCTGACTGTGACGCTCA 300  
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119  
Db 301 GCCTCCGACTCCAAACACAGACCATCTGATCTGGGCATAGAGTTCTCAGCCCTCGCGGCG 360  
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139  
Db 361 TCGGGGATGAGCTT---GGGCTGGTGAAGAGACCCAGCCCGCTGCCATCCACAG 417  
Qy 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159  
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Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179  
Db 478 ATGCACCTTCATGCAGGAGCACCTCTGCTACGATGCCATGGCGACAGCTCCAACTGGTC 537  
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199  
Db 538 ATCTTCGACCATGCTGGAGATCAAGAGCCCTCTTGGCCCTGGTGGCCACGGGGTC 597  
Qy 200 ArgAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219  
Db 598 CAAGCGGCACCTTGTGGGACAGCAAGACAGAGCTTCGTGGGATGCTGACCATCA 657  
Qy 220 AspPheIleLeuValLeuHisAsqTyrTyrArgSerProLeuValGlnIleTyrGluIle 239  
Db 658 GACTTCATCTTGGTGGTGCACCGCTATTACAGGTCCCGCTGGTCCAGATCTAGAGATT 717  
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259  
Db 718 GAAGACATAAGATTGAGACTGGAGGGAGATCTACCTTCAGGCTGCTTCAGGCTCTG 777  
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279  
Db 778 GTCTCCATCTCTCCATGATGAGCTGTTCGAGCTGTCTACGCGCTTCATCAAGACCG 837  
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299  
Db 838 ATCCACCGCTGCGGCTGACCCCTGTCTCGGGGCTGTGCTCCACATCTCCACAT 897  
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319  
Db 898 AAGCGGCTTCTCAAGTCTCTGCACATCTTTGGCACCTGTCTGCCCGGCTCTCTTCTC 957  
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Db 958 TACCGACCATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCGGTGGTCTGAA 1017  
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Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399  
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Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439  
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Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459  
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Qy 460 AspAlaLeuGlyAla 464  
Db 1378 GATGCCCTCGGGCC 1392  
RESULT 5  
US-09-950-022A-5  
; Sequence 5, Application US/09950022A  
; Patent No. 6919177  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950,022A  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 1873  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1392)  
; OTHER INFORMATION:  
US-09-950-022A-5  
Alignment Scores:  
Pred. No.: 4.48e-191 Length: 1873  
Score: 2095.00 Matches: 399  
Percent Similarity: 89.89% Conservative: 19  
Best Local Similarity: 85.81% Mismatches: 45  
Query Match: 83.44% Indels: 2  
DB: 3 Gaps: 2  
US-10-070-794A-30 (1-464) x US-09-950-022A-5 (1-1873)  
Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
Db 1 ATGAGCTTCTTAGACGACGAGAGAGCCGTTCTATGGCCATCCCGAGCTGTACCCAGC 60  
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
Db 61 TCAGAAAGAAGCCATGGGACACAGGGGAAACAGGCTCTAGATGGACAGGAGGAT 120  
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
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Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79  
Db 181 TCCACCGGACGAGGAGCCACATTTCCCAAGGCCACACCTTGGCCCAAGCCGCTCCCTTG 240  
Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99



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Db 241 GCCAGGTGGACACACCCCAACAGAGCGGGACATCTCCCTCTGACTGTGACGCTCA 300
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Db 301 GCCTCCGACTCCAAACACAGACCATCTGGATCTGGCATAGAGTTCTCAGCGCTCGCGCGC 360
Qy 120 TrpGluCysGluLeuGluGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGATGAGCTT---GGGCTGTGGAGAGAGCAGCCCGCTGCCATCCCCAGAG 417
Qy 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTATCCAGCGCTGGGTGGATGATGAGCTGCAGAGCCGGGGCCAGGTTCTAC 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCACCTTCATCAGGAGCACACCTGTCTACGATGCCATGGCGACAGCTCCAAACTGGTC 537
Qy 180 IlePheAspThrMetLeuGluIleLysAlaPheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCCCTTCCTTGGCCCTGGTGCCCAACGGCGTC 597
Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGGGGACCTTGTGGACAGCAGCAGAGAGCTTCGTGGGATGCTGACCATCACA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCATCTGTGTGTGTCACCGCTATTACAGGTCCCGCTGGTCCAGATCTACGAGATT 717
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAAGACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCCTCTG 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCNATGACAGCTGTTCCAGAGTGTCTAGCCCTCATCAAGACCGG 837
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCTTGGCGGCTCTGACACCTGTCTCCGGGGCTGTGCTCCACATCTCCACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTTCTCAAGTCTCTGCACATCTTGGCACCTTGTGCACCTGCTGCCCGCCCTCTCTCTC 957
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
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Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
Db 1018 ACGGCGCCCATCTGACCGCATGCGACATCTTCGTGGAGCCGCGGTGTCTGCGCTGCGCT 1077
Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 1078 GTGGTCAACAGAACTGGACAGGTAGTGGCCCTCTACTCTCGCTTTTGATGTATCCACCTG 1137
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCAACAAACATACACCACTGGACATGATGTGGAGAGCCCTGAGGCAGCGG 1197
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 419
Db 1198 ACACCTGTGTCTGGAAGGGGTCTTTCTCTGCCACGCCACGAGACCTTGGGGGAGTCAAT 1257
Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATTTGTCGGGAACAGGTGCACCCGCTGGTGTCTGTGGATGAGACCCAGCACCTT 1317
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGGCGTGGTCTCTCTGACATCTCTCAGGCTCTGGTCTCAGGCCCTGCTGGAATT 1377
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Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392
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## RESULT 6

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US-09-949-016-2390
; Sequence 2390, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2390
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2390
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Alignment Scores:
Pred. No.: 3 53e-99 Length: 1506
Score: 1088.50 Matches: 227
Percent Similarity: 68.15% Conservative: 79
Best Local Similarity: 50.56% Mismatches: 80
Query Match: 45.30% Indels: 63
DB: Gaps: 10
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US-10-070-794A-30 (1-464) x US-09-949-016-2390 (1-1506)

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Qy 11 SerTrpProSerProAlaValThrSerSerSerGluArgIleArgGlyLysArgArgAla 30
Db 54 ACGTTCCTCCCTGGAACTCTATAAGCAGCAGCCTGAACGGTTAGAGAAATCGCATCTATGCC 113
Qy 31 LysAlaLeuArgTrpThrArgGlnLysSerValGluGluGlyGluProProGlyGlnGly 50
Db 114 TCGTCT-----TCCCCCGGACACAGGG 137
Qy 51 GluGlyProArgSerArgProThrAlaGluSerThrGlyLeuGluAlaThrPheProLys 70
Db 138 CAG-----AGGTTCTGCCGTCTTCTTCCAGAGC-----CCGACC 173
Qy 71 ThrThrProLeuAlaGlnAlaAspProAlaGlyValGlyThrProThrGlyTrpAsp 90
Db 174 AGGCCTCCACTGGCATCA-----CCGACACACTAT--- 203
Qy 91 CysLeuProSerAspCysThrAlaSerAlaAlaGlySerSerThrAspAspValGluLeu 110
Db 204 ---GCTCCCTCCAAAGCGCGCGCTGGCGCGCCCTCGGA----- 242
Qy 111 AlaThrGluPheProAlaThrGluAlaTrpGluCysGluLeuGluGlyLeuLeuGlu 130
Db 243 -----CCGCGC---GAAGCC-----GGCATGCTGGAG--- 266
Qy 131 ArgProAlaLeuCysLeuSerProGlnAlaProPheProLysLeuGlyTrpAspAspGlu 150
Db 267 -----AAGCTGGAGTTCGAGGACGAA 287
Qy 151 ---LeuArgLysProGlyAlaGlnIleTyrMetArgPheMetGlnGluHisThrCysTyr 169
Db 288 CGAGTAGAAGACTCAGAAAGGGTGGTTTACATGCCATTATCATGAGTGCACACAGTTTAT 347
Qy 170 AspAlaMetAlaThrSerSerLysLeuValIlePheAspThrMetLeuGluIleLysLys 189
```







261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
Db TGCAATTTCTCTAATGCGCAGCTTGTTTGATGCTGCTCTTCAATTAATTCGGAATCAATC 544  
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
Db 545 CACAGGCTGCCAGGTATTGACCCAGAATCAGGCAATACTTTGTGTACATCCTCACCACCAAG 604  
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
Db 605 CGCATTTCTGAAGTTCCTCAAATGTTATCACTAGTGTCCCAAGCCAGAGTTCATGTCC 664  
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340  
Db 665 AAGTCTCTGGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGTTGTCGCACTACC 724  
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal 360  
Db 725 ACCCCCGTCTATGTGGCTCTGGGGATTTTGTACAGCATCAGTCTCAGCCCTGCCAGTG 784  
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380  
Db 785 GTGGATGAGAAGGGGGGTGTGGTGACATCTACTCCAAGTTTGATGTTATCAATCGCA 844  
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
Db 845 GCAGAAAAGACCTCAACAACCTAGATGTATCTGTGACTAAAGCCCTTGCACATCGATCA 904  
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420  
Db 905 CATTACTTTGAGGGTGTCTCAAGTGTCTACCTGTCATGAGACTCTGGAGACCATCATCAAC 964  
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
Db 965 AGGCTAGTGGGAAGCAGAGCTTCAACCATTTGTAGTGTGGATGAATAATGATGTGTGTCAG 1024  
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455  
1025 GGAATTGTATCACTGTCTGACATCTCTCGAGGCCCTGGTGTCTCACA 1069  
Db

## RESULT 10

```

RES001.410
US-09-949-016-5010
; Sequence 5010, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016

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Alignment Scores:		
Pred. No.:	5,328-92	Length: 1500
Score:	1017.00	Matches: 193
Percent Similarity:	82.5%	Conservative: 53
Best Local Similarity:	64.7%	Mismatches: 52
Query Match:	42.32%	Indels: 0
DB:	3	Gaps: 0

## RESULT 11

US-09-101-146-63  
; Sequence 63, Application US/09101146  
; Patent No. 6124125  
; GENERAL INFORMATION:  
; APPLICANT: Dartmouth College, St. Vincents Institute of  
; APPLICANT: Medical Research, Kemp et al.  
; TITLE OF INVENTION: NO. 6124125el AMP Activated Protein Kinase  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:

US-10-070-794A-30 (1-464) x US-09-949-016-16752 (1-20347)

QY	114	PheProAlaThrGluAlaTrpGluCysGluLeuGluGlyLeuLeuGluAlaArgProAla	133
Db	14838	 ::: TTTTCTGCTCTTTTGATGGGAG-----TTTTATGTGAAGGAGCTA	14882
QY	134	LeuCysLeuSerProGlnAlaProPheProLysLeuGlyTrpAspGluLeuArgLys	153
Db	14883	 ::: CTAACTATCCACCCCTATGCAGAGACCCCA-----GAA	14915
QY	154	ProGlyAlaGlnIleTyrMetArgPheMetGlnGluHisThrCysTrpAspAlaMetala	173
Db	14916	 ::: TCCAACAATAGCGTGATACTTCTCTCATGAAGTCTCATCGCTGCTATGACCTGATCCC	14975
QY	174	ThrSerSerLysLeuValIlePheAspThr-----	183
Db	14976	 ::: ACAAGCTCCAAATTGGTTGTATTGTATGTACGTCCCTCGCAGTGGTGAAATCCTCTTTTCC	15035
QY	183	-----	183
Db	15036	CTTCCCCCTTTGGAGCCTGTGGTTTAATACCTCTCATCTCATCTCAATCCTAAGGGTAATA	15095
QY	183	-----	183
Db	15096	TCCTTATCTTCTGTGAAGTAGTCTCATGTGTTTACCACCAATGCCCCAACACACTGTGTTCT	15155
QY	184	-----Met-----LeuGluI1	187
Db	15156	TTTTTACAGTCCTGCCCCCTGTGGATTGGCTTTATGATTATTACTGTCTGTGGCTACAGGT	15215
QY	187	eLysLysAlaPhePheAlaLeuValAlaAenGlyValArgAlaProLeuTrpAspSe	207
Db	15216	 ::: GAAGAAAGCTTTTTCGTTTGGTGACTAACGGGTGACGAGCTGCCCTTTATGGGATAG	15275
QY	207	rLysLysGlnSerPheVal-----	213
Db	15276	 ::: TAAGAAGCAAAAGTTTGTGGGTAAAGCAAAAGTTTCTGGAACACAATATTATTGGCATCTT	15335
QY	214	-----GLY-----	215
Db	15336	GTGTGGCGAGGGAGACAAGCTTCAGCGAGTGTGAGGGCTGTGTCTGTCTCTTAGGCA	15395
QY	215	etLeuThrIleThrAspPheIleLeuValLeuHisArgTyrTrpArgSerProLeu-----	233
Db	15396	 ::: TGCTGACCATCACTGATTTTCATCAATCTCTGCACCGCTACTATAAATCAGC-CTTGGTA	15454
QY	233	-----	233
Db	15455	AGGAACCTTAACCAATGACCAAAATCACTTTCCCTGCCCTAAATCCCTCATTTCTCATTT	15514
QY	233	-----	233
Db	15515	CTTTTCTCCAAGCAAGCCAGAGGGTTAAGAAAGCAGAGAGATCAGGTCTCAAAATCTT	15574
QY	234	-----ValGlnIleTyrGluIleGluGlnHisLysIleGluThrTrpA	248
Db	15575	 ::: GTTGCTTCTGCTTCAGGTACAGATCTATGAGCTAGAGAGACACAGATAGAACTTGA	15634
QY	248	rg-----	248
Db	15635	G-AGGTATGTAGAAATTGGGGTTATAAAGGATAAAGGATGGCGGGTTTCTGGGAAAC	15693
QY	249	-----GluIleTyrLeuGlnG	254
Db	15694	ACTTTTCCATGGTGGTATTTTGTGACCCATCCCTTTTCCCTTCAGAGGGTGTATCTCCAGG	15753
QY	254	lyCysPheLysProLeuValSerIleSerProAen-----	265
Db	15754	 ::: ACTCCTTTAAACCGCTGTCTGCATTTCTCTAATGCGAGGTGAGTTCACCATC	15813
QY	265	-----	265
Db	15814	TGTCCAAAAGGGGAAGAGATTTTGTTCATCAGCCCTAGCTAATGCGCTTAGACACCCAGGGA	15873



Db 16953 TTTTGTACAGTCAGTCCTCAGCCCTGCCAGTGGTGGATGAGAA-GGGTGAGAGATTG 17011  
Qy 364 ----- 364  
Db 17012 GGCAGAGGAGGGGAGAGATCCAGGCAAGTCAGGGTGGCTCTGGGAAGATCTGCTT 17071  
Qy 364 ----- 364  
Db 17072 TCCCTCAGCTTAGCCAGGAGGGTGAATCTATGATAGGGGAGCTTTAGATCCAGATC 17131  
Qy 365 -----GlnValValGlyLeuTySerArgPheA 375  
Db 17132 CTCCTTACTAGTCCTCTCTGCCCTAGGGCGTGGTGGATCATCTACTCCAAAGTTG 17191  
Qy 375 spValile----- 377  
Db 17192 ATGTTATCGTGAATGTTGGAGGGTCTGGAGGTAGGAGTGGTGGGGGGGGGCAC 17251  
Qy 377 ----- 377  
Db 17252 TGTAAATATGAGAGGAGAGAGGAGTCTCTCTGTGATCTAAGGGTCTTAGAAGCTTC 17311  
Qy 377 ----- 377  
Db 17312 CAGGCTTCAATCCTATTGAAAGGAATGAATGAGTTGGGTGGTGGCTGAC 17371  
Qy 377 ----- 377  
Db 17372 AATTGCCCTGATCCCTCTGTTGAGTTGGATGGTTCAGGGTTTGGAGGCTGCTCTCT 17431  
Qy 378 -----HisLeuAlaGlnPheTyra 386  
Db 17432 TGCTTCCCTGCAAGCTCCTCTCTGCTCTCCCAAGATCTGGCAGCAGAAAGACCTACA 17491  
Qy 386 snHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeuCysLeuGluGlyV 406  
Db 17492 ACAACCTAGATGATCTGTGACTAAAGCTTGGCAACATCGATCATCTACTTTGAGGGTG 17551  
Qy 406 alLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArgIleAla----- 423  
Db 17552 TTCTCAAGTGTACTCTGATGAGACTCTGGAGACCATCATCAACAGGCTAGT-GGAAGCA 17610  
Qy 424 -----ArgGlu----- 425  
Db 17611 GAGTAGGGAGGCCAGCAACCTAAAGAGCTGAGGGGAGCAGCCTTGGAGTGGGGTTT 17670  
Qy 425 ----- 425  
Db 17671 GGCAAGGAGATAGGGCAGAGGGGCTTCCCTGAGGCCAGCACTAAACATTCCTTTCT 17730  
Qy 426 -----GlnValHisArgLeuValLeuValLeuValAspGluThrGlnHisLeuL 440  
Db 17731 CCCTTGTGCTGTGCGCAGTTCCAGCTTGGAGTGGTGGATGAGAAATGATGTGTCA 17790  
Qy 440 euGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455  
Db 17791 AGGGAATTGTATCACTGTCTGACATCTCTGCAGGCCCTGGTGGCTCACA 17837

## RESULT 13

US-09-513-999C-1659  
; Sequence 1659, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59, US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513.999C  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1659

; LENGTH: 350  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 48..350  
US-09-513-999C-1659

## Alignment Scores:

Pred. No.: 3,06e-22 Length: 350  
Score: 312.00 Matches: 57  
Percent Similarity: 87.84% Conservative: 8  
Best Local Similarity: 77.03% Mismatches: 9  
Query Match: 12.98% Indels: 0  
DB: 3 Gaps: 0

US-10-070-794A-30 (1-464) x US-09-513-999C-1659 (1-350)

Qy 158 IletyRMetArgPheMetGlnGluHisThrCysTyRAspAlaMetAlaThrSerSerLys 177  
Db 129 GTGTATATCTCTTCATGAAGTCTCATCGCTGCTATGACCTGATCCACAAAGCTCCAAA 188  
Qy 178 LeuValIlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsn 197  
Db 189 TTGGTTGATTTGATACCTCCCTGCAGGTGAAGAAAGCTTTTGTGTTGGTACTAAC 248  
Qy 198 GlyValArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThr 217  
Db 249 GGTGTACAGCTGCCCTTTATGGATAGTAAGAAGCAAAAGTTTGTGGGATCTGACC 308  
Qy 218 IletyRAspPheIleLeuValLeuHisArgTyTyRArgSer 231  
Db 309 ATCACTGATTTTCATCAATATCTGACCCGCTACTATAATCA 350

## RESULT 14

US-09-248-796A-4769  
; Sequence 4769, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstein et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 4769  
; LENGTH: 762  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-4769

Alignment Scores:  
Pred. No.: 2,96e-16 Length: 762  
Score: 258.00 Matches: 69  
Percent Similarity: 50.00% Conservative: 55  
Best Local Similarity: 27.82% Mismatches: 82  
Query Match: 10.74% Indels: 42  
DB: 3 Gaps: 8

US-10-070-794A-30 (1-464) x US-09-248-796A-4769 (1-762)

Qy 134 LeuCysLeuSerProGlnAlaPropheProLysLeuGlyTrpAspAspGluLeuArgLys 153  
Db 52 TTGAGTTTGTGCGCTGAA-----CAAATTGAACATGAC-----CAAAA 90

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QY 154 ProGlyAlaGlnIleTyrMetArgPheMetGlnGluHisThrCysTyrAspAlaMetAla 173
Db 91 ATTGGGATCAAGGCTATTCGATTATTTTCAAAAGCAAAACATCTTACGATGCTTACCT 150
QY 174 ThrSerSerLysLeuValIlePheAspThrMetLeuGluIleLysAlaPhePheAla 193
Db 151 GTGAGTTATAGATAATTTGTTGGTACTTCAATTTGTAGTGAATAAGTCAATAATATT 210
QY 194 LeuValAlaGlnGlyValArgAlaProLeuTyrAspSerLysLysGlnSerPheVal 213
Db 211 TTATTACAATAATATAGTTCAGCACCGTTATGGATTAACCAACATCCAGATTCGCT 270
QY 214 GlyMetLeuThrIleThrAspPheIleLeuValLeuHisArgTyrTyrArgSerPro--- 232
Db 271 GGATTGTTAATCATCATCGGATTTTATCAATGTGATCAATCAATCAATTTTACAATCCAGAA 330
QY 233 -----LeuValGlnIleTyrGluIleGluGln----- 241
Db 331 AAGTTTGAACATAGTTGATCACTAACAATGGGTGGTAAAGAGAAATTTGAAAAGCCATA 390
QY 242 -----HisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 391 GGTGTAGATCAATCGAAACA----- 411
QY 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 412 GCATCAATACACCCATTCACGATCAATTAATGAAGCATGTGTCAAGATGTTGGAATCAAAA 471
QY 280 IleHisArgLeuProValLeuAspProValSerGlyAsn-----ValLeuHis 295
Db 472 GCTAGAGAATCCCATTAATTAATGATGAAGATGAAATAACTAAACCGTGAATTTGCTGTAGT 531
QY 296 IleLeuThrHisLysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArg 315
Db 532 GTGTAACTCAATACAGAAATTTGAATTTGTGGCTTG-----AATTGTAAGAA 582
QY 316 ProSerPheLeuTyrArgThrIleGlnAspLeu---GlyIleGlyThrPheArgAspLeu 334
Db 583 ACGAAATGTTATTGAACCCCTCAAGAAATTTGAGTGGTGGTGGTGAATTTGAAAAAGTTG 642
QY 335 AlaValValLeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArg 354
Db 643 TCTACATGACTACTGACACACCTGTCAAGAAGTCATTCATTTATTAACTGAGAAATCT 702
QY 355 ValSerAlaLeuProValValAsn 362
Db 703 GTCTCTTCATACCAATAAGTAGTGAC 726

RESULT 15
US-09-016-434-194
; Sequence 194, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
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; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PENITUT01
; CLONE: 1452972
; US-09-016-434-194

Alignment Scores:
Pred. No.: 3.37e-15 Length: 269
Score: 240.00 Matches: 47
Percent Similarity: 77.27% Conservative: 21
Best Local Similarity: 53.41% Mismatches: 20
Query Match: 9.99% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-30 (1-464) x US-09-016-434-194 (1-269)
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Db 1 GCCTTCATACATCCAGACACCTCCCATCATCAAAAGCCTTGAACATATTTGTGAAAAGACA 60
QY 355 ValSerAlaLeuProValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPhe 374
Db 61 ATATCAGCTCTGCCCTGTTGTGATGAGTCAGGAAAAGTTGTAGATATTTATTCCAAATTT 120
QY 375 AspValIleHisLeuAlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGlu 394
Db 121 GATGTAATTAATCTGCTGCTGAGAAAACATACATAACCTAGATATACCGTGACCCAG 180
QY 395 AlaLeuArgGlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSer 414
Db 181 GCCCTTCAGCACCGTTCACAGTATTTTGAAGGTGTTGTGAAGTGCATAAAGCTGGAATA 240
QY 415 LeuGlyGluValIleAspArgIle 422
Db 241 CTGGAGACCATCGTGGACAGAATA 264

Search completed: January 26, 2006, 03:33:18
Job time : 274.939 secs
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 26, 2006, 01:18:45 ; Search time 997.992 Seconds  
(without alignments)  
3844.711 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403

Sequence: 1 MSFLEQNSSSPSPAVTSS.....LSDILQALVLSPADIGALGA 464

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA Main -QMTS=fastcap -SUFFIX=p2n.rnpbm

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-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct

-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext

-HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US10070794 @CGN 1.1 2064 @runat\_24012006.164417.8900 -NCPU=6 -ICPU=3

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:

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7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*

8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*

9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*

10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2403	100.0	1470	9	US-10-503-175-1
2	2398	99.8	1647	3	US-09-826-581-5
3	2398	99.8	1647	7	US-10-705-137-5
4	2398	99.8	2781	7	US-10-473-670-30
5	2372	98.7	2290	9	US-10-756-149-1235
6	2013	83.8	1873	3	US-09-950-022-3
7	2013	83.8	1873	10	US-11-075-134-3

8	2011	83.7	1873	3	US-09-950-022-1	Sequence 1, Appli
9	2011	83.7	1873	10	US-11-075-134-1	Sequence 1, Appli
10	2010	83.6	1873	3	US-09-950-022-7	Sequence 7, Appli
11	2010	83.6	1873	10	US-11-075-134-7	Sequence 7, Appli
12	2007	83.5	1873	3	US-09-950-022-9	Sequence 9, Appli
13	2007	83.5	1873	10	US-11-075-134-9	Sequence 9, Appli
14	2005	83.4	1873	3	US-09-950-022-5	Sequence 5, Appli
15	2005	83.4	1873	10	US-11-075-134-5	Sequence 5, Appli
16	2000	83.2	1518	9	US-10-503-175-3	Sequence 3, Appli
17	1276	53.1	9100	9	US-10-503-175-5	Sequence 5, Appli
18	1276	53.1	26000	9	US-10-503-039-1	Sequence 1, Appli
19	1094	45.5	2223	9	US-10-466-162-13	Sequence 1, Appli
20	1088	45.3	1435	3	US-09-769-970-14	Sequence 14, Appli
21	1082.5	45.0	1167	9	US-10-466-162-11	Sequence 11, Appli
22	1022.5	42.6	1578	6	US-10-305-720-1113	Sequence 1113, Ap
23	1022.5	42.6	1578	9	US-10-505-680-407	Sequence 407, App
24	1022.5	42.6	1578	9	US-10-466-162-15	Sequence 15, Appli
25	1017	42.3	1691	3	US-09-825-297-2	Sequence 2, Appli
26	904.5	37.6	989	3	US-09-826-581-2	Sequence 2, Appli
27	904.5	37.6	989	7	US-10-705-137-2	Sequence 2, Appli
28	886	36.9	1467	9	US-10-450-763-20069	Sequence 20069, A
29	884	36.8	3261	10	US-11-097-143-25526	Sequence 25526, A
30	766.5	31.9	11527	5	US-10-108-605-70	Sequence 70, Appli
31	766.5	31.9	39651	10	US-11-097-143-25525	Sequence 25525, A
32	758	31.5	547	7	US-10-276-774-261	Sequence 261, App
33	705.5	29.4	2303	9	US-10-450-763-20071	Sequence 20071, A
34	640.5	26.7	1722	3	US-09-826-581-3	Sequence 3, Appli
35	640.5	26.7	1722	7	US-10-705-137-3	Sequence 3, Appli
36	501	20.8	602	5	US-10-106-698-2295	Sequence 2295, Ap
37	408	17.0	765	6	US-10-264-237-248	Sequence 248, App
38	374.5	15.6	2314	8	US-10-739-930-1178	Sequence 1178, Ap
39	373.5	15.5	2339	8	US-10-425-115-2938	Sequence 2938, Ap
40	369.5	15.4	1533	7	US-10-425-114-8857	Sequence 8857, Ap
41	358.5	14.9	3077	7	US-10-424-599-44858	Sequence 44858, A
42	357	14.9	1402	7	US-10-437-963-66100	Sequence 66100, A
43	353	14.7	1507	7	US-10-425-114-29527	Sequence 29527, A
44	352	14.6	1014	3	US-09-826-581-4	Sequence 4, Appli
45	352	14.6	1014	7	US-10-705-137-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-10-503-175-1  
; Sequence 1, Application US/10503175  
; Publication No. US20050172348A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersson, Leif  
; TITLE OF INVENTION: Transgenic animals expressing prkag3  
; FILE REFERENCE: 11145-020U51  
; CURRENT APPLICATION NUMBER: US/10/503,175  
; PRIOR FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: PCT/IB03/00912  
; PRIOR FILING DATE: 2003-01-31  
; PRIOR APPLICATION NUMBER: US 60/353,430  
; PRIOR FILING DATE: 2002-02-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1470  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1470)  
; OTHER INFORMATION:  
US-10-503-175-1  
Alignment Scores: 2,73e-256 Length: 1470  
Pred. No.: 2403.00 Matches: 464  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-070-794A-30 (1-464) x US-10-503-175-1 (1-1470)

Qy 1 MetSerPheLeuGluGlnGluAAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
Db 76 ATGAGCTCTCCCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAAGC 135

Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
Db 136 TCAGAAAGATCCGTGGGAACCGGAGGCGCCAAACCTTGAGATGGACAGGCAAGCTCG 195

Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
Db 196 GTGAGGAAGGGAGGCCACCAGGTGAGGGGAGAGTCCCGGTCCAGGCCAACTGCTGAG 255

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAAspProAla 80  
Db 256 TCCACCGGGCTGGAGGGCCACATCCCAAGACCCACACCTTGGCTCAAGCTGATCCCTGCC 315

Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100  
Db 316 GGGTGGGCATCCACCAACAGGTGGGACTGCCCTCCCTCTGACTGTACAGCCCTCAGCT 375

Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120  
Db 376 GCAGGCTCCAGCAGATGATGTGAGCTGGCCACGGAGTTCAGGCGCACAGAGGCGCTGG 435

Qy 121 GlnCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140  
Db 436 GAGTGTAGCTAGAGGGCTCTGGAAGAGAGGCTGCCCTGTGCTGCCCGCCAGGCC 495

Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTrpMet 160  
Db 496 CCATTTCCAGCTGGCTGGATGACGAACTGGGAAACCCGGCGCCAGATCTACATG 555

Qy 161 ArgPheMetGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuValIle 180  
Db 556 CGCTTCATGAGGAGCACACCTGTACGATGCCATGGCAACTAGTCTCCAGCTAGTCATC 615

Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
Db 616 TTCGACCATGCTGGAGATCAAGAGGCCCTCTTTGCTCTGGTGGCCAAAGGTGTGGCG 675

Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
Db 676 GCAGCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCACTGAC 735

Qy 221 PheIleLeuValLeuHisArgTrpTrpArgSerProLeuValGlnIleTrpGluIleGlu 240  
Db 736 TTCATCTCTGCTGTCATCGCTACTACAGGTCCCGCTGGTCCAGATCTATGAGATTGAA 795

Qy 241 GlnHisLysIleGluThrTrpArgGluIleTrpLeuGlnGlyCysPheLysProLeuVal 260  
Db 796 CAACATAAGATTGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTGTGTC 855

Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTrpThrLeuIleLysAsnArgIle 280  
Db 856 TCCATCTCTCTATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 915

Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
Db 916 CATCGCTGCTGCTTGTGACCGGTGTGAGCAACAGTACTCCACATCTCTCACACAAA 975

Qy 301 ArgLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTrp 320  
Db 976 GCGCTGCTCAAGTTCCTGACATCTTTGGTTCCTGTGCTGCCCGGCCCTCTCTCTCTAC 1035

Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340  
Db 1036 CGCACTATCCAAAGATTGGGCATCGGCACATTCGAGAGACTTGGCTGTGCTGGAGACA 1095

Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
Db 1096 GCACCATCTCTGACTGCATCGACATCTTTGTGGACCGGCTGTCTGCACTGCCTGTG 1155

Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTrpSerArgPheAspValIleHisLeuAla 380  
Db 1156 GTCAACGAATGTGTCAGGTCTGGGCTCTATTCCCGCTTTGATGTGATTCACTGGCT 1215

Qy 381 AlaGlnGlnThrTrpAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
Db 1216 GCCCAGCAAACTACACCACTGGACATGAGTGTGGAGAGCCCTTGAGGCGACAGACA 1275

Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420  
Db 1276 CTATGCTGGAGGAGTCTCTTCTCCAGCCCCACAGAGCTTGGGGAGTGTATCGAC 1335

Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
Db 1336 AGGATTGCTCGGAGCAGGTACACAGGCTGGTGTAGTGACGAGACCCAGCATCTCTTG 1395

Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460  
Db 1396 GGGCTGGTCTCCCTCTCCGACATCTTCAGGCATGGTGTCTCAGCCCTGTGGCATCGAT 1455

Qy 461 AlaLeuGlyAla 464  
Db 1456 GCCCTCGGGGCC 1467

RESULT 2  
US-09-826-581-5  
; Sequence 5, Application US/09826581  
; Patent No. US20020142310A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersson, Leif  
; APPLICANT: Luthman, L. Holger  
; APPLICANT: Marklund, Stefan  
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT  
; FILE REFERENCE: 11145-007001  
; CURRENT APPLICATION NUMBER: US/09/826,581  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: US 60/195,665  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1647  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (20)...(1486)  
US-09-826-581-5

Alignment Scores:  
Pred. No.: 1,17e-255 Length: 1647  
Score: 2398.00 Matches: 463  
Percent Similarity: 99.78% Conservative: 0  
Best Local Similarity: 99.78% Mismatches: 1  
Query Match: 99.79% Indels: 0  
DB: Gaps: 0

US-10-070-794A-30 (1-464) x US-09-826-581-5 (1-1647)

Qy 1 MetSerPheLeuGluGlnGluAAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
Db 95 ATGAGCTCTCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAAGC 154

Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
Db 155 TCAGAAAGATCCGTGGGAACCGGAGGCGCCAAAGCTTGAATGGACCAAGCAGAGTCTG 214

Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60

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Db 215 GTGAGGAAGGGAGCCACAGGTCAGGGGAAGGTCCCGGTCCAGGCCAGCTGCTGAG 274
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 275 TCACACGGGCTGGAGGCCACATTCCTCCACAGACCACACCTTGGCTCAAGCTGATCTCTGCC 334
Qy 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
Db 335 GGGGTGGGCATCTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCCTCAGCT 394
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120
Db 395 GCAGGCTCCAGCACAGATGATGTGGCTGGCCACGGAGTTCCTCCAGCACAGAGGCCCTGG 454
Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 455 GAGTGTGAGCTAGAGGCCCTGCTGGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 514
Qy 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 515 CCATTTCCTCCAGCTGGGCTGGGATGACGAACCTGGGAAACCCGGCGCCAGATCTACATG 574
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
Db 575 CGCTTTCATGAGGAGCACACCTGCTAGCATGCCATGGCACTAGCTCCAAGCTAGTGCATC 634
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 635 TTCGACACCATGCTGGAGATCAGAAGGCCCTCTTCTGCTGTGGTGGCAAGGTGTGGCG 694
Qy 201 AlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 695 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTCTGGGGATGCTGACCATCACTGAC 754
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 755 TTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 814
Qy 241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 815 CACATTAAGATTGAGACTGGAGGGAGATCTACTGCAAGGCTGCTTCAAGCCTCTGGTC 874
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 875 TCCATCTCTCTAATGATAGCTGCTTTGAAGCTGCTTACACCCCTCATCAAGAACCGGATC 934
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 935 CATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 994
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 995 CGCTGCTCAAGTCTCTGCACTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1054
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 1055 CGCACTATCAAGATTGGGCATCGGCACATTCGAGACTTGGCTGCTGCTGCTGCTGCTGCTG 1114
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1115 GCACCCATCTGACTGCACTGGACATCTTTGTGGACCGGCTGTGCTGCTGCTGCTGCTG 1174
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1175 GTCAACCAATGTGGTCAAGTCTGGGCTCTATTTCCTGCTTGTATGTGATTCCTGGCT 1234
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1235 GCCCAGCAAACTTACACCACTGACATGAGTGTGGGAGAGGCCCTGAGGCGAGAGACA 1294
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
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Db 1295 CTATGCTGGAGGAGTCTCTTCTGCTCCAGCCCCAGAGAGCTTTGGGGAGTGCATCGAC 1354
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1355 AGGATTGCTCGGAGCAGGTACACAGGCTGCTAGTGGACGAGACCCAGCATCTCTTG 1414
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1415 GGGGTGGTCTCTCCCTCTCCGACATCTTTCAGGCATGCTGCTGCTGCTGCTGCTGCTG 1474
Qy 461 AlaLeuGlyAla 464
Db 1475 GCCCTCGGGGCC 1486

RESULT 3
US-10-705-137-5
; Sequence 5, Application US/10705137
; Publication No. US20040121385A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007002
; CURRENT APPLICATION NUMBER: US/10705,137
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 09/826,581
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20) ... (1486)
US-10-705-137-5

Alignment Scores:
Pred. No.: 1,17e-255 Length: 1647
Score: 2398.00 Matches: 463
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 7 Gaps: 0

US-10-070-794A-30 (1-464) x US-10-705-137-5 (1-1647)
Qy 1 MetSerPheLeuGluGlnGluAenSerSerTyrProSerProAlaValThrSerSer 20
Db 95 ATGAGCTTCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACGAGCAGC 154
Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTyrThrArgGlnLysSer 40
Db 155 TCAGAAAGAAATCCGTGGGAAACGGAGGGCCAAAGCCTTGAGATGGACAAAGCAGAGTCG 214
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 215 GTGGAGAAAGGGAGGACCCAGGTCAGGGGGAAGGTCCCGGTCAGGCGCCAGCTGCTGAG 274
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 275 TCACCGGGCTGGAGGCCACATTCCTCCAGACCACACCCCTTGGCTCAAGCTGATCTGCC 334
Qy 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
Db 335 GGGGTGGGCATCTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCCTCAGCT 394
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120
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Db 395 GCAGGCTCCACGACAGATGATGGAGCTGCCACGGAGTTCCAGCCACAGAGGCCCTGG 454
Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 455 GAGTGTGAGCTAGAAAGCCCTGCTGGAAGAGAGGCGCTGCCCTGTGCTCCTGCTCCCGCAGGCC 514
Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 515 CCATTTCCCAAGCTGGGCTGGGATGACGAATCTGGGAAACCCGGCGCCAGATCTACATG 574
Qy 161 ArgPheMetGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuValIle 180
Db 575 CGTTTCATGACGAGGACACCTGCTAGTGCCATGSCNACTAGCTCCAGCTAGTATCATC 634
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 635 TTCGACACCATGCTGGAGATCAAGAAGCCCTTCCTGCTGCTGGTGGCCAAACGGTGTGCGG 694
Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 695 GCAGCCCTCTCATGGGACAGCAAGACGAGCTTTTGGGGGATGCTGACCATCACTGAC 754
Qy 221 PheIleLeuValLeuHisAspTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 755 TTCTATCTGCTGCTGCATCGCTACTACAGTCCCCCTGGTCCAGATCTATGAGATTGAA 814
Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 815 CAACATAAGATTGAGCCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTCTGGTC 874
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 875 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCCCTCATCAAGAACCGGATC 934
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 935 CATGCGCTGCTGCTTCTTGACCCGGTGTACGGCAACGTACTCCACATCCTCACACAAA 994
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 995 CGCCTGCTCAAGTCTCTGCACATCTTGTGTTCCCTGCTGCCCGGCCCTCTCTCTAC 1054
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 1055 CGCACTATCCAAGATTGGGCATCGGCATCTCGAGACTTGGCTGTGGTGTCTGAGACA 1114
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal 360
Db 1115 GCACCATCTCTGACTGCATCTGGACATCTTTTGGACCGCGGTGTCTGCACTGCCTGTG 1174
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1175 GTCAACGAATGTGTCAGGTCTGGGCTCTATTCCCGCTTTGTGATGTGATTCACCTGGCT 1234
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1235 GCCCAGCAAACTACAACACCTGACATGATGTGGGAGAGCCCTGAGGACAGGAGACA 1294
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
Db 1295 CTATGCTGGAGGAGTCTTCTTCCTGCCAGCCACGAGAGCTTGGGGAGTGTATCGAC 1354
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1355 AGGATTGCTCGGAGCAGGTACACAGGCTGTGTGTAGTGGACGAGACCCAGCATCTCTTG 1414
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1415 GCGGTGGTCTCCCTCTCGACATCTCTTACGGCACCTGGTGTCTCAGCCCTGCTGGCATCAT 1474
Qy 461 AlaLeuGlyAla 464
Db 1475 GCCTCGGGGCC 1486
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## RESULT 4

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US-10-473-670-30
; Sequence 30, Application US/10473670
; Publication No. US20040110180A1
; GENERAL INFORMATION:
; APPLICANT: RECIPON, Shirley A.; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: TANG, Y. Tom; THORNTON, Michael;
; APPLICANT: BOROWSKY, Mark L.; BAUGHN, Marian R.;
; APPLICANT: BURFORD, Neil; LEE, Soo Yeun;
; APPLICANT: BANDMAN, Olga; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; RAMKUMAR, Javalaxmi;
; APPLICANT: CHAWLA, Narinder K.; LU, Dzung Aina M.;
; APPLICANT: ARVIZO, Chandra S.; ISON, Craig H.;
; APPLICANT: DING, Li; LU, Yan;
; APPLICANT: GURURAJAN, Rajagopal; WALSH, Roderick T.;
; APPLICANT: GANDHI, Ameena R.; SWARNAKAR, Anita;
; APPLICANT: FORSYTHE, Ian J.; YUE, Henry;
; APPLICANT: AU-YOUNG, Janice K.; ELLIOTT, Vicki S.;
; APPLICANT: LEE, Sally
; TITLE OF INVENTION: KINASES AND PHOSPHATASES
; FILE REFERENCE: PI-0398 USN
; CURRENT APPLICATION NUMBER: US/10/473,670
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/10818
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/282,119
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/283,588
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,759
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/285,589
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/287,037
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/287,036
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/288,608
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/288,712
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/289,909
; PRIOR FILING DATE: 2001-05-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474666CB1
US-10-473-670-30
Alignment Scores:
Pred. No.: 2,65e-255 Length: 2781
Score: 2398.00 Matches: 463
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 7 Gaps: 0
US-10-070-794A-30 (1-464) x US-10-473-670-30 (1-2781)
Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20
Db 96 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC 155
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
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Db 156 TCAGAAAGATCCCTGGGAAACGAGGCGCCAAAGCCCTTGAGATGAGCAAGGACGAGTGC 215  
Qy 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
Db 216 GTGGAGGAAGGGAGGACACAGAGTTCAGGGGAAAGTCCCGGTCCAGGCCAGCTGCTGAG 275  
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
Db 276 TCCACCGGGCTGGAGGACACATTCCTCCCAAGACCAACACCTTGGCTCAAGCTGATCTCTGC 335  
Qy 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100  
Db 336 GGGGTGGGACCTCCACCAACAGGGTGGAGTGGCTCCCTCTGACTGTACAGCCCTCAGCT 395  
Qy 101 AlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120  
Db 396 GCAGGCTCCAGCACAGATGATGTGGAGTGGCCACGGAGTTCACAGCCACAGAGGCGCTGG 455  
Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140  
Db 456 GAGTGTGAGCTAGAGGCTGCTGGAAGAGAGGCGCTGCCCTGTGCTGTGCCCGCAGGCC 515  
Qy 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160  
Db 516 CCATTCCTCCAGCTGGGCTGGATGAGCACTCGGAACCCCGCGCCAGATCTCATG 575  
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180  
Db 576 CGCTTCATGCAGGAGCACACCTGTACGATGCCATGCACTAGTCCAGCTAGTATC 635  
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
Db 636 TTCACACCATGCTGGAGATCAAGAGGCTCTCTTGTCTGTGGTGGCCAAACGGTGTGGG 695  
Qy 201 AlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
Db 696 GCAGCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCAGTGC 755  
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240  
Db 756 TTCATCTGTGTGCTGCATGCTACTACAGGTCCCTCCCTGCTCCAGATCTATGAGATTGAA 815  
Qy 241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260  
Db 816 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTCTGGTC 875  
Qy 261 SerIleSerProLeuAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
Db 876 TCCATCTCTTAATGATAGCTGTTTGAAGCTGTCTACACCTTCATCAAGAACCGGATC 935  
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
Db 936 CATCGCTGCTGCTTCTTGACCGGTCTCAGGCAACGTACTCCACATCTCTCACACAAA 995  
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
Db 996 CGCTGCTCAAGTCTCTGCAATCTTGTGTCTGCTGCTGCCCGGCTCTCTCTCTAC 1055  
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340  
Db 1056 CGCACTATCAAGATTGGGCGATCGGCACATTCGAGACTTGGCTGTGGTGGAGACA 1115  
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
Db 1116 GCACCATCTGACTGACTGAGCATCTTGTGGACCGGCTGTCTGTGACTGCTGCTG 1175  
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380  
Db 1176 GTCAACGAATGTGTCAGTGTGGGCTCTATTTCGGCTTTGATGTGATTACCTGGCT 1235  
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
Db 1236 GCGGAGCAACCTTACACCACTGAGCATGAGTGTGGGAAAGCCCTGAGGCGAGGACA 1295

Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420  
Db 1296 CTATGCTCGAGGAGTCTCTTCTCTGCAGCCACAGAGAGTTCGGGGAAGTATCGAC 1355  
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
Db 1356 AGATTGCTCGGAGCAGGTACACAGGCTGGTGTAGTGGAGAGACCCAGCATCTCTTG 1415  
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460  
Db 1416 GGGTGGTCTCTCTCTCCGACATCTTCAGGCACTGGTGTCTGAGCCCTGCTGGCATCGAT 1475  
Qy 461 AlaLeuGlyAla 464  
Db 1476 GCCTCGGGGCC 1487

## RESULT 5

US-10-756-149-1235  
; Sequence 1235, Application US/10756149  
; Publication No. US20050181375A1

## GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha  
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND  
; FILE REFERENCE: file  
; CURRENT APPLICATION NUMBER: US/10/756,149

; NUMBER OF SEQ ID NOS: 5818  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1235

; LENGTH: 2290

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-10-756-149-1235

## Alignment Scores:

Pred. No.: 1-53e-252 Length: 2290  
Score: 2372.00 Matches: 457  
Percent Similarity: 99.35% Conservative: 3  
Best Local Similarity: 98.70% Mismatches: 3  
Query Match: 98.71% Indels: 0  
DB: Gaps: 0

US-10-070-794A-30 (1-464) x US-10-756-149-1235 (1-2290)

Qy 1 MetSerPheLeuGluGlnGluAenSerSerSerTyrProSerProAlaValThrSerSer 20  
Db 97 ATGAGCTTCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC 156  
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTyrThrArgGlnLysSer 40  
Db 157 TCAGAAAGAAATCCGTGGAAACCGAGGCGCAAGACCTTGAGATGGACAGGAGAAATCG 216  
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
Db 217 GTGAGGAGGGGAGGAGCCAGCTCAGGGGGAAGTCCCGGTCCAGGCCAGCTGCTGAG 276  
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
Db 277 TCCACCGGGCTGGAGGCCACATTCCTCCACAGACACACCTTGGCTCAAGCTGATCTCTGCC 336  
Qy 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100  
Db 337 GGGGTGGGCACTCCACCAAGGGTGGGACTGCTCCCTCTGACTGTACAGCTCAGCT 396  
Qy 101 AlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120  
Db 397 GCAGGCTCCAGCACAGATGATGTGGAGTGGCCACGAGTTCACGAGCCACAGAGGCTGG 456  
Qy 121 GluCysGluLeuGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAla 140







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Qy 200 ArgAlaalaProLeuTrpAspSerLysValGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGGACCTTTGTGGACAGCAAGACAGAGCTTCGTGGGATGCTGACCATCA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluile 239
Db 658 GACTTCATCTGTGGTGTCCACCGCTATTACAGGTCCCGCTGGTCCAGATCTACGAGATT 717
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCCAATGACAGCGCTGTCTAGCGCCCTCATCAAGAACCGG 837
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCTGCGGCTCTGGACCTGTCTCCGGGGCTGTGCTCCACATCTCCACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTCTCAAGTCTCTGCACATCTTGGCACCCTGTCTGCCCGCGCTCTCTCTC 957
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
Db 958 TACCGCACCATCCCAAGATTTCGGCATCGGCACATTCGAGACCTTGGCGGTGGTCTGAA 1017
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
Db 1018 ACGCGCCCATCTCTGACCGCATCTGACATCTTCGTGGACCGCGGTGTCTGCGCTGCT 1077
Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 1078 GTGGTCAACGAACTGGACAGTATGGGCTCTACTCTCGCTTTGTATGTATCCACCTG 1137
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCAACAAACATACACACCTGGACATGATGTGGAGAGCCCTGAGGACGCGG 1197
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValile 419
Db 1198 ACATGTGTCTGGAAGGCTCTTCTCTGCCACCGCCACAGACCTTGGGGGAAGTCATT 1257
Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATTGTCGGGAAACAGGTGCACCGCTGTGTCTCGTGGATGAGACCCAGCACCTT 1317
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGGCGGTGGTGTCTCTGACATCTTCTAGGCTCTGGTGTCTGAGCCCTGCTGGAATT 1377
Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGCC 1392
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## RESULT 8

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US-09-950-022-1
; Sequence 1, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
```

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; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; US-09-950-022-1
Alignment Scores: 1.58e-212 Length: 1873
Pred. No.: 2011.00 Matches: 400
Score: 2011.00 Conservative: 19
Percent Similarity: 90.11% Mismatches: 44
Best Local Similarity: 86.02% Indels: 2
Query Match: 83.69% Gaps: 2
DB: 3
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US-10-070-794A-30 (1-464) x US-09-950-022-1 (1-1873)

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Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGNCGAAGGAGAGAGCGGTTCATGGCCATCCCGAGCTGTAACCCAGC 60
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 61 TCAGAAAGAACCATATGGGGACACAGGGGAACAAAGGCCCTCTAGATGGACAGCAGGAGAT 120
Qy 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGAAAGGGGGGCTTCGGGGCCCGAGGGAAGGTCCCACTCCAGCCAGGCTGCTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACCGGGCAGGAGGCGCACATTCGCCAAGSCCACACCTTTGGCCCAAGCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCGAGGTGGACAAACCCCAACAGAGCGGACATCTCCCTCTGACTGTGCGAGCCTCA 300
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCTCGCGCGCG 360
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGGATGAGCTT---GGGCTGGTGAAGAGAACCCAGCCCGCTGGCCATCCCAAG 417
Qy 140 AlaProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTTTACCAGGCTGGGCTGGGATGATGAGCTGCAGAGAGCGGGGGCCAGGCTAC 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGACCTTCATGCGAGGAGCACACCTGTCTACATGCCATGGCGACCCAGCTCCAACTGTC 537
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATGCTGAGATCAAGAAGGCCCTTCTTTGGCTGGTGGCCAAACGCGCTC 597
Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGGACCTTTGTGGACAGCAAGAACAGAGCTTCGTGGGATGCTGACCATCA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluile 239
Db 658 GACTTCATCTGTGGTGTCTGACCGCTATTACAGGTCCCGCTGGTCCAGATCTACGAGATT 717
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
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Db 718 GAAGACATAGATTGAGACTTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCCTCTG 777
Qy ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTAGGCCCTCATCAAGACCGG 837
Qy IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db ATCCACCGCCCTGCCGCTCTGAGCCCTGTCTCCGGGCTGTCTCCACATCTCCACAT 897
Qy LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db AAGCGCTTCTCAAGTCTCTGACATCTTGGACCTCTGCTGCCCGCCCTCTCTCTC 957
Qy TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339
Db TACCGCACCATCCAAAGATTTCGGCATCGGCACATTCGAGACTTGGCGGTGTCTGGAA 1017
Qy ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
Db ACGCGCCCATCTCGACCGCATCTGACATCTTCGTGGACCGCGCTGTCTGTGCGCTGCT 1077
Qy ValValAsnGluCysGlyGlnValValGlyValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db GTGTCAACGAACCTGGACAGGTAGTGGGCTCTTACTCTCGCTTGTGTGATCCACCTG 1137
Qy AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db GCTGCCCAACAAACATACACCATCTGGACATGATGTGGAGAACCTCTGAGCAGCGG 1197
Qy ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 419
Db AACTGTGTCTGGAGGCTCTCTTCTCTGCGAGCCACAGACCTTGGGGGAAGTCAAT 1257
Qy AsparGileAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db GACCGGATGTTCGGGAACAGGTGACCGCTGTGTGCTGTGGATGAGCCACACCTT 1317
Qy LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db CTGGCGGTGTGTCTCTCTGACATCTTCTGAGCTCTGTGTCTGAGCCCTCTGTGGATT 1377
Qy AspAlaLeuGlyAla 464
Db GATGCCCTCGGGCC 1392
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## RESULT 9

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US-11-075-134-1
; Sequence 1, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use to the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P0468US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1392)
; OTHER INFORMATION:
US-11-075-134-1

Alignment Scores:
Pred. No.: 1,59e-212 Length: 1873
Score: 2011.00 Matches: 400
Percent Similarity: 90.11% Conservative: 19
Best Local Similarity: 86.02% Mismatches: 44
Query Match: 83.69% Indels: 2
DB: 2 Gaps: 2

US-10-070-794A-30 (1-464) x US-11-075-134-1 (1-1873)
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Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGAGCAAGGAGAGAGCGCTTCATGGCCATCCCGAGCTGTAAACCAACG 60
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 61 TCAGAAAGAAAGCCATGTTGGGACACAGGGGAACAAGGCCCTCTAGATGGACAAGCAGGAG 120
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGNAGGGGGCTCCGGGCCCGAGGAGAGTCCCGAGTCCAGTCCAGGCCAGTTGCTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACCGGGCAGGAGGGCCACATCCCCCAAGGCCACACCTTGGCCCAAGCCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCGAGGTGGACAAACCCCAACAGAGCGGGACATCTCCCTCTGTGAGTGTGACGCTCA 300
Qy 100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCCAAACACAGACCATCTGGATCTGGGCATAGAGTCTCAGCCTCGCGGCG 360
Qy 120 TrpGluCysGluLeuGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGATGAGCTT---GGGCTGGTGAAGAGAGCCAGCCCGCTGCCATCCCCAGAG 417
Qy 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTTACCCAGCTGGGCTGGGATGATGAGTGCAGAAAGCCGGGGCCAGGCTCTAC 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCACCTTCATGCAAGAGCACACCTGTCTAGTGCCATGGCCAGCCAGCTCCAAACTGGTC 537
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAGCCCTTCTTTCCTGCTGGTGGCAACGGGCTC 597
Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGGCACCTTGTGGGACAGCAAGACAGAGCTTCGTGGGGATGCTGACCATCACA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrThrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCATCTGTGTGCTGACACCTATTACAGGTCCCTCTGGTCCAGATCTACGAGATT 717
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGACATAAGATTGAGACCTGGAGGAGATCTACTCTCAAGGCTGCTTCAAGCCTCTG 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
```

```
Db 778 GTCTCCATCTCTCCCATGACAGCCTGTTGCAAGCTGTCTACGCCCTCATCAAGAACCGG 837
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAenValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCCTGCCGCTCTGGACCTGTCTCCGGGGCTGTGCTCCACATCTCTCACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTTCTCAAGTTCTCGACATCTTTGGCACCTTGGCACCTGTGCTCCCGCCCTCTCTC 957
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339
Db 958 TACCGCACCATCCAAAGATTGGGGCATCGGCACATTCGAGACTTGGCCGCTGGTGGAA 1017
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
Db 1018 ACGCGCCCATCTCTGACCGCACCTGGACATCTTCGTGACCGCGTGTGTCTGGCGCTGCCT 1077
Qy 360 ValValAsnGluCysGlyGlnValValIleValIleValIleValIleValIleHisLeu 379
Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGGCTCTTACTCTCGCTTTGATGTGATCCACTG 1137
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCAACAAACATACACCACTGGACATGATGTGGAGAGGCCCTGAGCGACGGG 1197
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 419
Db 1198 ACCTGTGTCTGGAAGGCTCTCTTCTCTCCAGCCACGAGACCTTGGGGGAAAGTCAAT 1257
Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATGTGCGGGAACAGGTGCACCGCTGTGTCTGTGGATGAGACCCACACCTT 1317
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGCGTGGTGTCTCTCTGACATCTCTCAGGCTCTGGTGGCTCAGCCCTGTGGAT 1377
Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392
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## RESULT 10

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US-09-950-022-7
; Sequence 7, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothechild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Maesoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-7
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## Alignment Scores:

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Pred. No.: 2,05e-212 Length: 1873
Score: 2010.00 Matches: 399
Percent Similarity: 90.11% Conservative: 20
Best Local Similarity: 85.81% Mismatches: 44
Query Match: 83.65% Indels: 2
DB: Gaps: 2

US-10-070-794A-30 (1-464) x US-09-950-022-7 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAenSerSerTyrProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGAGCAAGGAGAGAGCGGTTCATGTGCGCATCCCGAGCTGTAACACCGAGC 60
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTyrPheArgGlnLysSer 40
Db 61 TCAGAAAGAACCATGGGGACCAAGGGGAACAAGGCCCTCTAGATGGAGCAAGCGAGGAGAT 120
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGAGAGGGGGCTCCGGGCCGAGGAGAGGTCCCGAGTCCAGGCCAGTGTGCTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACGGGGCAGGAGGCCACATTCGCCAAGGCCACACCTTGGGCCCAAGCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCAGGTGGACAAACCCCAACAGAGCGGGACATCTCTCCCTCTGACTGTGCAGCCTCA 300
Qy 100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCCAAACACAGACCATCTGGATCTGGGCATAGAGTCTCAGGCTCGCGCGCG 360
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGATGAGCTT---GGGCTGGTGAAGAGAAGCCAGCCCGCTGCCATCCACAG 417
Qy 140 AlaProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTATCCAGGCTGGGCTGGGATGATGAGCTGCAGAAAGCGGGGGCCAGGTCTAC 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCATCTTATGCGAGGAGCACACTGTACGATGCCATGCCAGCTCCAAACTGGTC 537
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATGTCTGGAGATCAAGAAGGCCCTTCTTTGCCCTGGTGGCCACCGCATC 597
Qy 200 ArgAlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGACGGCGACCTTTGTGGGACAGCAAGAGCAGAGCTTCGTGGGGATGCTGACCATCA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCATCTTGGTGTGTCACCGCTATTACAGTCCCGCTCCAGATCTACGAGATT 717
Qy 240 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGAACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAenValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCCTGCCGCTCTGGACCTGTCTCCGGGGCTGTGCTCCACATCTCTCACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTTCTCAAGTTCTCGACATCTTTGGCACCTTGGCACCTGTGCTCCCGCCCTCTC 957
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Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339  
Db 958 TACCGCACCATCCAAAGATTGGGCATCGGCACATTCCGAGACTTGGCGTGTCTGGAA 1017  
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359  
Db 1018 ACGCGCGCCATCCCTGACCGCACTCGACATCTTCGTGGACCGCGGTGTCTGCGCTGCCT 1077  
Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379  
Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGCCCTCTACTCTCGCTTGTGTGATCCACTG 1137  
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399  
Db 1138 GCTGCCCAACAAACATACACACCTGACATGAATGTGGAGAAGCCCTGAGCGACGG 1197  
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 419  
Db 1198 ACCTGTGTCTGGAAAGCGCTCTTCTGCGCAGCCCAACGAGACCTTGGGGGAAGTCAAT 1257  
Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439  
Db 1258 GACCGGATTGTCGGGAACAGGTGCAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1317  
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459  
Db 1318 CTGGCGGTGTGTCTCTGACATCTTCTGAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1377  
Qy 460 AspAlaLeuGlyAla 464  
Db 1378 GATGCCCTCGGGCC 1392

## RESULT 11

US-11-075-134-7  
; Sequence 7, Application US/11075134  
; Publication No. US20050208551A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Novel PKAG3 Alleles and Use fo the Same as Genetic Markers for  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/11/075,134  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR FILING DATE: 2005-09-022  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 1873  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1392)  
; OTHER INFORMATION:  
US-11-075-134-7

## Alignment Scores:

Pred. No.: 2,05e-212 Length: 1873  
Score: 2010.00 Matches: 399  
Percent Similarity: 90.11% Conservative: 20  
Best Local Similarity: 85.81% Mismatches: 44

Query Match: 83.65% Indels: 2  
DB: 10 Gaps: 2  
US-10-070-794a-30 (1-464) x US-11-075-134-7 (1-1873)  
Qy 1 MetSerPheLeuGlnGlnAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
Db 1 ATGAGCTTCTTAGAGCAAGGAGAGAGCGCTTATCGGCATCCCGAGCTGTAAACACACAGC 60  
Qy 21 SerGluArgIleArgGlyLysArgArgAlaIleAlaLeuArgTrpThrArgGlnLysSer 40  
Db 61 TCAGAAAGAACCCATGGGACCCAGGGGAAACAAGGCCCTCTAGATGGACAAGGACGAGGAT 120  
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
Db 121 GTAGAGGAAGGGGGCCCTCCGGGCCCGAGGAGGAGTCCCGAGTCCAGGCCAGTGTCTGAG 180  
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79  
Db 181 TCCACCGGGGAGGAGGCCACATTTCCCAAGGCCACACCTTGGCCCAAGCGCTCCCTTTG 240  
Qy 80 AlaGlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSer 99  
Db 241 GCCAGGTGGACAAACCCCAAGAGCGGAGACATCTCTCCCTCTGACTGTGACGCTCA 300  
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119  
Db 301 GCCTCCGACTCCAAACACAGACCATCTGGATCTGGCATAGAGTTCTCAGCCTCCGGCGG 360  
Qy 120 TrpGluCysGluLeuGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139  
Db 361 TCGGGGGATGAGCTT---GGGCTGGTGAAGAGAGCAGCCCGCTGCCATCCACAG 417  
Qy 140 AlaProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159  
Db 418 GTGCTGTATCCAGGCTGGGCTGGGATGATGAGCTGCAGAAAGCGGGGGCCAGGCTCTAC 477  
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179  
Db 478 ATGCACCTTATGACGAGGACACACTGCTAGCATGCCATGCGGACCACTCCAACTGGTC 537  
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyVal 199  
Db 538 ATCTTCGACACCATGTGGAGATCAAGAGCGCTTCTTTGCCCTGTGTGGCAACGGCATC 597  
Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219  
Db 598 CGAGCGGCACCTTGTGGGACAGCAAGACAGAGCTTCGTGGGATGCTGACCATCACA 657  
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239  
Db 658 GACTTTCATCTTGTGTGTGACCCCTATTACAGGTCCCTTGTGTGTGTGTGTGTGTGTGT 717  
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrIleuGlnGlyCysPheLysProLeu 259  
Db 718 GAAGAACATAAGATTGAGACTCGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777  
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrIleuLysAsnArg 279  
Db 778 GTCTCCATCTCTCCCAATGACAGCCTGTTCGAGAGCTGTCTACGCCCTCATCAAGAACCG 837  
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299  
Db 838 ATCCACCGCTCGCGGTCTGGACCTGTCTCGGGGGCTGTGTCTCCACATCTCTCACACAT 897  
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319  
Db 898 AAGCGGCTTCTCAAGTTCTCTGACATCTTTGGCACCTTGTGGCACCTGTCTCGCCCGCTCT 957  
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339  
Db 958 TACCGCACCATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCGGTGTGTGTGTGTGT 1017

Qy	340	ThrAlaProIleuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	359
Db	1018	ACGGCGCCATCTCTGACCGACCTGGACATCTTGTTGGACGGGGTGCTGTGGCTGCCT	1077
Qy	360	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	379
Db	1078	GTGGTCAACGAACCTGGACAGGTAGTGGGCTCTACTCTGCCTTGTATGTATCCACCTG	1137
Qy	380	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	399
Db	1138	GCTGCCCAACAAACATACACCACCTGGACATGAATGTGGGAGAAGCCCTGAGGACGCG	1197
Qy	400	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle	419
Db	1198	ACACTGTCTGGAAGCGTCTTCTTCGCAGCCCCACGAGACCTTGGGGGGAAGTCATT	1257
Qy	420	AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	439
Db	1258	GACCGGATGTCCGGGAACAGGTGCACCGCTGTGTCTGTGGATGAGACCCAGCACCTT	1317
Qy	440	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	459
Db	1318	CTGGCGGTGGTGTCCCTCTCTGACATCTTTCAGGCTCTGTGTGCTCAGCCCTGCTGGAATT	1377
Qy	460	AspAlaLeuGlyAla	464
Db	1378	GATGCTCTCGGGGCC	1392

## RESULT 12

```

US-09-950-022-9
; Sequence 9, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Matek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits

```

Alignment Scores:		
Pred. No.:	4, 41e-212	1873
Score:	2007.00	399
Percent Similarity:	90.11%	Conservative: 20
Best Local Similarity:	85.81%	Mismatches: 44
Query Match:	83.52%	Indels: 2
DB:	3	Gaps: 2

US-10-070-794A-30 (1-464) x US-09-950-022-9 (1-1873)

**Qy**

1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer  
|||||  
|||||

**Dd**

1 ATGAGCTTCTTAGAGCAAGGAGAGACCGCTTCATGGCCATCCCGAGCTGTAAACCACGCG 60



Db 1138 GCTGCCCAACAAACATACACCTGGACATGAATGTGGAGAGCCCTGAGGAGCGG 1197  
Qy 400 ThrLeuGlyLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValle 419  
Db 1198 ACACGTGTCTGGAGGCGTCTCTCTCCAGCCACAGAGACCTTGGGGAGTCAAT 1257  
Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439  
Db 1258 GACCGGATGTCCGGGAAACAGGTGCACCGCTGGTGTCTCGTGGATGAGACCCAGCACCTT 1317  
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuValSerProAlaGlyLe 459  
Db 1318 GTGGCGGTGGTGTCTCTCTGACATCCTTCAGGCTCTGGTGTCTGAGCCCTGCTGGAAT 1377  
Qy 460 AspAlaLeuGlyAla 464  
Db 1378 GATGCCCTCGGGGCC 1392

## RESULT 13

US-11-075-134-9  
; Sequence 9, Application US/11075134  
; Publication No. US20050208551A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/11/075.134  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: US/09/950,022  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 9  
; LENGTH: 1873  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1392)  
; OTHER INFORMATION:  
US-11-075-134-9

Alignment Scores:  
Pred. No.: 4.41e-212 Length: 1873  
Score: 2007.00 Matches: 399  
Percent Similarity: 90.11% Conservative: 20  
Best Local Similarity: 85.81% Mismatches: 44  
Query Match: 83.52% Indels: 2  
DB: 10 Gaps: 2

US-10-070-794A-30 (1-464) x US-11-075-134-9 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
Db 1 ATGAGCTCTCTAGAGCAAGAGAGAGCGTTCATGGCCATCCCGAGCTGTAAACCCAGC 60  
Qy 21 SerGluArgIleArgGlyLeuArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
Db 61 TCAGAAAGACCATGGGGACCGGACCAAGGACCTCTAGATGACAGGAGGAGAT 120  
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGlyGlyProArgSerArgProThrAlaGlu 60

Db 121 GTAGAGGAAGGGGGCGCTCCGGGGCCCGAGGAAAGGTCCCCAGTCCAGGCCAGTTGCTGAG 180  
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79  
Db 181 TCCACCGGGCAGGAGGCCACATTCCTCCACAGGCCACACCTTGGCCCAAGCGCTCCCTTG 240  
Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99  
Db 241 GCCGAGGTGGACAAACCCCAACAGAGCGGGACATCTCCCTCTGACTGTGACGCTCA 300  
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119  
Db 301 GCCTCCGACCTCCACACAGACACCATCTGGATCTGGGCATAGAGTTCTCAGCCCTCGGCGCG 360  
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuLeuArgProAlaLeuCysLeuSerProGln 139  
Db 361 TCGGGGGATGAGCTT---GGCTGGTGAGAGAGCAGCCCGCTGCCCATCCACAG 417  
Qy 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleThr 159  
Db 418 GTGCTGTACCCAGGCTGGGCTGGGATGATGAGCTGCAGAGCGGGGGCCAGGCTTAC 477  
Qy 160 MetArgPheMetGlnGluHisThrCysTyrrAspAlaMetAlaThrSerSerLysLeuVal 179  
Db 478 ATGCACCTTCATGCAGGAGCACACCTGCTAGCATGCCATGGCGACAGCTCCAAACTGGTC 537  
Qy 180 IlePheAspThrMetLeuGluLeuLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199  
Db 538 ATCTTCGACACCATCTGGAGATCAGAGGCCCTCTTTGGCCCTGGTGGCCACAGGCGTC 597  
Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219  
Db 598 CAAGCGGCACCTTTGTGGGACAGCAAGAGCAGAGCTTCGTGGGGATGCTGACCATACA 657  
Qy 220 AspPheIleLeuValLeuHisArgTyrrArgSerProLeuValGlnIleThrGluIle 239  
Db 658 GACTTCATCTGTGGTGTGCACCGCTATTACAGGTCCCGCTGTCAGATACAGAGATT 717  
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrrLeuGlnGlyCysPheLysProLeu 259  
Db 718 GAAGAACAATAGATTGAGACTGGAGGAGATCTACCTTCAGGCTGCTTCAGGCTCTG 777  
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrrThrLeuIleLysAsnArg 279  
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTAGGCCCTCATCAAGAACCGG 837  
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299  
Db 838 ATCCACCGCTCGCGGTCTGGACCCCTGTCTCCGGGGCTGTGTCTCCACATCTCCACACAT 897  
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319  
Db 898 AGCGGCTTCTCAAGTTCTTGACATCTTTGGACCCCTGTGTCGCCCGGCTCTCTCTC 957  
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339  
Db 958 TACCGCACCATCCAAAGATTGGGACATCGGCACATTCGAGACTTGGCGGTGGTCTGGAA 1017  
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359  
Db 1018 ACGCGGCCCATCTCGACCGCATCTTCGTGGACCGGCTGTGTCTGCGCTGCGCT 1077  
Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrrSerArgPheAspValIleHisLeu 379  
Db 1078 GTGTCAACGAACACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGATGATCCACTG 1137  
Qy 380 AlaAlaGlnGlnThrTyrrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399  
Db 1138 GCTGCCCCAACAAACATACACCACTGGACATGAATGTGGGAGAGCCCTGAGGACGCGG 1197  
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValle 419

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Db      1198 ACATGTGTCTGGAGGGCTCCTTCTTCCTGCCAGCCCCACAGACCTTGGGGAGTGCATT 1257
Qy      420 AspArgIleAlaAArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db      1258 GACCGGATTGTCGGGAACAGGTGCACCGCTGGTCTCGTGGATGAGACCCAGCACCTT 1317
Qy      440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db      1318 CTGGCGGTGGTGTCTCTGACATCCTTCAGGCTCTGGTCTCAGCCCTGCTGGAAATT 1377
Qy      460 AspAlaLeuGlyAla 464
Db      1378 GATGCCCTCGGGGCC 1392

RESULT 14
US-09-950-022-5
; Sequence 5, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-5

Alignment Scores:
Pred. No.:      7,36e-212      Length:      1873
Score:          2005.00      Matches:      399
Percent Similarity: 89.8%      Conservative: 19
Best Local Similarity: 85.81%      Mismatches: 45
Query Match:      83.44%      Indels:      2
DB:              3          Gaps:      2

US-10-070-794A-30 (1-464) x US-09-950-022-5 (1-1873)
Qy      1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20
Db      1 ATGAGCTTCTAGAGCAAGGAGGAGAGCGCTTCATGGCCATCCCGAGCTGTAAACCAACGAGC 60
Qy      21 SerGluArgIleArgGlyIysArgArgAlaIysAlaLeuArgTrpThrArgGlnLysSer 40
Db      61 TCAGAAAGAACGCATCGGGACCCAGGGGAACAAGGCTCTAGATGACCAAGGACGAGGAT 120
Qy      41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db      121 GTAGAGGAGGGGGGCTCCGGGCCGAGGAAAGTCCCCAGTCCAGGCCAGTTGCTGAG 180
Qy      61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db      181 TCCACCGGGCAGGAGGCCACATTCCTCCCAAGGGCCACACCTTGGCCCAAGCCGCTCCCTTG 240
Qy      80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99

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Db      241 GCCAGGTGGACAACACCCCAACAGAGCGGACATCTCCCTCTGACTGTGCAGCCTCA 300
Qy      100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db      301 GCCTCCGACATCCAAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCTCCGGCGCG 360
Qy      120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db      361 TCGGGGGATGAGCTT---GGGCTGGTGAAGAGAGACAGCCCGCTGCCATCCACAGAG 417
Qy      140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db      418 GTGCTGTTACCCAGGCTGGCTGGGATGATGAGCTGCAGAAGCGGGGGCCAGGCTCTAC 477
Qy      160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db      478 ATGCATTTTCATGCGAGGAGCACACCTGCTACGATGCCATGGCACCAGCTCCAAATCGTTC 537
Qy      180 IlePheAspThrMetLeuGluIleLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db      538 ATCTTCGACACCATGCTGGAGATCAAGAGCCCTCTTTGCCCTGGTGGCAACAGCGGTC 597
Qy      200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db      598 CGAGCGCACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGATGCTGACCATCACA 657
Qy      220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db      658 GACTTCATCTTGGTGTGCACCGCTATTACAGGTCCCGCTGGTCCAGATCTACGAGATT 717
Qy      240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db      718 GAAGAACAATAGATTGAGACCTCGAGGGAGATCTACTCTTCAGGCTGCTTCAGGCTCTG 777
Qy      260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db      778 GTCTCCATCTCTCCCAATGACAGCGCTGTTGAAGCTGTCTACGCGCTCATCAAGAACGG 837
Qy      280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db      838 ATCCACCGCTTCGCGGCTCTCGACCTGTCTCCGGGGCTGTGCTCCACATCCTCACACAT 897
Qy      300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db      898 AAGCGCTTCTCAAGTTCCTGCACATCTTTGGACCCCTGCTGCCCGGCCCTCTCTCTC 957
Qy      320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339
Db      958 TACCGCACCATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCGCTGGTGTGGAA 1017
Qy      340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
Db      1018 ACGCGCCCATCTCTGACCGCATCTGTCGAGACCGCGGTGTGCTGCGCTGCTCT 1077
Qy      360 ValValAsnGluCysGlyValValGlyValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db      1078 GTGTGTCAACGAAACTGGACAGTAGTGGGCTCTACTCTCTCGTTTGTATGTATCCACCTG 1137
Qy      380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db      1138 GCTGCCCAACAAACATACACACCATGATGATGGGAGAGAGCCCTCAGGCGAGCGG 1197
Qy      400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlySerLeuGlyValIle 419
Db      1198 ACATGTGTCTGGAGGCGCTCTTCTTCGCGAGCCCAAGACCTTGGGGAGTGCATT 1257
Qy      420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db      1258 GACCGGATTGTCGGGAACAGGTGCACCGCTGGTGTCTCGTGGATGAGACCCAGCACCTT 1317
Qy      440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db      1318 CTGGCGGTGGTGTCTCTGACATCCTTCTGAGCTCTGGTCTCAGGCTCTGAGCCCTGCTGGAAATT 1377

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Qy 460 AspAlaLeuGlyAla 464  
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 15  
US-11-075-134-5  
; Sequence 5, Application US/11075134  
; Publication No. US20050208551A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothechild, Max  
; APPLICANT: Ciohanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use to the Same as Genetic Markers for  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/11/075,134  
; PRIOR FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: US/09/950,022  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 1873  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1392)  
; OTHER INFORMATION:  
US-11-075-134-5

Alignment Scores:  
Pred. No.: 7,356-212 Length: 1873  
Score: 2005.00 Matches: 399  
Percent Similarity: 89.89% Conservative: 19  
Best Local Similarity: 85.81% Mismatches: 45  
Query Match: 83.44% Indels: 2  
DB: 10 Gaps: 2

US-10-070-794A-30 (1-464) x US-11-075-134-5 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
Db 1 ATGAGCTTCTAGAGCAAGGAGAGCGGTCATGGGCCATCCGAGCTGTAAACACCGAGC 60

Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
Db 61 TCAGAAAGAGCCATGGGACCGAGGCAACAGGCGCTCTAGATGCACAGCGAGGAT 120

Qy 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
Db 121 GTAGAGAGGGGGGCGCTCCGGGCGGAGGAAAGTCCCCAGTCCAGGCCCATGTTGCTGAG 180

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79  
Db 181 TCCACCGGGCAGGAGGCCACATCCCAAGGCCACACCTTGGCCCAAGCGCTCCCTTG 240

Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99  
Db 241 GCCGAGGTGGCAACACCCCAACAGAGCGGAGCATCTCCCTCTGACTGTGCGAGCCTCA 300

Qy 100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119  
Db 301 GCCTCCGACTCCAAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCCTCGGCGGC 360

Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139  
Db 361 TCGGGGGATGAGCTT---GGGCTGGTGAAGAAGCAGCCCGCTGCCATCCACAGAG 417

Qy 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159  
Db 418 GTGCTGTATCCAGGCTGGGCTGGGATGATGAGCTGCAGAAAGCGGGGGCCAGGCTTAC 477

Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179  
Db 478 ATGCATTTATGCAGGAGCACACCTGTACATGCCATGGCAGCAGCTCCAAACTGGTC 537

Qy 180 IlePheAspThrMetLeuGluLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199  
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGCGCTTCTTGGCTGGTGGCCCAAGCGGTC 597

Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219  
Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGGATGCTGACCATCACA 657

Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239  
Db 658 GACTTCATCTTGTGTGTCACCGCTATTACAGTCCCGCTGGTCCAGATCTACAGATT 717

Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259  
Db 718 GAAGAACATAAGATTGAGACTTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCGCTCTG 777

Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279  
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGACCGG 837

Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299  
Db 838 ATCCACCGCTTGGGCTCTGGACCTGTCTCCGGGGCTGTGCTTCCATCTCTCACAT 897

Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319  
Db 898 AAGCGGCTTCTCAAGTTCTTGCCACATCTTTGGCACCTGTCTGCCCGCGCTCTCTCTC 957

Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339  
Db 958 TACCGCACCATCCAAAGATTGGGCGCATCGGCACATTCGAGACTTGGCGCTGGAA 1017

Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359  
Db 1018 ACGGCGCCATCTTGACCGCACTGGACATCTTGTGACCGCGGTGTCTGCGCTGCT 1077

Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379  
Db 1078 GTGGTCAACGAACCTGGACAGGTAGTGGGCTCTTACTCTCGCTTGTGTGATCCACCTG 1137

Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399  
Db 1138 GCTGCCCCAACAAACATACACACCTGAGATGAATGTGGGAGAGCCCTGAGCAGCGG 1197

Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyValIle 419  
Db 1198 ACATGTGTCTGGAAGCGTCTTCTGTCAGCCCCCAGAGACCTTGGGGAGAGTCAAT 1257

Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439  
Db 1258 GACCGGATGCTCCGGGAACAGGTGACCGCTGCTGTGCTCGTGGATGAGACCCAGCCTT 1317

Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459  
Db 1318 CTGGCGGTGGTGTCCCTCTCTGACATCTCTTTCAGGCTCTGTGTGCTCAGCCCTGCTGGAATT 1377

Qy 460 AspAlaLeuGlyAla 464  
Db 1378 GATGCCCTCGGGGCC 1392

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Job time : 1031.99 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 26, 2006, 03:26:13.; Search time 1080.05 Seconds  
(without alignments)  
356.862 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6059551 seqs, 415333918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62  
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10070794 @CGN 1 1 352 @runat 24012006 164418 8933  
-NCPU=6 -ICPU=3 -NO MWAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:  
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2: /cgn2\_6/ptodata/1/pubpna/US06 NEW PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US07 NEW PUB.seq:  
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6: /cgn2\_6/ptodata/1/pubpna/US10 NEW PUB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq:  
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11: /cgn2\_6/ptodata/1/pubpna/US15 NEW PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023	42.6	1628	8	US-11-136-527-2210
2	500.5	20.8	1321	7	US-10-750-185-28770
3	500.5	20.8	1321	7	US-10-750-623-28770
4	461.5	19.2	568	8	US-11-128-061-330
5	461.5	19.2	568	8	US-11-128-061-3972
6	461.5	19.2	568	8	US-11-128-049-330
7	461.5	19.2	568	8	US-11-128-049-3972

8	234.5	9.8	1500	8	US-11-041-776-79	Sequence 79, Appl
9	113.5	4.7	3439	8	US-11-000-688-851	Sequence 851, App
10	110.5	4.6	3175	7	US-10-995-561-464	Sequence 454, App
11	110.5	4.6	3464	7	US-10-995-561-465	Sequence 465, App
12	110.5	4.6	3468	7	US-10-995-561-466	Sequence 466, App
13	109.5	4.6	6594	8	US-11-075-185-38	Sequence 38, Appl
14	109.5	4.6	78869	8	US-11-075-185-1	Sequence 1, Appl
15	108	4.5	2736	7	US-10-821-234-55	Sequence 55, Appl
16	107.5	4.5	1494	7	US-10-467-657-5005	Sequence 5005, Ap
17	107.5	4.5	3145	7	US-10-821-234-327	Sequence 327, App
18	106.5	4.4	1454	8	US-11-024-959-85	Sequence 85, Appl
19	106.5	4.4	2301	8	US-11-151-601-9	Sequence 9, Appl
20	106.5	4.4	2797	8	US-11-075-400-17	Sequence 17, Appl
21	106.5	4.4	3552	8	US-11-151-601-7	Sequence 7, Appl
22	106.5	4.4	6594	8	US-11-075-185-38	Sequence 38, Appl
23	106.5	4.4	78869	8	US-11-075-185-1	Sequence 1, Appl
24	106	4.4	1486	8	US-11-055-822-955	Sequence 955, App
25	106	4.4	1692	8	US-11-055-822-953	Sequence 933, App
26	106	4.4	4461	7	US-10-750-185-45911	Sequence 45911, A
27	106	4.4	4461	7	US-10-750-623-45911	Sequence 45911, A
28	105.5	4.4	1366	7	US-10-955-054A-82	Sequence 82, Appl
29	105	4.4	1400	8	US-11-136-527-7875	Sequence 7875, Ap
30	105	4.4	1663	8	US-11-136-527-3779	Sequence 3779, Ap
31	104	4.3	1519	7	US-10-750-185-52488	Sequence 52488, A
32	104	4.3	1519	7	US-10-750-623-52488	Sequence 8239, Ap
33	103.5	4.3	1662	7	US-10-467-657-8239	Sequence 49, Appl
34	103.5	4.3	7474	8	US-11-069-834-49	Sequence 6, Appl
35	102	4.2	2862	8	US-11-156-953-6	Sequence 124, App
36	101.5	4.2	2305	8	US-11-064-774A-124	Sequence 79, Appl
37	101	4.2	1588	8	US-11-080-991-79	Sequence 48, Appl
38	101	4.2	4015	6	US-10-826-585-48	Sequence 4, Appl
39	101	4.2	4015	8	US-11-120-544B-4	Sequence 12, Appl
40	101	4.2	7916	8	US-11-054-168B-12	Sequence 37, Appl
41	100.5	4.2	2279	7	US-10-509-121-37	Sequence 38, Appl
42	100.5	4.2	2301	7	US-10-509-121-38	Sequence 230, App
43	100.5	4.2	7216	8	US-11-136-527-290	Sequence 60819, A
44	100	4.2	1976	7	US-10-770-726-30	
45	100	4.2	2174	7	US-10-750-185-60819	

#### ALIGNMENTS

RESULT 1

US-11-136-527-2210  
; Sequence 2210, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2210  
; TYPE: DNA  
; LENGTH: 1628  
; ORGANISM: Rattus norvegicus  
US-11-136-527-2210

Alignment Scores:  
Pred. No.: 7.86e-77 Length: 1628  
Score: 1023.00 Matches: 196  
Percent Similarity: 79.75% Conservative: 56  
Best Local Similarity: 62.03% Mismatches: 64  
Query Match: 42.57% Indels: 0  
DB: 8 Gaps: 0  
US-10-070-794A-30 (1-464) x US-11-136-527-2210 (1-1628)

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Qy 140 AlaProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 61 GCTCCAGCTCGGAGAGTAAGAACTCTCAAGAGACCCCGGAATCGAACAGTAGTGTGTAC 120
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 121 ACCACCTTCATGAAGTCTCATCGTGTATGACCTGATCCCAAGCTCCAGCTGGTG 180
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 181 GTATTTCATCTCGCTGCAGGTAAGAAAGCCCTCTTTCCTCGGTGACTTAACCGGTGT 240
Qy 200 ArgAlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 241 CGTCTGCCCTTTGTGGGATAGTAAGAACGAGAGCTTTGTGGGCATGCTGACCATCACT 300
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 301 GACTTCATCAATATTCGACCCGATATCAAGTCAGCCCTGGTGGAGATCTATGAAGTAC 360
Qy 240 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 361 GAGGAGCAAGATAGAGACTTGGAGAGGCTTACCTGCAAGACTCCTTTAAGCCACTT 420
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 421 GTCTGCAATTTCTCAAAATGCCAGCTTGTGATGCTGTCTTCAATTAATTCGAAATGAG 480
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 481 ATCCACAGSITTCAGTTATGACCCGAGTCAGGCAACACTTGTACATTTCTTACTCAC 540
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 541 AAGCGATCTCAAGTTCCTCAAGTTGTTATCACTGAGTTCCCGCAAGCCGGAATTCATG 600
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339
Db 601 TCTAAGTCTCTGGAGAGACTACAGATTGGCCACCTACGCCAATATTTGCCATCGTCCGTACC 660
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
Db 661 ACTACACTCTCTATGTGGCTCTGGGCATCTTTGTACAGCCAGCTCTCGCCTTGCT 720
Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 721 GTGGTGGATGAGAAAGGGCGTGTGGTGACATCTACTCAAAGTTTGATGTGATTAATTG 780
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 781 GCAGCAGAAAAGACATACAAACCTAGATGTCTGTGACAAAAGCCCTACAGCACCGG 840
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyValIle 419
Db 841 TCACACTACTTCGAGGGTGTCTCAAGTGTCTACCTACATGAGACTCTAGAGCAATCATC 900
Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 901 AATAGACTGGTGGRAGCAGAGGTTCCCGTCTGGTGGTGGTGAATGAACATGACGTGGTC 960
Qy 440 LeuGlyValValSerSerAspIleLeuGlnAlaLeuValLeuSer 455
Db 961 AMGGCATGTGATCTGCTGTGACATCTTACAGGCTCTGGTGTCTCACA 1008

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RESULT 2

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US-10-750-185-28770
; Sequence 28770, Application US/10750185
; Publication NO. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David

```

```

; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28770
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Bovine 19866880603844
; US-10-750-185-28770

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Alignment Scores: 1-57e-32 Length: 1321

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Pred. No.: 500.50 Matches: 136
Score: 53.27% Conservative: 43
Best Similarity: 40.48% Mismatches: 89
Query Match: 20.83% Indels: 69
Gaps: 5

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US-10-070-794A-30 (1-464) x US-10-750-185-28770 (1-1321)
Qy 168 CysTyrAspAlaMetAlaThrSerSerLysLeuValIlePheAspThrMetLeuGluIle 187
Db 101 TGCTATGACCTGATCTTCACAAGCTCCCAATTTGGTTATTTGCTATTCCTTCGACGTA 160
Qy 188 LysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAlaAlaProLeu-TrpAspSe 207
Db 161 TACAG-----TGCCCCCTCTCTGGATAC 184
Qy 207 rLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisAr 227
Db 185 TAAAGCAAGAGACTTGTGGCATGTGATTTATCCCAATTTCAATATTCATCTGCACTA 244
Qy 227 gTyrTyrArgSerProLeuVal-GlnIleTyrGluIleGluGlnHisLysIleGluThrT 247
Db 245 TTACTATATGTGACCTTGGTTCAGAGCTATGAGCTGGAAGATACAAATAGAACTT 304
Qy 247 rPArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIleSerProAsnAspS 267
Db 305 GAAAGGAGGTGATATACAGGACTTCTTTAAACCACTTGTCTGATTTCTTCTAATGCCA 364
Qy 267 erLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuA 287
Db 365 ACTTGTTTAATGCTGCTTTTCAATTAATTCAGAACAGATCCACAGGCTGCCAGTTGTG 424
Qy 287 spProValSerGlyAsnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuH 307
Db 425 ACCCAGAAATCAAGCAACATCTTTGACACCCCTCACCCCAAGTGCATCTCATGTTCCTCA 484
Qy 307 isIlePheGlySerLeuLeuProArgProSerPheLeuTyrArgThr-IleGlnAspLeu 326
Db 485 AAGTGTATTACCTGAGCTCTT-AAGCCAGAAATTCATGTCTAAGTCTAATAGAGAT--- 540
Qy 327 GlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAlaProIleLeuThrAla 346
Db 541 -----TAGCTTCTATGCCAGCATTTGCCATGTTCTGTCACTATGACCCCACTGACCGCT 594
Qy 347 LeuAspIlePheValAspArgValSerAlaLeuProValValAsnGluCysGlyGln 366
Db 595 CTGGGCATC-----TCTGTACAGGATCTGCCA---GTGAATGAGAGAGGTGAG 639
Qy 367 ValValGlyLeuTyrSerArgPhe----- 374
Db 640 GTGGTGAACATCTATTCCACATTTGATGTTATCTGTGTAAGTCACTTCACTTCAGTCACGTCCA 699
Qy 374 ----- 374

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Db 700 ACTCTTTGGGATCCTCTGGACTGTAGCCGGTACAGGCTTCTCTGTCCAGGACTTCCAG 759  
Qy 375 -----AspValIleHisLeuAlaAala 381  
Db 760 GCAAGAACACTAGAGTGGGTACCATTTCTTCTCAGTGTATTCATCCATCAGGCAGCA 819  
Qy 382 GlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 401  
Db 820 TAAAGATCTACCAACACCTAGATGTGCTGTAGTCAAGCCCTGAAAGATCGATCAG 879  
Qy 402 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGluValIleAspArg 421  
Db 880 TACTTTAATGATAGCTCAAGTGGACCTGATGAGGCTCTGGAGACCTTCTCAGCAGG 939  
Qy 422 IleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuGly 441  
Db 940 CTAGTGAAGCAGGAGTACCGACTCGTGGTGGTGGATGAGATGATGATCAAGGGA 999  
Qy 442 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455  
Db 1000 ACTGTATACCATCTGTCTCCTGTAGACCCCTGGTGTCTACA 1041

RESULT 3  
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; Sequence 28770, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28770  
; LENGTH: 1321  
; TYPE: DNA  
; ORGANISM: Bovine 19866880603844  
US-10-750-623-28770

Alignment Scores:  
Pred. No.: 1.57e-32 Length: 1321  
Score: 500.50 Matches: 136  
Percent Similarity: 53.27% Conservative: 43  
Best Local Similarity: 40.48% Mismatches: 89  
Query Match: 20.83% Indels: 69  
DB: 7 Gaps: 5

US-10-070-794A-30 (1-464) x US-10-750-623-28770 (1-1321)

Qy 168 CysTyrAspAlaMetAlaThrSerSerLysLeuValIlePheAspThrMetLeuGluIle 187  
Db 101 TGTATGACCTGAGTCTCACAAGCTCCAAATTTGGTGTATTTGCTACTTCCCTGCAGGTA 160  
Qy 188 LysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAlaProLeu-TrpAspSe 207  
Db 161 TACAG-----TTGCCCTTCTGGATC 184  
Qy 207 rLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisAr 227  
Db 185 TAAAGCAAGGACTTGTGGCAGTGTGATATCACCAATTTTCATCAATATCTGCACTA 244  
Qy 227 gTyrTyrArgSerProLeuVal-GlnIleTyrGluIleGluGlnHisLysIleGluThr 247  
Db 245 TTACTATATGACGCTTGGTTCAGAGCTATGAGCTGGGAAGATACAAAATAGAACTT 304

Qy 247 rPArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIleSerProAsnAsps 267  
Db 305 GAAAGAGGTGTATATACAGGACTTCTTTAAACACCATTTGCTGCAATTTCTTCTTAATGCCA 364  
Qy 267 erLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuA 287  
Db 365 ACTTGTATATGCTGCTTTTTCATTAATTCAGAACAGATCCACAGGCTGCCAGTTGTTG 424  
Qy 287 spProValSerGlyAsnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuH 307  
Db 425 ACCAGATCAGCAACATCTTGTACACCTCACCCACAAGTGCATTTCTATGTTCTCTCA 484  
Qy 307 islePheGlySerLeuLeuProArgProSerPheLeuTyrArgThr-IleGlnAspLeu 326  
Db 485 AAGTGTATACCTGAGCTCTT-AAGCCAGAATTTATGTCTAAGTCTTAATAGAAGAT--- 540  
Qy 327 GlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAlaProIleLeuThrAla 346  
Db 541 -----TAGCTTCTATGCCAGCATTTGCCATTTCTGCACCTATGACCCACTGCACCGCT 594  
Qy 347 LeuAspIlePheValAspArgValSerAlaLeuProValValLeuGluCysGlyGln 366  
Db 595 CTGGCATC-----TCTGTACAGGATCTGCCA---GTGAATGAGGAAGGTCCAG 639  
Qy 367 ValValGlyLeuTyrSerArgPhe----- 374  
Db 640 GTGGTGAACATCTATTCCACATTTGATGTTATCTGTGCTAAGTCACTTTCAGTCAGCTCCA 699  
Qy 374 ----- 374  
Db 700 ACTCTTTGGGATCCTCTGGACTGTAGCCGGTACAGGCTTCTCTGTCCATGGGACTTCCAG 759  
Qy 375 -----AspValIleHisLeuAlaAala 381  
Db 760 GCAAGAACACTAGAGTGGGTACCATTTCTTCTCAGTGTATTCATCCATCAGGCAGCA 819  
Qy 382 GlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 401  
Db 820 TAAAGATCTACCAACACCTAGATGTGCTGTAGTCAAGCCCTGAAAGATCGATCAG 879  
Qy 402 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGluValIleAspArg 421  
Db 880 TACTTTAATGATAGCTTCAAGTCCGACCTGTCATGAGGCTCTGGAGACCTTTCTCAGCAGG 939  
Qy 422 IleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuGly 441  
Db 940 CTAGTGAAGCAGGAGTACCGACTCGTGGTGGTGGATGAGATGATGATCAAGGGA 999

## RESULT 4

US-11-128-061-330  
; Sequence 330, Application US/11128061  
; Publication No. US20060003958A1  
; GENERAL INFORMATION:  
; APPLICANT: Melville, Mark W.  
; APPLICANT: Charlebois, Timothy S.  
; APPLICANT: Mounts, William M.  
; APPLICANT: Hann, Louane E.  
; APPLICANT: Sinacore, Martin S.  
; APPLICANT: Leonard, Mark W.  
; APPLICANT: Brown, Eugene L.  
; APPLICANT: Miller, Christopher P.  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
; FILE REFERENCE: 01997.027701  
; CURRENT APPLICATION NUMBER: US/11/128,061  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US 60/570,425  
; PRIOR FILING DATE: 2004-05-11

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; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 330
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; US-11-128-061-330

Alignment Scores:
Pred. No.: 9.77e-30 Length: 568
Score: 461.50 Matches: 104
Percent Similarity: 59.32% Conservative: 36
Best Local Similarity: 44.07% Mismatches: 40
Query Match: 19.21% Indels: 57
DB: 8 Gaps: 2

US-10-070-794A-30 (1-464) x US-11-128-061-330 (1-568)
Qy 221 PheilleuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 3 TTTATCAACATCTCGCACCGATACATAAGTCGGCCTTGGTGCAGATCTATGAACGGAA 62
Qy 241 GlnHisIleValLeuThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 63 GAACACAGATAGAAACTTGGAGAGAGTATACCTACAGGACTCTTTAGACCCCTTGTGTC 122
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 123 TGCATTTCTCCAAATGC-CAGATCACTGAG----- 151
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 151 ----- 151
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 152 -----TTCCCAAGCCAGAAATTCATGTCT 175
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 176 AAGTCTCTGGAAGAGCTACAGATTGGCACCATTGCCAACATTGTCTATGTCCTGCTACTACC 235
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 236 ACACCTGTCTATGTGGCTCTAGGCATCTTTGTACAGACCAGAGTCTCTGCGCTGCTGTG 295
Qy 361 ValAsnGluCysGlyGlnValHisArgLeuValGlyLeuTyrSerArgPheAspValIle-HisLeuAl 380
Db 296 GTGGATGAG-----AAAGAATTGGC 316
Qy 380 aAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgTh 400
Db 317 AGCAGAAAAGACCTATAACAACCTGGATATATCTGTGACAAAAGCTCTACAAACCCGGTC 376
Qy 400 rLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAs 420
Db 377 TCACCTACTTTGAGGGTGTCTCAAGTGTCTATCTACAGGAGACTCTGGAGACTATCATTTAA 436
Qy 420 PArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLe 440
Db 437 TAGACTGTGTGAGCAGAGGTTTACCGCTGTGTGGTGTGGTGTGGATGAGACGCTGGTCAA 496
Qy 440 uGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455
Db 497 GGGCATCGATCGCTGTCGATATCTCGAGGCTCTCGAGGCTCTGTGTGCTCACA 542

RESULT 5
US-11-128-061-3972
; Sequence 3972, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
```



Db 437 TAGACTGGTGAAGCAGAGGTTACCGCTCTGGTGGTGGATGAGAACGACGTGGTCAA 496  
 Qy 440 uGlyValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455  
 Db 497 GGGCATCGTATCGTGTCCGATATCCTGCGAGCTCTGGTGTCTACA 542

## RESULT 6

US-11-128-049-330  
 ; Sequence 330, Application US/111128049  
 ; Publication No. US20060010513A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Melville, Mark W.  
 ; APPLICANT: Charlebois, Timothy S.  
 ; APPLICANT: Mounts, William M.  
 ; APPLICANT: Hann, Louane E.  
 ; APPLICANT: Sinacore, Martin S.  
 ; APPLICANT: Leonard, Mark W.  
 ; APPLICANT: Brown, Eugene L.  
 ; APPLICANT: Miller, Christopher P.  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
 ; FILE REFERENCE: 01997.027700  
 ; CURRENT APPLICATION NUMBER: US/11/128,049  
 ; PRIOR FILING DATE: 2005-05-11  
 ; PRIOR FILING DATE: 2004-05-11  
 ; NUMBER OF SEQ ID NOS: 7285  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 330  
 ; LENGTH: 568  
 ; TYPE: DNA  
 ; ORGANISM: Cricetus griseus  
 US-11-128-049-330

Alignment Scores:  
 Pred. No.: 9,77e-30 Length: 568  
 Score: 461.50 Matches: 104  
 Percent Similarity: 59.32% Conservative: 36  
 Best Local Similarity: 44.07% Mismatches: 40  
 Query Match: 19.21% Indels: 57  
 DB: 8 Gaps: 2

US-10-070-794A-30 (1-464) x US-11-128-049-330 (1-568)

Qy 221 PheileuValLeuHisArgTyrArgSerProLeuValGlnIleTyrGluileGlu 240  
 Db 3 TTTATCAACATCTGCGACCGATCTATAAGTCGGCTTGGTGCAGATCTATGACTGAA 62  
 Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260  
 Db 63 GAACACAGATAGAACTTGGAGAGGTATACCTACAGACTCTCTTTAAGCCCTTGTC 122  
 Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
 Db 123 TGCATTTCTCAAATGC-CAGATCACTGAG----- 151  
 Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
 Db 151 ----- 151  
 Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
 Db 152 -----TTCCCAAGCCAGAAATTCATGTCT 175  
 Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340  
 Db 176 AAGTCTCGAAGAGCTACAGATTGGCACCTATGCCAACATTGCTATGGTCCGTACTACC 235  
 Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
 Db 236 ACACCTGTCTATGGCTCTAGGCACTTTGTACAGACCAGAGTCTCTGCCCTCGCTGTG 295  
 Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle-HisLeuAl 380

Db 296 GTGCATGAG-----AAAGAATTTGGC 316  
 Qy 380 aAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGlnAlaLeuArgGlnArgTh 400  
 Db 317 AGCAGAAAAGACCTATAACACCTGGATATATCTGTGACAAAGCTCTACAAACCCGTC 376  
 Qy 400 rLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAs 420  
 Db 377 TCACACTTTGAGGGTGTCTCAAGTGTATCTACAGAGACTCTGGAGACTATCATTA 436  
 Qy 420 pArgIleAlaArgGlnValHisArgLeuValLeuValaspGluThrGlnHisLeuLe 440  
 Db 437 TAGACTGGTGGAAAGCAGAGGTTACCGCTCTGGTGGTGGATGAGAACGACGTGGTCAA 496  
 Qy 440 uGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455  
 Db 497 GGGCATCGTATCGTGTCCGATATCTGCGAGGCTCTGGTGTCTACA 542

## RESULT 7

US-11-128-049-3972  
 ; Sequence 3972, Application US/111128049  
 ; Publication No. US20060010513A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Melville, Mark W.  
 ; APPLICANT: Charlebois, Timothy S.  
 ; APPLICANT: Mounts, William M.  
 ; APPLICANT: Hann, Louane E.  
 ; APPLICANT: Sinacore, Martin S.  
 ; APPLICANT: Leonard, Mark W.  
 ; APPLICANT: Brown, Eugene L.  
 ; APPLICANT: Miller, Christopher P.  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
 ; FILE REFERENCE: 01997.027700  
 ; CURRENT APPLICATION NUMBER: US/11/128,049  
 ; PRIOR FILING DATE: 2005-05-11  
 ; PRIOR FILING DATE: 2004-05-11  
 ; NUMBER OF SEQ ID NOS: 7285  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 3972  
 ; LENGTH: 568  
 ; TYPE: DNA  
 ; ORGANISM: Cricetus griseus  
 US-11-128-049-3972

Alignment Scores:  
 Pred. No.: 9,77e-30 Length: 568  
 Score: 461.50 Matches: 104  
 Percent Similarity: 59.32% Conservative: 36  
 Best Local Similarity: 44.07% Mismatches: 40  
 Query Match: 19.21% Indels: 57  
 DB: 8 Gaps: 2

US-10-070-794A-30 (1-464) x US-11-128-049-3972 (1-568)

Qy 221 PheileuValLeuHisArgTyrArgSerProLeuValGlnIleTyrGluileGlu 240  
 Db 3 TTTATCAACATCTGCGACCGATCTATAAGTCGGCTTGGTGCAGATCTATGACTGAA 62  
 Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260  
 Db 63 GAACACAGATAGAACTTGGAGAGGTATACCTACAGACTCTCTTTAAGCCCTTGTC 122  
 Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
 Db 123 TGCATTTCTCAAATGC-CAGATCACTGAG----- 151  
 Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
 Db 151 ----- 151

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Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 152 -----TTCCCCAAGCCAGAAATTCATGCT 175
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
Db 176 AAGTCTCTGGAGAGCTACAGATTGGCACTATCCACATCTGTATGGTCCGTACTACC 235
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 236 ACACCTGTCTATGTGGCTCTAGGCATCTTTGTACAGACCGAGTCTCTGGCCTGCCTGTG 295
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle-HisLeuAl 380
Db 296 GTGGATGAG-----AAGAATTTGGC 316
Qy 380 aAlaGlnGlnThrTyrAenHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgTh 400
Db 317 AGCAGAAAGACCTATACACCTGGATATATCTGTGACAAAGCTCTACACACCGGTC 376
Qy 400 rLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAs 420
Db 377 TCACTACTTTGAGGGTGTCTCAAGTGTCTATCTACAGGAGACTCTGGAGACTATCATTA 436
Qy 420 pArgIleAlaArgGlnGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLe 440
Db 437 TAGACTGGTGAAGCAGAGGTTCCACCGTCTGGTGGTGGATGAGAACGACGTGGTCAA 496
Qy 440 uGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455
Db 497 GGGCATCGTATCGTCTCCGATATCTCGACGGCTCTGGTGTCTACA 542

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RESULT 8

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US-11-041-776-79
; Sequence 79, Application US/11041776
; Publication No. US20050272057A1
; GENERAL INFORMATION:
; APPLICANT: ABRAHAMSEN, MITCHELL
; APPLICANT: FREIJE, WADIAH
; TITLE OF INVENTION: SMALL SEGMENTS OF DNA DETERMINE ANIMAL IDENTITY AND
; TITLE OF INVENTION: SOURCE
; FILE REFERENCE: 34579-97951
; CURRENT APPLICATION NUMBER: US/11/041,776
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: 60/538,791
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/539,728
; PRIOR FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 79
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1500)
; OTHER INFORMATION: nucleotides 1501-3000 of PRKAG_STS3
US-11-041-776-79

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Alignment Scores:
Pred. No.: 7.85e-10 Length: 1500
Score: 234.50 Matches: 97
Percent Similarity: 25.28% Conservative: 16
Best Local Similarity: 21.70% Mismatches: 46
Query Match: 9.76% Indels: 290
DB: 8 Gaps: 6

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US-10-070-794A-30 (1-464) x US-11-041-776-79 (1-1500)

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Qy 84 ThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAlaAlaGlySer 103
Db 71 ACACCTTGGAGTGTCTGGGGAGGGGTACCTTCAGYACCTCTGGCCACGACGCTTAGA 130

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Qy 104 SerThrAspAspValGluLeuAlaThrGluPheProAlaThrGlu-AlaTyrGluCysG1 123
Db 131 TCTGGAAACAATGTGACACAGATCTCTGTGAGGCGATGCCAGNACGTGGGAGAGGCA 190
Qy 123 uLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAlaPro-PheP 143
Db 191 GACAGCAGGCTCATGTAGAGGCGAGGCCCGGG-----AGGCGCCCGGTGGA 235
Qy 143 roLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMetArgPheM 163
Db 236 AGAACCTTGGCTGGCAGGCGGACCTCTGAGGCGCAGGGAACG---ATTACACCTCAA--- 288
Qy 163 etGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePheAspT 183
Db 289 -----CTGTTCTCTC 298
Qy 183 hrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAlaAlap 203
Db 299 CGGCGCTCAG-ATCAAGAAGSCCTTCTTCTTGTGGTGGCCAACGGGCTCCGAGCGGCAC 357
Qy 203 roLeuTyrAspSerLysLysGlnSerPheVal----- 213
Db 358 CTTTGTGGGACAGCAAGACAGAGCTTCTGTGGTGTGAGGGGCTGGGGAGGAGGAGGT 417
Qy 213 ----- 213
Db 418 GGYGGGAAGGAATAGGGGACCTTGTGGGTGATTTCTAGGGCCGAGCTCTGACAYACC 477
Qy 213 ----- 213
Db 478 ACAGGCTTSAACCAAGCAGGCGGCTGCGTGGRRSGGAGGAGCATVTGACCCCGGT 537
Qy 213 ----- 213
Db 538 CTCCYGTGGCCRGCTGGGAGATCTCAACTGTAGGAGAGCTGTGACCAGCTGACCCCTCC 597
Qy 213 ----- 213
Db 598 AGCTCTACTACCCCAAGTCTCCTGTCGAGGTGCTTAAGTAAGAGAGACAGCGGAGGA 657
Qy 213 ----- 213
Db 658 AGGAAGTCAGAAAATAGAGAAGCAGGCGAGAGAGAGAGAAATCAACAGGGGAAGCATAA 717
Qy 213 ----- 213
Db 718 GAGGGACAACCCCATTTTTCAGGCACGCGGAGGGGCTGCCCTCTCTCTCTTTTGGCCAC 777
Qy 213 ----- 213
Db 778 CCTCAGTAAAGGATGTGGGCGAGGTTGGGGGAGGGGCGGCGGCTGACCCCATTTGCTCC 837
Qy 214 -----GlyMetLeuThrIleThrAspPheIleLeuValLeuHisA 227
Db 838 CCCCYYTTTGGCCCCSYACAGGGATGCTGACCATCACAGACTTCTATCTTGGTGTGCACC 897
Qy 227 rGlyTyrArgSerProLeu----- 233
Db 898 GCTATTACAGGTCCCCCT-GGTGAAGAGTGTCTGGGGGTCTGGGAACACCCATCTGGG 956
Qy 233 ----- 233
Db 957 CTGGGGTGAAGAGGATTACAGGGACCTCGCTGACTTTTGGGAGTTCCGTTGCTGCTTT 1016
Qy 234 --ValGlnIleTyrGluIleGluGlnHisLysIleGluThrTyrArg----- 248
Db 1017 AGGTCCAGATCTACGAGATTGAAGAAATAAGATTGAGACCTTGGAGGGGTGAGCAGGCGA 1076
Qy 248 ----- 248
Db 1077 GGGGACSGKCAAGGGGCTGAGGGGTGTGTGGTGTAGGTGTGTGGCCCAAGACCTCAGGGAG 1136

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QY 248 ----- 248
Db 1137 AGCATGCCAGTGGAGGTTTCTTGGAGGAAGCGGGAGGAGGTTGATCGGAGCCAGGGG 1196
QY 248 ----- 248
Db 1197 ATCTAAGGAGGAGACAGTCTGGGGTGGCCACCTGAGCGGGGGTGGTGGCCCTTTTG 1256
QY 249 -----
Db 1257 TGCTGATTTCTGGCTTCTTCTGACAGATCTACCTTCAAGGCTGCTTCAAGCCTCTGTCT 1316
QY 261 erlleSerProAsnAsp 266
Db 1317 CCATCTCTCCCAATGAC 1333

RESULT 9
US-11-000-688-851
; Sequence 851, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-K-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 851
; LENGTH: 3439
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; NAME/KEY: misc feature
; LOCATION: (1)-(3439)
; OTHER INFORMATION: collagen, type vi, alpha 2(COL6A2) gene.
US-11-000-688-851

Alignment Scores:
Pred. No.: 50 Length: 3439
Score: 113.50 Matches: 44
Percent Similarity: 39.74% Conservative: 16
Best Local Similarity: 29.14% Mismatches: 52
Query Match: 4.72% Indels: 39
DB: 8 Gaps: 8

US-10-070-794A-30 (1-464) x US-11-000-688-851 (1-3439)
QY 14 SerProAlaValThrSerSerGluArgIleArgGlyLysArgAlaLysAlaLeu 33
Db 1128 GCCCCGACGGTTACCCGGGGAAGCAGGAGTCCAGGGAGCGAGGACCAAGCGGCA 1187
QY 34 ArgTTPThrArgGlnLysSerValGluGluGluProGlyGlnGlyGluPro 53
Db 1188 AGGGGAGCC-----CTGGCGCCGAGGAGCGAGAGGCCCCCGGAGAAATCGGGGCCA 1241
QY 54 ArgSerArgProThrAlaGluSerThrGlyLeuGluAlaThrPheProLysThrPro 73
Db 1242 AGG-----GAAGCAAGGGGTATCAAGGCAACATGGAGCCCGAGGAAGTC 1286
QY 74 LeuAlaGlnAlaAspPro----AlaGlyValGlyThrProThrGlyTrpAspCysLeu 92
Db 1287 CTGCTGTGAAGGAGGACCAAGCGGGCGCTGGGC----- 1319
QY 93 ProSerAspCysThrAlaSerAlaAlaGlySerSerThrAspValGlu----- 109
Db 1320 CCGCGGACCCAAAGGCGAGCGGGGCGCAGGGGAGACCCCGGACCAAGGGGAGCCCGCAG 1379
```

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QY 110 -----LeuAlaThrGluPheProAlaThrGlu 118
Db 1380 GCAGCGATGCCCCCAAGGGGGAAGAGGACCTGCGCCCTGAGGGCCCCCGCG----- 1433
QY 119 AlaTTPGluCysGluLeuGluGlyLeuLeuGluGluArgPro-----AlaLeuCys 135
Db 1434 GCCTGG-----CTGGAGAGGTTGGCAACAAGAGGACCAAGGAGACCGAGGCTTGC 1484
QY 136 LeuSerProGlnAlaProPheProLysLeuGly 146
Db 1485 CTGACCCAGAGGCCCCCAGGAGGCTCTTGGGG 1517

RESULT 10
US-10-995-561-464
; Sequence 464, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 3175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-464

Alignment Scores:
Pred. No.: 80.2 Length: 3175
Score: 110.50 Matches: 44
Percent Similarity: 39.07% Conservative: 15
Best Local Similarity: 29.14% Mismatches: 53
Query Match: 4.60% Indels: 39
DB: 7 Gaps: 8

US-10-070-794A-30 (1-464) x US-10-995-561-464 (1-3175)
QY 14 SerProAlaValThrSerSerGluArgIleArgGlyLysArgAlaLysAlaLeu 33
Db 1159 GCCCCGACGGTTACCCGGGGAAGCAGGAGTCCAGGGAGCGAGGACCAAGCGGCA 1218
QY 34 ArgTTPThrArgGlnLysSerValGluGluGluGluProGlyGlnGlyGluPro 53
Db 1219 AGGGGAGCC-----CTGGCGCCGAGGAGCGAGGCCCCCGGAGAAATCGGGGCCA 1272
QY 54 ArgSerArgProThrAlaGluSerThrGlyLeuGluAlaThrPheProLysThrPro 73
Db 1273 AGG-----GAAGCAAGGGGTATCAAGGCAACARTGGAGCCCGAGGAAGTC 1317
QY 74 LeuAlaGlnAlaAspPro----AlaGlyValGlyThrProThrGlyTrpAspCysLeu 92
Db 1318 CTGCTGTGAAGGAGGACCAAGCGGGCGCTGGGC----- 1350
QY 93 ProSerAspCysThrAlaSerAlaAlaGlySerSerThrAspValGlu----- 109
Db 1351 CCGYGAGACCCAAAGGCGAGCGCGGCGGAGAGACCCCGGACCAAGGAGCGGCCAG 1410
QY 110 -----LeuAlaThrGluPheProAlaThrGlu 118
Db 1411 GCAGCGATGCCCCCAAGGGGGAAGAGGAGACCTGCGCCCTGAGGGGCCCCCGCG----- 1464
QY 119 AlaTTPGluCysGluLeuGluGlyLeuLeuGluGluArgPro-----AlaLeuCys 135
Db 1465 GCCTGG-----CTGGAGAGGTTGGCAACAAGGAGGACCAAGGAGCGGAGGCTTGC 1515
QY 136 LeuSerProGlnAlaProPheProLysLeuGly 146
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; AFFILIATION: CARLISLE, MICHAEL ET AL.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; SEQ ID NO 38
; LENGTH: 6594
; SOFTWARE: PatentIn version 3.3

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; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 78869
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-1

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Pred. No.:          9.57e+03      Length:      78869
Score:             109.50        Matches:     126
Percent Similarity: 34.36%       Conservative: 74
Best Local Similarity: 21.65%    Mismatches:  196
Query Match:       4.56%         Indels:     186
DB:                8            Gaps:        29

US-10-070-794A-30 (1-464) x US-11-075-185-1 (1-78869)

Qy      7 GluAenSerSerSerTrpProSerProAlaValThrSerSerSerGluArgGly 26
Db      48271 GAACGCTCCGTAGACACCCAGTCCGACTGCAGCGTCTCGAGCCAGCAATCCGAGT 48212

Qy      27 LysArgArgAlaLysAlaLeuArg-----
Db      48211 CGTCCGAGCTCAGCTTCGCTTCGAGCTCGGCGCGCGCCCTTCGCCGAACGGATCGACGG 48152

Qy      35 -----TrpThrArgGlnLysSerValGluGluGluProProGlyGlnGlyGlu 51
Db      48151 CGATCACCTTGGACCAAGCGGAGCTCTCCACGA-----GGGCTTCCAGCGCGGCGG 48098

Qy      52 GlyProArgSerArgProThrAlaGluSerThr-----GlyLeu 64
Db      48097 GCTCCGCTGCGAGACCAACGCCCGCGCGTGAAGATGGGGCTCCCTTTGAGGACGA 48038

Qy      65 GluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAlaGlyValGlyThr 84
Db      48037 GCAGCGCGAGCCCTTCCTCGCGGCGAGCAGCCGAGCTTCAACGCCG-----TCTCGA 47984

Qy      85 ProProThr-GlyTrpAspCysLeuProSerAspCysThrAlaSerAlaLagLysSerSe 104
Db      47983 CCGCGCTCGCGGG-----GCCCCCGCGGGAAGA 47954

Qy      104 rThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrpGluCysGluLe 124
Db      47953 CCGCGCGAAGTCCGTCTCGCGCGGTATGCGCG----- 47920

Qy      124 uGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAlaProPheProLy 144
Db      47919 -----CTCGAGATCCGCCCACTAGTCTC-----CCTCGTGATGT 47888

Qy      144 sLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleThrMetArgPheMetG1 164
Db      47887 CGTGGTCCCGAGGACCGACTGCGCATCTCGAGCCGGTGTGCTCCGAAACGACGCGC 47828

Qy      164 nGluHis-----ThrCysTrpAspAlaLys 172
Db      47827 TCGTACGAGGTACAGTTGATGATGACCCGGCGGAGCTTCGTCATCTCGCTCGATCTCAT 47768

Qy      172 tAlaThrSerSerLysLeuValIlePheAspThrMetLeuGluIleLysLysAlaPhePh 192
Db      47767 AGCCGCGTCCGTCGCGTTCGCGCGCGCGCAGTCCGAAACGCGTCGAG----- 47716

Qy      192 eAlaLeuValAlaAenGlyValArgAlaAlaProLeuTrpAspSerLysLysGlnSerPh 212
Db      47715 -CGATCCAGGACGCGGGTTCACATAGTCCGGTGCCTTCCTCGGCGCGCGGCGGCGG 47657

Qy      212 eValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisArgTyrTrpArgSerPr 232
Db      47656 CCACGGCGATCCGCGCGAGGTTCCGGTGTCTGTTCTGTCACGACGCGCGGGAATCGCC 47597
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RESULT 15

US-10-821-234-55/c

; Sequence 55, Application US/10821234

; Publication No. US20050255114A1

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; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 55
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-55

Alignment Scores:
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Score: 108.00 Matches: 48
Percent Similarity: 38.51% Conservative: 19
Best Local Similarity: 27.59% Mismatches: 60
Query Match: 4.49% Indels: 47
DB: 7 Gaps: 10

US-10-070-794A-30 (1-464) x US-10-821-234-55 (1-2736)

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Qy 22 -----GluArgIleArgGlyLysArgArgAlaLysAla 32
Db 2351 CGTTTGTGCTCGCGGTACGGTACAGTACGATCCCGGTCCCGGCCCGCTCGCGCTCG 2292
Qy 33 LeuArgTrpThrArgGlnLysSerValGluGlyGluPro----- 46
Db 2291 CTCGGTGGTTCGCGCGTCCGCTCCCGGTACAGTACCGGCCCTTTTCTCTGGACCGTCA 2232
Qy 47 -----ProGlyGlnGlyGluGlyProArgSer----- 59
Db 2231 GGGCCGTACGCCCGAGCTCCCTCGAGGCCCATCATCAGGGGGCGGTCACCGCCCTCG 2172
Qy 60 GluSerThrGlyLeuGluAlaThrPheProLysThrThr-ProLeuAlaGlnAlaAspPr 79
Db 2171 GAGGCTCCGCCATGTCCGCCACCGCCCGCCAGCTCCCTCTGCGCTCCCGCT---CC 2115
Qy 79 oAlaGlyValGlyThrProThrGlyTrpAspCysLeu-----ProSerAs 95
Db 2114 CGCCGGG---CCCGCTCCCGACTCCGGC-----TGCTTCGCGCTTCCGGTCCCGGTCC 2064
Qy 95 pCysThrAlaSerAlaAlaGlySerSerThr-----AspAspValGluLe 110
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Qy 110 uAlaThrGluPheProAlaThrGluAlaTrpGluCysGluLeuGluGluGlu 130
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Search completed: January 26, 2006, 08:30:49  
Job time : 1122.05 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 25, 2006, 22:06:06 ; Search time 7342.54 Seconds  
(without alignments)  
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Title: US-10-070-794A-30  
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Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2403	100.0	2115	40	US-10-070-794A-29
3	2398	99.8	1647	1	PCT-US03-34114A-73
4	2398	99.8	1647	33	US-09-826-581-5
5	2398	99.8	1647	54	US-10-695-614A-73
6	2398	99.8	1647	55	US-10-705-137-5
7	2398	99.8	2301	42	US-10-170-235-24862
8	2398	99.8	2781	1	PCT-US02-10818-30
					Sequence 1, Appli
					Sequence 29, Appli
					Sequence 73, Appli
					Sequence 5, Appli
					Sequence 73, Appli
					Sequence 5, Appli
					Sequence 24862, A
					Sequence 30, Appli

9	2398	99.8	2781	51	US-10-473-670-30	Sequence 30, Appl
10	2394	99.6	2109	40	US-10-070-794A-3	Sequence 3, Appl
11	2391	99.5	2314	1	PCT-US01-27760A-386	Sequence 386, App
12	2391	99.5	2314	1	PCT-US01-27760A-386	Sequence 386, App
13	2391	99.5	2314	29	US-09-687-527-420	Sequence 420, App
14	2391	99.5	2314	50	US-10-399-103-386	Sequence 386, App
15	2391	99.5	2314	50	US-10-399-103A-386	Sequence 386, App
16	2374	98.8	2301	79	US-60-452-680-32	Sequence 32, Appl
17	2374	98.8	2522	63	US-10-932-349-6	Sequence 6, Appl
18	2374	98.8	2522	81	US-60-500-337-7	Sequence 6, Appl
19	2374	98.8	2612	63	US-10-932-349-7	Sequence 7, Appl
20	2374	98.8	2612	81	US-60-500-337-7	Sequence 7, Appl
21	2372	98.7	2290	1	PCT-US03-34114A-75	Sequence 75, Appl
22	2372	98.7	2290	3	PCT-US03-02638A-4	Sequence 4, Appl
23	2372	98.7	2290	37	US-09-949-003C-782	Sequence 782, App
24	2372	98.7	2290	54	US-10-695-614A-75	Sequence 75, Appl
25	2372	98.7	2290	61	US-10-756-149-1235	Sequence 1235, Ap
26	2013	83.8	1873	66	US-11-075-134-3	Sequence 3, Appl
27	2011	83.7	1873	40	US-10-070-794A-27	Sequence 27, Appl
28	2011	83.7	1873	66	US-11-075-134-1	Sequence 1, Appl
29	2011	83.7	2022	40	US-10-070-794A-31	Sequence 31, Appl
30	2010	83.6	1873	66	US-11-075-134-7	Sequence 7, Appl
31	2007	83.5	1873	66	US-11-075-134-9	Sequence 9, Appl
32	2005	83.4	1873	66	US-11-075-134-5	Sequence 5, Appl
33	2002	83.3	1867	40	US-10-070-794A-1	Sequence 1, Appl
34	2000	83.2	1518	52	US-10-503-175-3	Sequence 3, Appl
35	1835	76.4	2612	42	US-10-144-771-21737	Sequence 21737, A
36	1835	76.4	2612	78	US-60-360-207-21737	Sequence 21737, A
37	1298.5	54.0	13413	37	US-09-949-003C-4472	Sequence 4472, Ap
38	1278.5	53.2	21722	63	US-10-932-349-18998	Sequence 18998, A
39	1278.5	53.2	21722	81	US-60-500-337-18998	Sequence 18998, A
40	1276	53.1	9100	52	US-10-503-175-5	Sequence 5, Appl
41	1276	53.1	26000	52	US-10-503-039-1	Sequence 1, Appl
42	1099	45.7	2297	77	US-60-278-232-699	Sequence 699, App
43	1098.5	45.7	2205	75	US-60-172-373-4233	Sequence 4233, Ap
44	1094	45.5	2223	1	PCT-US02-01048-13	Sequence 13, Appl
45	1094	45.5	2223	1	PCT-US03-34114A-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1

US-10-503-175-1

Sequence 1, Application US/10503175

GENERAL INFORMATION:

APPLICANT: Andersson, Leif

APPLICANT: Marklund, Stefan

TITLE OF INVENTION: Transgenic animals expressing prkag3

FILE REFERENCE: 11145-020DS1

CURRENT APPLICATION NUMBER: US/10/503,175

PRIOR FILING DATE: 2004-07-30

PRIOR APPLICATION NUMBER: PCT/IB03/00912

PRIOR FILING DATE: 2003-01-31

PRIOR APPLICATION NUMBER: US 60/353,430

PRIOR FILING DATE: 2002-02-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1470

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1470)

OTHER INFORMATION:

US-10-503-175-1

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Score: 2403.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

Length: 1470

Matches: 464

Conservative: 0

Mismatches: 0

Indels: 0

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Db 1456 GCGCTCGGGGCC 1467

## RESULT 2

US-10-070-794A-29  
; Sequence 29, Application US/10070794A  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSSON, Leif  
; APPLICANT: LOOFT, Christian  
; APPLICANT: KALM, Ernst  
; APPLICANT: MILAN, Denis  
; APPLICANT: ROBE, Annie  
; APPLICANT: ROGEL-GAILLARD, Claire  
; APPLICANT: IANNUCELLI, Nathalie  
; APPLICANT: GELLIN, Joel  
; APPLICANT: LE ROY, Pascale  
; APPLICANT: CHARDON, Patrick  
; TITLE OF INVENTION: VARIANTS OF THE GAMMA CHAIN OF AMPK, DNA SEQUENCES ENCODING  
; FILE OF INVENTION: THE SAME, AND USES THEREOF  
; FILE REFERENCE: 11145-023US1  
; CURRENT FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US/10/070,794A  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT/EP00/09896  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: EP 00401388.4  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: EP 99402236.3  
; PRIOR FILING DATE: 1999-09-10  
; NUMBER OF SEQ ID NOS: 42  
; SEQ ID NO 29  
; LENGTH: 2115  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1395)  
US-10-070-794A-29

## Alignment Scores:

Pred. No.:	9,51e-306	Length:	2115
Score:	2403.00	Matches:	464
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	40	Gaps:	0

US-10-070-794A-30 (1-464) x US-10-070-794A-29 (1-2115)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20

Db 1 ATGAGCTTCTAGAGCAAGAAAAACAGCAGCTCTATGGCCATCACCAGCTGTGACAGCAGC 60  
Qy 21 SerGluArgIleArgGlyLysArgArgAlaIleAlaLeuArgTrpThrArgGlnLysSer 40  
Db 61 TCAGAAAGATCCGTGGAAACAGAGGGCCAAAGCCCTTGAGATGGACAGAGCAGAGTCG 120  
Qy 41 ValGluGluGlyGluProProGlyGlnGlyProArgSerArgProThrAlaGlu 60  
Db 121 GTGGAGAGAGGGAGCCACAGCTCAGGGGAGAGTCCCGGTCCAGGCCAACCTGCTGAG 180  
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
Db 181 TCCACCGCGGTGGAGGCCACATTCCTCCCAAGACACACCTTGGCTCAAGCTGATCTCTGCC 240  
Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100  
Db 241 GGGGTGGGCACTCCACACAGAGGTGGGACTGCTCCCTCTGACTGTGTACAGCCCTCAGCT 300  
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120  
Db 301 GCAGGCTCCAGCACAGATGATGTGGAGTGGCCACGGAGTTCCTCCAGCCACAGAGGCTGG 360  
Qy 121 GluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAla 140  
Db 361 GAGTGTGAGCTAGAAGGCCCTGTGGAGAGAGAGGCTGCTGCTGTGCTGTCCCGCAGGCC 420  
Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160  
Db 421 CCATTTCCCAAGCTGGGCTGGGATGACAACTCGGAAACCCCGCGCCAGAGTCTACATG 480  
Qy 161 ArgPheMetGlnGlnHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180  
Db 481 CGCTTTCATGCGAGGAGCACACCTGCTACGATGCCATGSCAACTAGTCCCAAGTAGTCAATC 540  
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
Db 541 TTCGACACCATGCTGGAGATCAAGAAGGCCCTTCTTCTGCTGTGGTGGCAACGGTGTGCGG 600  
Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
Db 601 GCAGCCCTCTATGGGACACAAAGACAGAGCTTTTGTGGGATGCTGACCATCAGTAC 660  
Qy 221 PheIleLeuValLeuHisArgTyrTrpArgSerProLeuValGlnIleTyrGluIleGlu 240  
Db 661 TTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260  
Db 721 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTCTGCTC 780  
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
Db 781 TCCATCTCTCTAATGATAGCCCTTTTGAAGCTGTGTACACCTCTCATCAAGAACCGGATC 840  
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
Db 841 CATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
Db 901 CGCTGCTCAAGTTCCTGTCACATCTTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340  
Db 961 CGCATTATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGTGGAGACA 1020  
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal 360  
Db 1021 GCACCATCTCTGACTGACATGACATCTTTGTGGACCGGGTGTGTCTGCTGCTGCTGCTG 1080  
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380

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Db 1081 GTCACCAATGTGGTCAAGTCTGGGGCTCTATTCCCGCTTTGATGTGATTACCTGGCT 1140
Qy 381 AlaGlnGlnThrTyrAenHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1141 GCCCAGCAAACTTACACCACTTGGACATGATGTGGGAGAACCTTGGAGCAGAGACA 1200
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValLeuAsp 420
Db 1201 CTATGTCTGGAGGAGTCTTCTTCTCCAGCCCCACAGAGCTTGGGGGAAGTGTATCGAC 1260
Qy 421 ArgLeuAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1261 AGGATTGCTCGGAGCAGGTATACACAGGCTGGTGTGTAGTGACGACGACCATCTCTTG 1320
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1321 GGCGTGTCTCCCTCTCCGACATCTTTCAGGCACCTGGTGTCTCAGCCCTGTGGCATCGAT 1380
Qy 461 AlaLeuGlyAla 464
Db 1381 GCCCTCGGGCC 1392

RESULT 3
PCT-US03-34114A-73
; Sequence 73, Application PC/TUS0334114A
; GENERAL INFORMATION:
; APPLICANT: CuraGen Corporation at al.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE PROTEIN ACTIVITY
; FILE REFERENCE: Cura 951 (PCT)
; CURRENT APPLICATION NUMBER: PCT/US03/34114A
; CURRENT FILING DATE: 2003-10-27
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 73
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1486)
PCT-US03-34114A-73

Alignment Scores:
Pred. No.: 2.6e-305 Length: 1647
Score: 2398.00 Matches: 463
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.79% Indels: 0
Db: 1 Gaps: 1

US-10-070-794A-30 (1-464) x PCT-US03-34114A-73 (1-1647)
Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTyrProSerProAlaValThrSerSer 20
Db 95 ATGAGCTCTCCCTAGACAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACACGACG 154
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTyrThrArgGlnLysSer 40
Db 155 TCAGAAAGATCCGTGGGAACGGAGGGCCAAAGCCTTTGAGATGACAAGGCAGAGTCG 214
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 215 GTGGAGGAAGGGAGCCACAGGTGAGGGGAAGGTCCCGGTCCAGGCCAGCTGCTGAG 274
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 275 TCCACCGGGCTGGAGCCACATTCCTCCAGACACACACCTTGGCTCAAGCTGATCTCTGCC 334
Qy 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
Db 335 GGGGTGGGCACCTCCACCAACAGGTGGGAGTGCCTCCCTCTGAGCTGTACAGCCTCAGCT 394
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
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Db 395 GCAGGCTCCAGCACACATGATGTGGAGCTGGCCACGAGTTCCAGCCACAGAGGCGCTGG 454
Qy 121 GluCysGluLeuGlnGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 455 GAGTGTGAGCTAGAGGCTGTCTGGAGAGAGAGGCTGCTGCTGTGCTGCTGCTGCTGCTGCT 514
Qy 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 515 CCATTTCCTCCAGCTGGGCTGGGATGACAACTCCGGAAACCCCGGCCGAGATCTCATG 574
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerTysLeuValIle 180
Db 575 CGCTTCATGCAGGAGCACACCTGCTACGATGCCATGSCAACTAGTCCAAAGCTAGTCATC 634
Qy 181 PheAspThrMetLeuGluLeuLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 635 TTCGACACCATGCTGGAGATCAAGAAGGCTCTCTTTGCTGTGGTGGCCAAAGGTGTGCGG 694
Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 695 GCAGCCCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCAGTCAC 754
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 755 TTCACTCTGTGTGTGCATCGTACTACAGGTCCTCCCTGCTGCAGATCTATGAGATTGAA 814
Qy 241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 815 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTCTGGTC 874
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 875 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 934
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 935 CATGCCCTGCTGCTTCTTGACCCGGTGTCAAGCAACGCTACTCCACATCTCCACACAAA 994
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 995 CGCCTGCTCAAGTTCTCTGTCACATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1054
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
Db 1055 CGCCTATCCAAAGATTGGGGCATCGGCACATTCGAGACTTGGCTGTGGTGTGGAGACA 1114
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1115 GCACCCATCTGACTGCACTGGACATCTTTGTGGACCGGCTGTGTCTGCACTGCTGTG 1174
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1175 GTCAACGAATGTGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1235 GCCCAGCAAACTTACACCACTGAGCATGATGTGGGGAAGCCCTGAGGACGAGGACA 1294
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
Db 1295 CTATGTCTGGAGGAGTCTTCTTCTCCAGCCCCACGAGAGCTTGGGGGAAGTGTATCGAC 1354
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1355 AGGATTGTCTGGAGCAGGTATACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1414
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1415 GCGGTGGTCTCCCTCTCTCGACATCTTTCAGGCACCTGGTGTGTGTGTGTGTGTGTGTGT 1474
Qy 461 AlaLeuGlyAla 464
```

Db 1475 GCCCTCGGGCC 1486

RESULT 4

US-09-826-581-5

; Sequence 5, Application US/09826581

; GENERAL INFORMATION:

; APPLICANT: Andersson, Leif

; APPLICANT: Luthman, L. Holger

; APPLICANT: Marklund, Stefan

; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT

; FILE REFERENCE: 11145-007001

; CURRENT APPLICATION NUMBER: US/09/826.581

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: US 60/195,665

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 1647

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (20)...(1486)

US-09-826-581-5

Alignment Scores:

Pred. No.: 2,66-305 Length: 1647

Score: 2398.00 Matches: 463

Percent Similarity: 99.78% Conservative: 0

Best Local Similarity: 99.78% Mismatches: 1

Query Match: 99.79% Indels: 0

DB: 33 Gaps: 0

US-10-070-794A-30 (1-464) x US-09-826-581-5 (1-1647)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20

Db 95 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATCGGCATCACCAGCTGTGACAGCAGC 154

Qy 21 SerGluArgLeuArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40

Db 155 TCAGAAAGATCCCTGGGAACGGAGGGCCAAAGCCTTGAGATGGACAGCAGAGTCG 214

Qy 41 ValGluGluGluProProGlyGlnGlyGlnGlyProArgSerArgProThrAlaGlu 60

Db 215 GTGAGGAAGGGAGCCAGCAGCTCAGGGGAGAGTCCCGGTCCAGCCAGCTGTCTAG 274

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80

Db 275 TCCACCGGGCTGGAGGGCCACATTCGCCAAGACCACACCTTTGGCTCAAGCTGATCTCTGCC 334

Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100

Db 335 GGGGTGGGCACTCCACCAACAGGTGGAGTGCCTCCCTCTGACTGTACAGCTCAGCT 394

Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120

Db 395 GCAGGCTCCAGCAGATGATGGAGCTGGCCAGCAGGATTCACAGCCACAGAGGCTGG 454

Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140

Db 455 GAGTGTGAGCTAGAAAGCCCTGCTGGAAGAGAGGCTGCCCTGTGCTGTCCCGCAGGCC 514

Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnLysMet 160

Db 515 CCATTTCCCAAGCTGGGCTGGATGACAACTGGGAACCCGGCCGCGCCAGATCTCATG 574

Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValLe 180

Db 575 CGCTTCATGCAGGAGCACCTGCTACGATGCCATGCTAGCTCCAGCTAGCTATC 634

Qy 181 PheAspThrMetLeuGluLeuLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200

Db 635 TTCACACCATGCTGGAGATCAAGAGGCTTCTTTGCTCTGGTGGCCACCGTGTGGG 694

Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrLeuThrAsp 220

Db 695 GCAGCCCTCTTAGGGACAGCAAGACAGAGCTTTGTGGGATGCTGACCATCAGTAC 754

Qy 221 PheLeuLeuValLeuHisArgTyrTyrArgSerProLeuValGlnLysLeuGluLeu 240

Db 755 TTCATCTGCTGCTGATCGTCTACTACAGGTCCCTCCCTGGTCCAGATCTATGAGATTGAA 814

Qy 241 GlnHisLysLeuGluThrTrpArgGluLeuTyrLeuGlnGlyCysPheLysProLeuVal 260

Db 815 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTCTTCAAGCCCTCTGCTC 874

Qy 261 SerLeuSerProAsnAspSerLeuPheGluAlaValTyrThrLeuLysLysAsnArgLys 280

Db 875 TCCATCTCTCTAATGATGACCTGTTTGAAGCTGTCTACACCTCATCAAGACCGGATC 934

Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisLysLeuThrHisLys 300

Db 935 CATCGCTGCTGCTGTTCTTGACCCGGTGTGAGCAACGCTACTCCACATCTCCACACAAA 994

Qy 301 ArgLeuLeuLysPheLeuHisLysLysPheGlySerLeuLeuProArgProSerPheLeuTyr 320

Db 995 CGCTGCTCAAGTTCTCTGACATCTTTGGTTCCCTGCTGCCCGGCTCTCTCTCTCTAC 1054

Qy 321 ArgThrLeuGlnAspLeuGlyLysGlyThrPheArgAspLeuAlaValLeuGluThr 340

Db 1055 CGCATATCCAGATTGGGACATCGGCATCTCCAGACTTGGCTGTGGTCTGGAGACA 1114

Qy 341 AlaProLeuLeuThrAlaLeuAspLysPheValAspArgValSerAlaLeuProVal 360

Db 1115 GCACCATCTGACTGCTGACATCTTTGTGGACCGGCTGTGTGCTGCTGCTGCTG 1174

Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValLysLeuAla 380

Db 1175 GTCAACGAATGTGCTGAGTGTGGGCTCTATTTCGCGCTTTGATGTGATTTACCTGGCT 1234

Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400

Db 1235 GCCAGCAAACTTACAAACCTTGGACCTGGACNTGAGTGTGGGAGAGCCCTGAGCAGAGACA 1294

Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValLysAsp 420

Db 1295 CTATGCTGGAGGAGTCTCTTTCTGCGACCCCGCAGAGCTTGGGGAAGTGTGCTGAC 1354

Qy 421 ArgLeuAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440

Db 1355 AGGATTGCTCGGAGCAGGTTACACAGGCTGTGTAGTGGACGAGACCCAGCATCTCTTG 1414

Qy 441 GlyValValSerLeuSerAspLysLeuGlnAlaLeuValLeuSerProAlaGlyLysAsp 460

Db 1415 GGGTGTGCTCTCCCTCTCCGACATCTTTCAGGCACTGTGTGCTGCTGCTGCTGCTG 1474

Qy 461 AlaLeuGlyAla 464

Db 1475 GCCCTCGGGCC 1486

RESULT 5

US-10-695-614A-73

; Sequence 73, Application US/10695614A

; GENERAL INFORMATION:

; APPLICANT: Berghs, Constance

; APPLICANT: Catterton, Elina

; APPLICANT: Ellerman, Karen E.

; APPLICANT: Ort, Tatiana A.

; APPLICANT: Rieger, Daniel K.

; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE PROTEIN ACTIVITY

; FILE REFERENCE: Cura 951 [PCT]

; CURRENT APPLICATION NUMBER: US/10/695,614A

; CURRENT FILING DATE: 2003-10-27

; NUMBER OF SEQ ID NOS: 151

; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 73  
; LENGTH: 1647  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (20) .. (1486)  
US-10-695-614A-73

Alignment Scores:  
Pred. No.: 2,6e-305 Length: 1647  
Score: 2398.00 Matches: 463  
Percent Similarity: 99.78% Conservative: 0  
Best Local Similarity: 99.78% Mismatches: 1  
Query Match: 99.79% Indels: 0  
DB: Gaps: 0

US-10-070-794A-30 (1-464) x US-10-695-614A-73 (1-1647)

```
Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20
Db 95 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACGAGCAGC 154
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 155 TCAGAAAGAAATCCGTGGGAAACGGAGGGCCAAAGCCTTGAGATGGCAAGGCAAGATCG 214
Qy 41 ValGluGluGlyGluProProGlyGlnGlyProArgSerArgProThrAlaGlu 60
Db 215 GTGAGGAGGAGGAGCCACAGGTTCAGGGGAGAGGTCCCGGTTCAGGCCAGCTGTGAG 274
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 275 TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACACACACCTTGGCTCAAGCTGATCCTGCC 334
Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
Db 335 GGGGTGGGCACCTCCACCAACAGGGTGGGACTGCGCTCCCTCTGACTGTACAGCCTCAGCT 394
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db 395 CGAGCTCCAGCAGCAGATGATGGAGTGGCCACGGAGTTCACGACCCACAGAGGCCCTGG 454
Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 455 GAGTGTGAGCTAGAAGGCTGCTGGAAGAGAGGCTGCGCTGTGCTGTCCCGCAGGCC 514
Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 515 CCATTTCCTCAAGCTGGGTGGGATGACGAACCTGCGGAAACCCGGCGCCAGATCTACATG 574
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
Db 575 CGCTTCATCAGGAGCAGCACCTGTACAGTGCATGGCACTAGCTCCAGCTAGTCAATC 634
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 635 TTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGTCTGTGGTGGCCAAAGGTGTGGG 694
Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 695 CGAGCCCTCTATGGGACGACGAAGAGCAGAGCTTTGTGGGATGCTGACCATCACTGAC 754
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 755 TTATCTCTGGTGTGATCGCTACTACAGTTCCTCCCTGGTCCAGATCTATGAGATTGAA 814
Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 815 CAACATAAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGTCTCAAGCCTCTGGTC 874
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
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Db 875 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 934
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 935 CATCGCTGCTGTTCTTGACCGGTGTTCAGGCAACGTACTCCACATCTCCACACAAA 994
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 995 CGCTGCTCAAGTTCCTGACATCTTTGGTTCCCTGTCTGCCCGGCCCTCTTCTCTCTAC 1054
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
Db 1055 CGCACTATCCAAAGTTTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGGAGACA 1114
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1115 GCACCATCTGACTGCTGACATGGACATCTTTGTGTGACCGGGCTGTCTGCACCTGCCTGTG 1174
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1175 GTCAACGAATGTGTGAGTGTGGGCTCTATTTCCTGCTTGTGATTCACCTGGCT 1234
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuA:rgGlnArgThr 400
Db 1235 GCCCAGCAACCTACACCACTGGACATGATGATGGGAGAGCCCTGAGCAGAGGACA 1294
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
Db 1295 CTATGTCTGGAGGAGTCTCTTCTGTCAGCCCCACGAGAGCTTGGGGGAAGTATCGAC 1354
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1355 AGGATTCTCGGAGCAGGTACACAGGCTGGTGTGTAGTGGACGAGAGCCAGCATCTCTTG 1414
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1415 GGCTGTGCTCCCTCTCCGACATCTTCAGGACCTGCTGCTCAGCCCTGCTGGCATCGAT 1474
Qy 461 AlaLeuGlyAla 464
Db 1475 GCCCTCGGGGCC 1486
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## RESULT 6

US-10-705-137-5  
; Sequence 5, Application US/10705137  
; GENERAL INFORMATION:  
; APPLICANT: Andersson, Leif  
; APPLICANT: Luthman, L. Holger  
; APPLICANT: Marklund, Stefan  
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT  
; FILE REFERENCE: 11145-007002  
; CURRENT APPLICATION NUMBER: US/10705,137  
; CURRENT FILING DATE: 2003-11-10  
; PRIOR APPLICATION NUMBER: US 09/826,581  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: US 60/195,665  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1647  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (20) ... (1486)  
US-10-705-137-5

Alignment Scores:  
Pred. No.: 2,6e-305 Length: 1647  
Score: 2398.00 Matches: 463  
Percent Similarity: 99.78% Conservative: 0

Best Local Similarity: 99.78% Mismatches: 1  
Query Match: 99.79% Indels: 0  
DB: 55 Gaps: 0  
US-10-070-794A-30 (1-464) x US-10-705-137-5 (1-1647)

QY 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
DB 95 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCGAGTGTGACGAGC 154  
QY 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
DB 155 TCAGAAAGATCCGTGGAAACGGAGGCCAAGCCCTTGATGGACACAGCAGAGTCG 214  
QY 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
DB 215 GTGAGGAGAGGGAGCCACAGGTTCAGGGGAGGTCCCGGTCCAGGCCAGCTGTGAG 274  
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
DB 275 TCACACGGGCTGGAGGCCACATTCGCCAAGACACACCCCTTGGCTCAAGCTGATCCTGCC 334  
QY 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100  
DB 335 GGGGTGGGCACTCCACACAGGGTGGGACTGCTCCCTCTGACTGTACAGCTCAGCT 394  
QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120  
DB 395 GCAGGCTCCAGCACAGATGATGGAGCTGCCACGGAGTTCACGACCACAGAGGCTGG 454  
QY 121 GluCysGluLeuGluGlyLeuLeuGluGluGluArgProAlaLeuCysLeuSerProGlnAla 140  
DB 455 GAGTGTGAGCTAGAAGCCCTGCTGGAAAGAGAGGCTGCCCTGTGCTGCTGCCGCGAGCC 514  
QY 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160  
DB 515 CCATTTCCCAAGCTGGCTGGGATGACAACTCGGAAACCCGGCCCGCCAGATCTCATG 574  
QY 161 ArgPheMetGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuValIle 180  
DB 575 CGCTTCATGCAGGAGCACACTGCTACGATGCCATGCACTAGCTCCAAAGCTAGTCATC 634  
QY 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
DB 635 TTCGACACCATGCTGGAGATCAAGAGGCCCTCTCTTCTGCTGTGGGCCAACCGTGTGCGG 694  
QY 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
DB 695 GCAGCCCTCTATGGGACACAGAGCAGAGCTTTGTGGGATGCTGACCATCAGCTGAC 754  
QY 221 PheIleLeuValLeuHisArgTyrTrpArgSerProLeuValGlnIleTyrGluIleGlu 240  
DB 755 TTCATCTCTGTGCTGCTACTACAGGTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 814  
QY 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260  
DB 815 CAACATAAGATTGAGACCTGGAGGAGATCTAGCTGCAAGGCTGCTTCAAGCCCTGCTGTC 874  
QY 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
DB 875 TCATCTCTCTAATGATACCTGTTGAAGCTGTCTACACCTCATCAAGAACCCGGATC 934  
QY 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
DB 935 CATCGCTGCTGCTTCTTGAACCGGTGTGAGGCAACGCTACTCCACATCTCTCACACAAA 994  
QY 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
DB 995 CGCTGCTCAAGTCTCTGACATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1054  
QY 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340  
DB 1055 CGCATTATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGGGAGACA 1114

QY 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
DB 1115 GCACCCATCTGACTGCACTGGACATCTTTGTGGACCGCGTGTGTCTGCACTGCCCTGTG 1174  
QY 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380  
DB 1175 GTCAACGAATGTGTGAGTCGTGAGTCGTGGGCTCTATTCCCGCTTTGATGTTCACCTGGCT 1234  
QY 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
DB 1235 GCCCAGCAACCTTCAACCACTTGGACATGATGTGTGGAGAGCCCTTGAGGCAGAGGACA 1294  
QY 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420  
DB 1295 CTATGTCTGGAGGGAGTCTTCTCTCCAGCCCCACGAGAGCTTGGGGAGTGTATCGAC 1354  
QY 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
DB 1355 AGATTGCTCGGAGCAGGTACACAGGCTGTGTAGTGACGAGACCCAGCATCTCTTG 1414  
QY 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460  
DB 1415 GGGTGGTCTCCCTCTCCGACATCTTTCAGGCACTGGTGTCTCAGCCCTGCTGGCATCGAT 1474  
QY 461 AlaLeuGlyAla 464  
DB 1475 GCCTCGGGGCC 1486

RESULT 7  
US-10-170-235-24862  
; Sequence 24862, Application US/10170235  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN  
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF  
; FILE REFERENCE: CL001380  
; CURRENT APPLICATION NUMBER: US/10/170,235  
; CURRENT FILING DATE: 2003-03-17  
; NUMBER OF SEQ ID NOS: 42514  
; SEQ ID NO 24862  
; LENGTH: 2301  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-170-235-24862

Alignment Scores:  
Pred. No.: 5,24e-305 Length: 2301  
Score: 2398.00 Matches: 463  
Percent Similarity: 99.78% Conservative: 0  
Best Local Similarity: 99.78% Mismatches: 1  
Query Match: 99.79% Indels: 0  
DB: 42 Gaps: 0

US-10-070-794A-30 (1-464) x US-10-170-235-24862 (1-2301)

QY 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
DB 95 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCGAGTGTGACGAGC 154  
QY 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
DB 155 TCAGAAAGATCCGTGGAAACGGAGGCCAAGCCCTTGATGGACACAGCAGAGTCG 214  
QY 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
DB 215 GTGAGGAGAGGGAGGCCACAGGTTCAGGGGAGGTCCCGGTCCAGGCCAGCTGTGAG 274  
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
DB 275 TCACACGGGCTGGAGGCCACATTCGCCAAGACACACCCCTTGGCTCAAGCTGATCCTGCC 334  
QY 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100



Db 335 GGGTGGGCACTCACCAACAGGCTGGGACTGCTCCCTCTGACTGTACAGCTCAGCT 394  
Qy 101 AlaGlySerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120  
Db 395 GCAGGCTCCAGCACAGATGATGGAGCTGGCCACGAGTTCACAGCCACAGAGGCGCTGG 454  
Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGluAla 140  
Db 455 GAGTGTGAGCTAGAAGCGCTGCTGAAAGAGAGGCGCTCCCTGTGCTGCTCCCGCAGGCC 514  
Qy 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160  
Db 515 CCATTTCCCAAGCTGGGCTGGGATGAGCACTGGGAACCCGGCGCCAGATCTACATG 574  
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180  
Db 575 CGCTTCATGCAGGAGCACACCTGTACGATGCCATGGCACTAGCTCCAAGTAGTCATC 634  
Qy 181 PheAspThrMetLeuGluIleLysGlyAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
Db 635 TTCGACACCATGCTGGAGATCAAGAGCGCTTCTTGTCTGTGGCCAAAGCGGTGTCGG 694  
Qy 201 AlaAlaProLeuTyrAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
Db 695 GCAGCCCTCTATGGGACAGCAAGCAGAGCTTTGTGGGATGCTGACCATCCTGAC 754  
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240  
Db 755 TTCATCTGTGTGCTGCATCGTACTACAGGTCCCCCTGGTCCAGATCTATGAGATTGAA 814  
Qy 241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260  
Db 815 CAACATAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTCTGTC 874  
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
Db 875 TCCATCTCTCAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 934  
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
Db 935 CATCGCTGCTGCTTGTACCGCTGTGCGCAAGCTACTCCACATCTCCACACACAAA 994  
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
Db 995 CGCTGTCTCAAGTTCTCTGCATCTTTTGGTTCCTGTGCTGCGCGCGCTCTCTCTCTAC 1054  
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340  
Db 1055 CGCACTATCCAAGATTGGGCATCGGCATTCGAGACTTGGCTGTGCTGTGGAGACA 1114  
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
Db 1115 GCACCATCTCTGACTGCATGGACATCTTTTGGACCGCGGTGTCTGTGCACTGCTGTG 1174  
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380  
Db 1175 GTCAACGAATGTGTCAGTCTGCGGCTCTATTTCCTGCTTGTGATGTCACTGCTGCT 1234  
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
Db 1235 GCCCAGCAAACTCAACCACTGGACATGATGTGGAGAGAGCCCTGAGCGAGAGGACA 1294  
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420  
Db 1295 CTATGCTGGAGGAGTCTTTCTCTGCCAGCCCGCAGAGCTTGGGGAGTGTGATCGAC 1354  
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
Db 1355 AGGATTGCTCGGAGCAGGTACACAGGCTGTGTGTGTGAGCAGACCCAGCATCTCTTG 1414  
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460

Db 1415 GGGTGGTCTCTCCCTCTCCGACATCTTTCAGGCACTGGTGTCTCAGCCCTGCTGGCATCGAT 1474  
Qy 461 AlaLeuGlyAla 464  
Db 1475 GCCCTCGGGGCC 1486

## RESULT 8

PCT-US02-10818-30  
; Sequence 30, Application PC/TUS0210818

; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: Recipon, Shirley A.  
; APPLICANT: Burrill, John D.  
; APPLICANT: Marcus, Gregory A.  
; APPLICANT: Zingler, Kurt A.  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Thornton, Michael  
; APPLICANT: Borowsky, Mark L.  
; APPLICANT: Baughn, Mariah R.  
; APPLICANT: Burford, Neil  
; APPLICANT: Lee, Soo Yeun  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hafalia, April J.A.  
; APPLICANT: Yao, Monique G.  
; APPLICANT: Ramkumar, Jayalaxmi  
; APPLICANT: Wadia, Narinder K.  
; APPLICANT: Lu, Dyung Aina M.  
; APPLICANT: Arvizu, Chandra S.  
; APPLICANT: Ison, Craig H.  
; APPLICANT: Ding, Li  
; APPLICANT: Lu, Yan  
; APPLICANT: Gururajan, Rajagopal  
; APPLICANT: Walsh, Roderick T.  
; APPLICANT: Gandhi, Ameena R.  
; APPLICANT: Swarnakar, Anita  
; APPLICANT: Forsythe, Ian J.  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice K.  
; APPLICANT: Elliott, Vicki S.  
; APPLICANT: Lee, Sally  
; TITLE OF INVENTION: KINASES AND PHOSPHATASES  
; FILE REFERENCE: PI-0398 PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/10818  
; CURRENT FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/282,119; 60/283,588; 60/283,759; 60/285,589; 60/287,037; 60/287,036; 60/288,608; 60/288,712; 60/289,909; 60/292,246  
; PRIOR FILING DATE: 2001-04-06; 2001-04-13; 2001-04-13; 2001-04-20; 2001-04-27;  
; 2001-04-27; 2001-05-04; 2001-05-04; 2001-05-09; 2001-05-17  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PERL Program  
; SEQ ID NO 30  
; LENGTH: 2781  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 7474666CB1  
PCT-US02-10818-30

Alignment Scores:  
Pred. No.: 7,8e-305 Length: 2781  
Score: 2398.00 Matches: 463  
Percent Similarity: 99.78% Conservative: 0  
Best Local Similarity: 99.78% Mismatches: 1  
Query Match: 99.79% Indels: 0  
DB: 1 Gaps: 0

US-10-070-794A-30 (1-464) x PCT-US02-10818-30 (1-2781)

Qy 1 MetSerPheLeuGluGlnGlnSerSerSerTyrProSerProAlaValThrSerSer 20  
Db 96 ATGAGCTCTTAGACAAAGAAACAGCAGCTCATGGCCATCACCGAGTGTGTGACGACG 155



QY 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTfTrpThrArgGlnLysSer 40  
DB 156 TCAGAAAGATCCCGTGGGAAACGAGGCGCCAAAGCCTTGAGATGGACAGAGTCG 215  
QY 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
DB 216 GTGAGGAGAGGGAGGACCAAGGTTCAGGGGAGAGTCCCGGTCCAGCCAGCTGTGAG 275  
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
DB 276 TCCACCGGCTGGAGGCCACATTCCTCCCAAGACACACCTTGGCTCAAGCTGATCTCTGCC 335  
QY 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100  
DB 336 GGGGTGGGCACTCCACCAACAGGTGGGACTGCCCTCCCTCTGACTGTACAGCCTCAGCT 395  
QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120  
DB 396 GCAGGCTCCAGCACAGATGATGGAGCTGGCCACGAGTTCCAGCCACAGAGGCTCGG 455  
QY 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140  
DB 456 GAGTGTGAGCTAGAGGCTGTCTGGAAGAGAGGCTGCCCTGTGCTGCTGCCCGCAGGCC 515  
QY 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160  
DB 516 CCATTTCCCAAGCTGGGCTGGGATGAGCAATGCGGAAACCCGCGCCGAGATCTACATG 575  
QY 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180  
DB 576 CGCTTCATGAGGAGCACACTGTCTAGTCCATGCACTAGCTCAAGCTAGTATC 635  
QY 181 PheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyValArg 200  
DB 636 TTCGACACCATGCTGGAGATCAAGAAGCCCTCTTCTGCTGTGGTGGCAAGGTGTGGG 695  
QY 201 AlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
DB 696 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGATGCTGACCATCATCTGAC 755  
QY 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240  
DB 756 TTATCTGTGTGTGATCTGCTACTACAGTTCCTGCTGGTGGTGGATCTATGAGATGAA 815  
QY 241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260  
DB 816 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTCTTCAAGCCTCTGTCTC 875  
QY 261 SerIleSerProLeuAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
DB 876 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCTCATCAAGAACCGGATC 935  
QY 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
DB 936 CATCGCTGCTGCTGTCTTGACCGGTGTGAGGCAACGTCTCACATCTCTCACACACAA 995  
QY 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
DB 996 CGCTGTCTCAAGTCTCTGACATCTTTGTTCTGCTGCTGCCCGGCTCTCTCTCTAC 1055  
QY 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340  
DB 1056 CGCACTATCAAGATTTGGGCTGCGCACATTCGAGACTTGGCTGTGGTGTCTGGAGACA 1115  
QY 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
DB 1116 GCACCCATCTGATCTGACCTGGACATCTTTGTGACCGGCTGTCTGCACTGCTGTG 1175  
QY 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380  
DB 1176 GTCAACGAATGTGGTCAAGTGTGGGCTCTATTCGCGCTTTGATGTGATTCACCTGGCT 1235  
QY 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400

DB 1236 GCCCAGCAAACTTACACACCTGGACATGATGTGGGAGAACCTTGGAGCGAGGACA 1295  
QY 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp 420  
DB 1296 CTATGTCTGGAGGAGTCTCTTCTCCAGCCCCCAGAGAGCTTGGGGGAAGTGTATCGAC 1355  
QY 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
DB 1356 AGGATTGCTCGGAGCAGGTACACAGGCTGGTGTCTAGTGGACGAGACCCAGCATCTCTTG 1415  
QY 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460  
DB 1416 GGGGTGTCTCTCCCTCTCCGACATCTTTCAGGCACTGTGTCTCAGCCCTGTCTGGCATCGAT 1475  
QY 461 AlaLeuGlyAla 464  
DB 1476 GCCCTCGGGGCC 1487  
RESULT 9  
US-10-473-670-30  
; Sequence 30. Application US/10473670  
; GENERAL INFORMATION:  
; APPLICANT: RECIPON, Shirley A.; BURRILL, John D.;  
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;  
; APPLICANT: TANG, Y. Tom; THORNTON, Michael;  
; APPLICANT: BOROWSKY, Mark L.; BAUGHN, Mariah R.;  
; APPLICANT: BURFORD, Neil; LEE, Soo Yeun;  
; APPLICANT: BANDMAN, Olga; HAPALIA, April J.A.;  
; APPLICANT: YAO, Monique G.; RAMKUMAR, Jayalaxmi;  
; APPLICANT: CHAWLA, Nandira K.; LU, Byung Aina M.;  
; APPLICANT: ARVIZU, Chandra S.; ISON, Craig H.;  
; APPLICANT: DING, Li; LU, Yan;  
; APPLICANT: GURURAJAN, Rajagopal; WALSH, Roderick T.;  
; APPLICANT: GANDHI, Ameena R.; SWARNAKAR, Anita;  
; APPLICANT: FORSYTHE, Ian J.; YUE, Henry;  
; APPLICANT: AD-YOUNG, Janice K.; ELLIOTT, Vicki S.;  
; APPLICANT: LEE, Sally  
; TITLE OF INVENTION: KINASES AND PHOSPHATASES  
; FILE REFERENCE: PI-0198 USN  
; CURRENT APPLICATION NUMBER: US/10/473,670  
; CURRENT FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: PCT/US02/10818  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: US 60/282,119  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/283,588  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/283,759  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/285,589  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: US 60/287,037  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/287,036  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/288,608  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: US 60/288,712  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: US 60/289,909  
; PRIOR FILING DATE: 2001-05-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PERL Program  
; SEQ ID NO 30  
; LENGTH: 2781  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 7474666CB1  
US-10-473-670-30

## Alignment Scores:

Pred. No.: 7,8e-305 Length: 2781  
Score: 2398.00 Matches: 463  
Percent Similarity: 99.78% Conservative: 0  
Best Local Similarity: 99.78% Mismatches: 1  
Query Match: 99.79% Indels: 0  
DB: 51 Gaps: 0

US-10-070-794A-30 (1-464) x US-10-473-670-30 (1-2781)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
Db 96 ATGAGCTCTCCCTAGAGCAGAGAAACAGCAGCTCATGCGCATCACCGCTGTGACAGCAGC 155  
Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
Db 156 TCAGAAAGATCCCTGGGAAACGAGGCGCCAAAGCCTTGAGATGGACAAAGCAGAGTCG 215  
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
Db 216 GTGAGGAAGAGGAGCCACCAAGGTGAGGGGAAAGGTCCTCCGCTCAGGCGCAGCTGAG 275  
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
Db 276 TCCACCGGCTGGAGGCCACATTCCTCCAGACCAACCTTGGCTCAAGCTGATCTCTGCC 335  
Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100  
Db 336 GGGGTGGGCACTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTATACAGCCTCAGCT 395  
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120  
Db 396 GCAGGCTCCAGCAGACAGATGATGTGGAGCTGGCCACGGAGTTCCTCCAGCCACAGAGGCTGG 455  
Qy 121 GluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAla 140  
Db 456 GAGTGTGAGCTAGAGGCTCTGAGAGAGGCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTG 515  
Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTrpMet 160  
Db 516 CCATTTCCAAAGCTGGGCTGGGATGACGAACTGGCGAAACCCGCGCCAGATCTACATG 575  
Qy 161 ArgPheMetGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuValIle 180  
Db 576 CGCTTCATGAGGAGCACACCTGCTACATGCCATGCCATGAGTCTCAAGCTAGTCATC 635  
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
Db 636 TTCGACACATGCTGGAGATCAAGAGGCTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 695  
Qy 201 AlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
Db 696 GCAGCCCTCTATGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCACTGAC 755  
Qy 221 PheIleLeuValLeuHisArgTrpTrpArgSerProLeuValGlnIleTrpGluLeuGlu 240  
Db 756 TTCACTCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 815  
Qy 241 GlnHisLysIleGluThrTrpArgGluIleTrpLeuGlnGlyCysPheLysProLeuVal 260  
Db 816 CACATATAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGTTCAAGCTCTGCTC 875  
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValThrLeuIleLysAsnArgIle 280  
Db 876 TCCATCTCTCTCTATATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 935  
Qy 281 HisArgLeuProValLeuAspProValSerGlyAnValLeuHisIleLeuThrHisLys 300  
Db 936 CATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 995  
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTrp 320

Db 996 CGCCTGCTCAAGTTCTCTGCACATCTTTTGGTTCCTGCTGCCCGCCCTCTCTCTCTAC 1055  
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340  
Db 1056 CGCATTATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCTGGTGGTGGAGACA 1115  
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
Db 1116 GCACCATCTCTGACTGCATCTGGACATCTTTGTGGACCGGCTGTGTCTGCACCTGCTGTG 1175  
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTrpSerArgPheAspValIleHisLeuAla 380  
Db 1176 GTCAACGAATGTGCTCAGGTCTGGGCTCTATTCCCGCTTGTATGTGATTCACCTGGCT 1235  
Qy 381 AlaGlnGlnThrTrpAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
Db 1236 GCCCAGCAACCTTACACCACTGGACATGAGTGTGGGAAAGCCCTTGAGCAGAGACA 1295  
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp 420  
Db 1296 CTATGCTCGAGGAGTCTCTTCTGCGAGCCGCCAGAGCTTGGGGAGTGCATCGAC 1355  
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
Db 1356 AGGATTCTCGGAGCAGGTACACAGGCTGTGTCTAGTGGACGAGACCCAGCATCTCTTG 1415  
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460  
Db 1416 GGCGTGTCTCTCTCTCCGACATCTTCAGGACATGCTGTCTCAGCCCTGCTGCGATCGAT 1475  
Qy 461 AlaLeuGlyAla 464  
Db 1476 GCCCTCGGGGCC 1487

RESULT 10  
US-10-070-794A-30  
; Sequence 3, Application US/10070794A  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSSON, Leif  
; APPLICANT: LOOFT, Christian  
; APPLICANT: KALM, Ernst  
; APPLICANT: MILAN, Denis  
; APPLICANT: ROBIC, Annie  
; APPLICANT: ROGEL-GAILLARD, Claire  
; APPLICANT: IANNUCELLI, Nathalie  
; APPLICANT: GELIN, Joel  
; APPLICANT: LE ROY, Pascale  
; APPLICANT: CHARDON, Patrick  
; TITLE OF INVENTION: VARIANTS OF THE GAMMA CHAIN OF AMPK, DNA SEQUENCES ENCODING  
; TITLE OF INVENTION: THE SAME, AND USES THEREOF  
; FILE REFERENCE: 11145-023US1  
; CURRENT APPLICATION NUMBER: US/10/070,794A  
; CURRENT FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT/EP00/09896  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: EP 00401388.4  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: EP 99402236.3  
; PRIOR FILING DATE: 1999-09-10  
; NUMBER OF SEQ ID NOS: 42  
; SEQ ID NO 3  
; LENGTH: 2109  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (472) .. (1389)  
US-10-070-794A-30  
Alignment Scores: 1.48e-304 Length: 2109  
Pred. No.: 2394.00 Matches: 462  
Score: 99.78% Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.63% Indels: 0  
DB: 40 Gaps: 0  
US-10-070-794A-30 (1-464) x US-10-070-794A-3 (1-2109)

Qy 3 PheLeuGluGlnGluAenSerSerSerTrpProSerProAlaValThrSerSerSerGlu 22  
Db 1 TTCTAGAGCAGAGAAACAGAGCTCATGGCCATCACCAGCTGTGACAGCAGCTCAGAA 60  
Qy 23 ArgileArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSerValGlu 42  
Db 61 AGATTCCTGGGAAACGAGAGGCCAAGCCCTTGAGATGGACAGAGAACTCGGTGGAG 120  
Qy 43 GluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGluSerThr 62  
Db 121 GAAGGGAGGCCACAGGTCAGGGGAGGTCCCGGTCCAGGCCAATCTGTGAGTCCACC 180  
Qy 63 GlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAaspProAlaGlyVal 82  
Db 181 GGGCTGGAGGCCACATTCGCCAAGACCACACCTTGGCTCAAGCTGATCTCTGCCGGGTG 240  
Qy 83 GlyThrProProThrGlyTrpAaspCysLeuProSerAaspCysThrAlaSerAlaAlaGly 102  
Db 241 GGCACTCCACACAGGGTGGGACTGCTCCCTCTGACTGTACAGCCCTAGCTGCAGGC 300  
Qy 103 SerSerThrAaspValGluLeuAlaThrGluPheProAlaThrGluAlaTrpGluCys 122  
Db 301 TCCAGCACAGATGATGGAGCTGCCACGAGGTTCCAGCCACAGAGGCTGGGAGTGT 360  
Qy 123 GluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAlaProPhe 142  
Db 361 GAGCTAGAAGCCCTGTGGAAGAGAGGCTGCCCTGTGCTGTGCCGAGGCCATTT 420  
Qy 143 ProLysLeuGlyTrpAaspGluLeuArgLysProGlyAlaGlnLleTrpMetArgPhe 162  
Db 421 CCCAAGCTGGCTGGGATGAGAACTCGGAAACCCGGCGGCCAGATCTCATGCGCTTC 480  
Qy 163 MetGlnGluHisThrCysTrpAaspAlaMetAlaThrSerSerLysLeuValLlePheAasp 182  
Db 481 ATGCAGGAGCACACTGCTAGGATGCCATGCACTAGCTCCAGCTAGTCACTTCGAC 540  
Qy 183 ThrMetLeuGluLleLysLysAlaPhePheAlaLeuValAlaAenGlyValArgAlaAla 202  
Db 541 ACCATGTGGAGATCAAGAAGCCCTCTTGTCTGTGGTGGCAACGCTGTGGGGCAGCC 600  
Qy 203 ProLeuTrpAaspSerLysLysGlnSerPheValGlyMetLeuThrLleThrAaspPheile 222  
Db 601 CCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGGATGCTGACCATCATCTTCATC 660  
Qy 223 LeuValLeuHisArgTrpTrpArgSerProLeuValGlnLleTrpGluGlnHis 242  
Db 661 CTGGTGTGATCGCTACTACAGTCCCTCCCTGTGTCAGATCATGAGATGGAACACAT 720  
Qy 243 LysileGluThrTrpArgGluLleTrpLeuGlnGlyCysPheLysProLeuValSerile 262  
Db 721 AAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTCAAGCCTCTGTGCTCCATC 780  
Qy 263 SerProAenAaspSerLeuPheGluAlaValTrpThrLeuLysLysAenArgLleHisArg 282  
Db 781 TCTCTAATGATAGCCCTTTGAAGCTGTGTACACCTCATCAAGAACCGGATCCATCGC 840  
Qy 283 LeuProValLeuAaspProValSerGlyAenValLeuHisLleLeuThrHisLysArgLeu 302  
Db 841 CTGCCTGTTCTTGACCCGGGTGTCAGGCNAAGTACTCCACATCTCCACACACAAACGGCTG 900  
Qy 303 LeuLysPheLeuHisLlePheGlySerLeuLeuProArgProSerPheLeuTrpArgThr 322  
Db 901 CTCAAGTCTCTGACATCTTTGGTTCCCTGTGCTGCCCGGCCCTCTTCTCTACCGCACT 960  
Qy 323 IleGlnAaspLeuGlyLleGlyThrPheArgAaspLeuAlaValValLeuGluThrAlaPro 342  
Db 961 ATCAAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGTGGAGACAGCACCC 1020

Qy 343 IleLeuThrAlaLeuAaspLlePheValAaspArgValSerAlaLeuProValValAen 362  
Db 1021 ATCTGACTGACTGGACATCTTTGTGACCGCGGTGTGTCTGCACTGCCTGTGTGTCAAC 1080  
Qy 363 GluCysGlyGlnValValGlyLeuTrpSerArgPheAaspValLleHisLeuAlaGln 382  
Db 1081 GAATGTGTGTGAGTGTGGGCTCTATTCGCGCTTTGATGTGATTCACCTGGCTGCCAG 1140  
Qy 383 GlnThrTrpAenHisLeuAaspMetSerValGlyGluAlaLeuArgGlnArgThrLeuCys 402  
Db 1141 CAACCTTACCAACACCTTGGACATGAGTGTGGAGAGCCCTTGAGGACAGACACTATGT 1200  
Qy 403 LeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValLleAaspArgile 422  
Db 1201 CTGGAGGGAGTCTCTTCTTCCAGCCACAGAGAGCTTGGGGAAGTGTATCGACAGATT 1260  
Qy 423 AlaArgGluGlnValHisArgLeuValLeuValAaspGluThrGlnHisLeuLeuGlyVal 442  
Db 1261 GCTCGGAGCAGGTTACACAGGCTGTGTAGTGGACGAGACCCAGCATCTCTTGGCGTG 1320  
Qy 443 ValSerLeuSerAaspLleLeuGlnAlaLeuValLeuSerProAlaGlyLleAaspAlaLeu 462  
Db 1321 GTCTCCCTCTCCGACATCTTTCAGGCACTGTGTCTGAGCCCTGCTGGCATCGATGCCCTC 1380  
Qy 463 GlyAla 464  
Db 1381 GGGGCC 1386

RESULT 11  
PCT-US01-27760-386  
; Sequence 386, Application PC/TUS0127760  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCES: 21272-115/785  
; CURRENT APPLICATION NUMBER: PCT/US01/27760  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 09/687,527  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 892  
; SOFTWARE: Custom  
; SEQ ID NO 386  
; LENGTH: 2314  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (22)..(1491)  
PCT-US01-27760-386

Alignment Scores:  
Pred. No.: 4,52e-304 Length: 2314  
Score: 2391.00 Matches: 461  
Percent Similarity: 99.78% Conservative: 2  
Best Local Similarity: 99.35% Mismatches: 1  
Query Match: 99.50% Indels: 0  
DB: 1 Gaps: 0  
US-10-070-794A-30 (1-464) x PCT-US01-27760-386 (1-2314)

Qy 1 MetSerPheLeuGluGlnGluAenSerSerSerTrpProSerProAlaValThrSerSer 20  
Db 97 ATGAGCTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCAGCAGCTGTGACAGCAGC 156  
Qy 21 SerGluArgileArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
Db 157 TCAGAAAGAATCCGTGGGAAACGAGGGCCAAAGCCCTTGAGATGGACAGCAGAGATCG 216  
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
Db 217 GTGGAGAAAGGGGAGGCCACAGGTCAGGGGGAAGGTCCCGGTCAGGCCAGCTGTGAG 276

QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
DB 277 TCCACCGGGCTGGAGGCCACATATCCCAAGACCACACCTTGGCTCAAGCTGATCTCTGCC 336  
QY 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100  
DB 337 GGGGTGGGCACCTCCACCAACAGGGTGGACATGCTCCCTCTGACTGTACAGCTCAGCT 396  
QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120  
DB 397 GCAGGCTCCAGCAGACAGATGATGGAGCTGGCCACGGAGTTCCACGACACAGAGGCTGG 456  
QY 121 GluCysGlnLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140  
DB 457 GAGTGTGAGCTAGAAGGCTGCTGGAAAGAGAGGCTGCTCCCTGTGCTCCCGCAGGCC 516  
QY 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160  
DB 517 CCATTTCCCAAGCTGGGCTGGATGACGAACCTGGGAAACCCGGCGCCGATCTACATG 576  
QY 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180  
DB 577 CGCTTCATCGAGGAGCACACCTGCTACGATGCCATGCACTAGCTCCAGCTAGTCAATC 636  
QY 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
DB 637 TTCACACCATGCTGGAGATCAAGAAGGCTTCTTGTCTGGTGGCCAAACGGTGTGGCG 696  
QY 201 AlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
DB 697 GCAGCCCTCTATGGGACAGCAGACGAGCTTGTGGGATGCTGACCATCACTGAC 756  
QY 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240  
DB 757 TTCATCTCTGTGTCATCGCTACTACAGGTCCCGCTGGTCCAGATCTATGATGATCAA 816  
QY 241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260  
DB 817 CAACATAGATGGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTCTGCTC 876  
QY 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
DB 877 TCCATCTCTCTATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGACCGGATC 936  
QY 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
DB 937 CATCGCTGCTGCTTCTTGAACCGGTGTGAGCAACGTACTCCACATCTCCACACAAA 996  
QY 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
DB 997 CGCCTGCTCAAGTTCCTGCACATCTTGGTTCCTGCTGCGCCGCGCTCTCTCTCTAC 1056  
QY 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340  
DB 1057 CGCACTATCCAAAGATTGGGCATCGGCATATCCGAGACTTGGCTGTGTGCTGGAGACA 1116  
QY 341 AlaProfileLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
DB 1117 GCACCATCTCTGACTGCACCTGACATCTTGTGGACCGCGGTGTCTGTGCACTGCTGTG 1176  
QY 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380  
DB 1177 GTCACGAATGTGGTGTGAGTGTGGGCTCTATATCCCGCTTGTGTGATTCACCTGGCT 1236  
QY 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
DB 1237 GCCCAGCAAACTCAACCACTGGACATGATGTGGGAGAGCCCTGAGGCAGAGGACA 1296  
QY 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420  
DB 1297 CTATGCTGGAGGAGTCTTTCTCTGCCACGCCACGAGCTTGGGGAGTGTGATCGAC 1356  
QY 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440

DB 1357 AGATTGCTCGGAGCAGGTACACAGCTGCTAGTGACGAGACCCAGCATCTCTTG 1416  
QY 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460  
DB 1417 GCGTGTGCTCTCCCTCTCCGACATCTTCCAGGCATGCTGCTGCTGCTGCTGCTGCTG 1476  
QY 461 AlaLeuGlyAla 464  
DB 1477 GCCTCGGGGCC 1488  
RESULT 12  
PCT-US01-27760A-386  
; Sequence 386, Application PC/TUS0127760A  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-115/ 785  
; CURRENT APPLICATION NUMBER: PCT/US01/27760A  
; CURRENT FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 09/687,527  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 892  
; SOFTWARE: Custom  
; SEQ ID NO 386  
; LENGTH: 2314  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (22)..(1491)  
PCT-US01-27760A-386  
Alignment Scores:  
Pred. No.: 4.52e-304 Length: 2314  
Score: 2391.00 Matches: 461  
Percent Similarity: 99.78% Conservative: 2  
Best Local Similarity: 99.35% Mismatches: 1  
Query Match: 99.50% Indels: 0  
Gaps: 1  
US-10-070-794A-30 (1-464) x PCT-US01-27760A-386 (1-2314)  
QY 1 MetSerPheLeuGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
DB 97 ATGAGCTCTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCCAGCTGTGACCCAGCAGC 156  
QY 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
DB 157 TCAGAAAGATCCCTGGGAAACGGAGGGCCAAAGCCTTGAGATGGACAAGGCAGAGTGC 216  
QY 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
DB 217 GTGGAGGAAGGGAGGACACACAGGTCCAGGGGAAGGTCCCGGTCCAGGCCAGCTGCTGAG 276  
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
DB 277 TCCACCGGCTGGAGGCCACATTTCCCAAGACCACACCTTGGCTCAGCTGATCTGCTGCC 336  
QY 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100  
DB 337 GGGGTGGGCACCTCCACCAACAGGGTGGGACTGCTCCCTCTCTGACTGTACAGCTCAGCT 396  
QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120  
DB 397 GCAGGCTCCAGCAGACAGATGATGGAGCTGGCCACGGAGTTCCCGCAGCCACAGAGGCTGG 456  
QY 121 GluCysGlnLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140  
DB 457 GAGTGTGAGCTAGAAGGCTGCTGGAAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 516  
QY 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160

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Db 517 CCATTCTCCAGCTGGGCTGGAGTGAAGAACTGGGAAACCCCGGGCCAGATCTACATG 576
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValile 180
Db 577 GCGTTTCATCGAGGAGCACACCTGTACGATGCCATGCACTAGCTCCAGCTAGTCAATC 636
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 637 TTCACACCACTGCTGGAGATCAAGAAGCCCTCTTTGCTCTGTGGTGGCAACGGTGTGG 696
Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 697 GCACCCCTCTATCGGACAGCAGCAGAGCAGCTTTTGGGGATGCTGACCATCAGTAC 756
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 757 TTCATCTCTGCTGCTGCTGCTACTACAGGTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 816
Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 817 CAACATAGATTTGAGCCTGGAGGAGATCTTACCTGCAAGGCTGCTTCAAGGCTCTGCTC 876
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 877 TCCATCTCTCTAATGATAGCTCTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 936
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 937 CATCGCTGCTGCTGCTTGTACCCGGTGTGAGGAGCTTCTCCACATCTCTCACACAAA 996
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 997 CGCCTGCTCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1056
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 1057 CGCACTATCAAGATTTGGGATCGGATCGGACATCTTGTGACCGGGCTGTCTGCACTGCTG 1116
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1117 GCACCCATCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1176
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1177 GTCAACCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1236
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1237 GCCCAGCAACCTTCAACACCACTTGAATGATGATGATGATGATGATGATGATGATGATG 1296
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp 420
Db 1297 CTATGCTGGAGGAGTCTTCTTCTGCGACCCACAGAGCTTGGGGAGTATGATGATGAT 1356
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1357 AGGATGCTCGGAGCAGGTACACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1416
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1417 GGGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1476
Qy 461 AlaLeuGlyAla 464
Db 1477 GCCCTCGGGGCC 1488
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## RESULT 13

US-09-687-527-420

; Sequence 420, Application US/09687527

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Zhou, Ping

```
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 795
; CURRENT APPLICATION NUMBER: US/09/687,527
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 420
; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(1491)
US-09-687-527-420
Alignment Scores:
Pred. No.: 4,52e-304 Length: 2314
Score: 2391.00 Matches: 461
Percent Similarity: 99.78% Conservative: 2
Best Local Similarity: 99.35% Mismatches: 1
Query Match: 99.50% Indels: 0
DB: 29 Gaps: 0
US-10-070-794A-30 (1-464) x US-09-687-527-420 (1-2314)
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Qy 1 MetSerPheLeuGlnGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20
Db 97 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACACGCTGTGACAGCAGC 156
Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 157 TCAGAAAGATTCGTGGAAACGGAGGGCCANAGCCTTGAGATGACAGGACAGAGTCG 216
Qy 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 217 GTGGAGAGAGGAGGAGCAGCAGCTCAGGGGAAAGTCCCGGTCCAGGCCAGCTGCTGAG 276
Qy 61 SerThrClyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 277 TCCACCGGGCTGGAGGCCACATTTCCCAAGACCAACACCTTGGCTCAAGCTGATCTCTGCC 336
Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
Db 337 GGGGTGGGCACTCCACACAGGGTGGGACTGCTCCCTCTGACTGTACAGCTCAGCT 396
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db 397 GCAGGCTCCAGCACAGATGATGTGGAGTGGCCAGCAGAGTTCACAGCCACAGAGGCTGG 456
Qy 121 GlnCysGluLeuGlnGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 457 GAGTGTGAGCTAGAAGGCTGCTGGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 516
Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 517 CCATTTCCCAAGCTGGGCTGGATGACAACTGCGGAAACCCGGCGCCAGATCTACATG 576
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValile 180
Db 577 CGCTTTCATCGAGGAGCACACCTGCTACGATGCCATGCACTAGTCTCAAGCTAGTCAATC 636
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 637 TTCGACACCATGCTGGAGATCAAGAAGGCCCTTCTTTGCTCTGCTGCTGCTGCTGCTGCTG 696
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Qy 201 AlaAlaProLeuTrpAspSerLysGlyGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 697 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGATGCTGACCATCACTGAC 756

Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 757 TTCATCTCTGGTGGCTGCGATCGCTACTACAGGTCCCTCCCTGGTCCAGATCTATGAGATTGAA 816

Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 817 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTCTTCAAGCCTCTGTC 876

Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 877 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 936

Qy 281 HisArgIleuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 937 CATCGCCTGCTGCTTCTTGAACCGGTGTACGGCAACGTACTCCACATCCTCACACAAA 996

Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 997 CGCTGTCTCAAGTTCCTGACATCTTTGGTTCCTGTGCTGCCCGCCCTCTCTCTAC 1056

Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 1057 CGCACTATCCAAAGATTGGGCATCGGCACATTCGAGACATTGGCTGTGGTCTGGAGACA 1116

Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal 360
Db 1117 GCACCCATCTGACTGCACTGGACATCTTTGTGGACCGCGGTGTCTGCACTGCCCTGTG 1176

Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1177 GTCAAGAAATGTGTGCTGAGTGTGGGCTCTATTCCCGCTTTGATGATTCACCTGGCT 1236

Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1237 GCCCAGCAAACTCAACACCTGACATGATGATGTGGGAGAGCCCTGAGGACAGAGACA 1296

Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp 420
Db 1297 CTATGTCTGGAGGAGTCTCTTCTGCTGCCAGCCACAGAGCTTGTGGGAAAGTATCGAC 1356

Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1357 AGGATTGCTCGGAGCAGGTACACAGGCTGGTGTAGTGGACGAGACCCAGCATCTCTTG 1416

Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1417 GCGGTGGTCTCCCTCTCGACATCCTTCAGGCACTGGTGTCTCAGCCCTGTGGCATCGAT 1476

Qy 461 AlaLeuGlyAla 464
Db 1477 GCGCTCGGGGCC 1488

```

```

RESULT 14
US-10-399-103-386
; Sequence 386, Application US/10399103
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-115/ 785
; CURRENT APPLICATION NUMBER: US/10/399,103
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 09/687,527
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 892
; SOFTWARE: Custom
; SEQ ID NO 386
; LENGTH: 2314
; TYPE: DNA

```

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(1491)
US-10-399-103-386

```

```

Alignment Scores:
Pred. No.: 4,52e-304 Length: 2314
Score: 2391.00 Matches: 461
Percent Similarity: 99.78% Conservative: 2
Best Local Similarity: 99.35% Mismatches: 1
Query Match: 99.50% Indels: 0
DB: Gaps: 0

```

US-10-070-794a-30 (1-464) x US-10-399-103-386 (1-2314)

```

Qy 1 MetSerPheLeuGluGlnGlnAsnSerSerTrpProSerProAlaValThrSerSer 20
Db 97 ATGAGCTTCTAGAGCAAGAAAACAGCAGCTCATGGCCATCACCCAGCTGTGACCCAGCAG 156

Qy 21 SerGluArgIleArgGlyLysArgArgAlaIysAlaLeuArgTrpThrArgGlnLysSer 40
Db 157 TCAGAAAAGATCCGTGGGAAACCGAGGGCCAAAGCCTTGAGATGGACAAAGCGCAAGATCG 216

Qy 41 ValGluGluGlyGluProGlyGlnGlyGlyProArgSerArgProThrAlaGlu 60
Db 217 GTGAGGAAGAGGGAGGCCAGCAGGTACAGGGGAAGGTCCCGGTCCAGGCCAGCTGTGAG 276

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 277 TCCACCGGGCTGGAGGCCACATTCGCCAAGACCACACCTTGGCTCAAGCTGATCTCTGCC 336

Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
Db 337 GGGGTGGGCATCTCACCAACAGAGGTGGGACTGCCCTCCCTCTGACTGTACAGCCTCAGCT 396

Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db 397 GCAGGCTCCAGACACAGATGATGTGGAGCTGGCCACGAGGTTCACGAGCCACAGAGCCTGG 456

Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 457 GAGTGTGAGCTAGAAAGCCCTGCTGGAAGAGAGAGGCTGCCCTGTGCTGTCCCCGAGGCC 516

Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 517 CCATTTCCCAAGCTGGGCTGGGATGACAACTGCGGAAACCCCGGCGCCAGATCTACATG 576

Qy 161 ArgPheMetGlnGlnHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
Db 577 CGCTTCATCGAGGAGCACACCTGTACATGCCATGGCACTAGCTCCAAGCTAGTCATC 636

Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 637 TTCGACACCATGCTGGAGATCAAGAGGCCCTTCTTGTCTGTGGTGGCCAAAGCGGTGTGGCG 696

Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 697 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGGATGTGCTACCATCACTGAC 756

Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 757 TTCATCTCTGGTGGCTGCGATCGCTACTACAGGTCCCTCCCTGGTCCAGATCTATGAGATTGAA 816

Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 817 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTCTTCAAGCCTCTGTC 876

Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 877 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 936

Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300

```

```

Db      937 CATGCCTGCTGTTCTTGACCCCGGTGTACGCAACGTAATCCACATCTCCACACAAA 996
Qy      301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db      997 CGCTCTGCTCAAGTTCCTGCACATCTTGGTTCCCTGCTGCCCGCCCTCTTCTCTAC 1056
Qy      321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db      1057 CGCACTATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTCTGGAGACA 1116
Qy      341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db      1117 GCACCACTCTGACTGACATGGAATCTTGTGGACCGCGGTGTCTGCACTGCCCTGTG 1176
Qy      361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db      1177 GTCAACGAATGTGCTAGGTGCTGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1236
Qy      381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db      1237 GCCCAGCAAACTACAACCACTGACATGATGTGGGAGAACCTTGAGGACAGGACA 1296
Qy      401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
Db      1297 CTATGCTGAGGGAGTCTCTTCTGCGACGCCACGAGAGCTTGGGGGAAGTATCGAC 1356
Qy      421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db      1357 AGGATGCTCGGAGCAGGTACACAGGCTGGTGTAGTGACGAGACCCGACATCTCTTG 1416
Qy      441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db      1417 GGGGTGCTCTCCCTCTCCGACATCTTCAGGCACTGGTGTCTGAGCCCTGCTGGCATCGAT 1476
Qy      461 AlaLeuGlyAla 464
Db      1477 GCCCTCGGGGCC 1488

```

## RESULT 15

```

US-10-399-103A-386
; Sequence 385, Application US/10399103A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-115/ 785
; CURRENT APPLICATION NUMBER: US/10/399,103A
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: PCT/US01/27760
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 09/687,527
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 892
; SOFTWARE: Custom
; SEQ ID NO 386
; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(1491)
US-10-399-103A-386

```

## Alignment Scores:

```

Pred. No.: 4,52e-304 Length: 2314
Score: 2391.00 Matches: 461
Percent Similarity: 99.78% Conservative: 2
Best Local Similarity: 99.35% Mismatches: 1
Query Match: 99.50% Indels: 0
DB: 50 Gaps: 0

```

US-10-070-794A-30 (1-464) x US-10-399-103A-386 (1-2314)

```

Qy      1 MetSerPheLeuGluGlnGluAenSerSerSerTyrProSerProAlaValThrSerSer 20
Db      97 ATGAGCTTCTTAGAGCAAGAAAAACAGCAGCTCATGGCCATCACCAGCTGTGACGACGAG 156
Qy      21 SerGluArgIleArgGlyIysArgAlaAlaValLeuArgTyrThrArgGlnLysSer 40
Db      157 TCAGAAGAATCCGTGGGAAACGAGGGCCAAAGCCTTGAGATGGACAAAGCAAGATCG 216
Qy      41 ValGluGluGlyGluProProGlyGlnGlyProArgSerArgProThrAlaGlu 60
Db      217 GTGGAGGAAGGGAGCCACCAGGTGAGGGGAAAGTCCCCGGTCCAGGCCAGCTGCTGAG 276
Qy      61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db      277 TCCACCGGGCTGGAGGCCACATTCGCCAAGACCACACCTTGGCTCAAGCTGATCTCTGCC 336
Qy      81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
Db      337 GGGGTGGGCACTCCACCAAGGGTGGGACTGCTCCCTCTGACTGTACAGCCTCAGCT 396
Qy      101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120
Db      397 GCAGGCTCCAGCACACATGATGTGGAGTGGCCACCGAGTTCACAGCCACAGAGCCCTGG 456
Qy      121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db      457 GAGTGTGAGCTAGAAAGCCCTGCTGGAAGAGAGGCGCTGCCCTGTGCTGCTGCCGAGGCC 516
Qy      141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db      517 CCATTTCCTCCAAAGCTGGGCTGGGATGACAACTCGGAAACCCCGCGCCAGATCTACATG 576
Qy      161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
Db      577 CGCTTCATCGAGAGGACACACCTCTACGATGCCATGGCACTAGCTCCAGCTAGTCAATC 636
Qy      181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db      637 TTCGACACCATGCTGGAGATCAAGAAGGCCCTCTTTGCTCTGGTGGCAACGGTGTGGG 696
Qy      201 AlaAlaProLeuTyrAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db      697 GCAGCCCTCTATGGGACACAAAGACAGAGCTTTGTGGGATGCTGACCATCAGTAC 756
Qy      221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db      757 TTCATCTCTGCTGTGATCTGCTACTACAGTCCCTGCTGCTGCTGATGATGATGAA 816
Qy      241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db      817 CAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTC 876
Qy      261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db      877 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCCGGATC 936
Qy      281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db      937 CATCGCTCTGCTGTTCTTGACCCGGTGTGAGGCAAGCTACTCCACATCTCCACACAAA 996
Qy      301 ArgLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db      997 CGCCTGCTCAAAGTTCCTGACATCTTTGGTTCCTGCTGCCCGGCCCTCTCTCTCTAC 1056
Qy      321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db      1057 CGCACTATCCAAAGATTGGGCATTCGACATTCGAGACTTGGCTGTGGTGGAGACA 1116
Qy      341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db      1117 GCACCACTCTGACTGACATGGAATCTTTGTGGACCGCGGTGTGTGACGCTGCTGTG 1176
Qy      361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380

```

Db		1177	GTCAACGAATGTGTCAAGTCGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT	1236
Qy		381	AlaGlnGlnThrTyrAanHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr	400
Db		1237	GCCCAGCAACCTACACCACTGGACATGAGTGTGGGAGAGCCCTGAGGCAGAGGACA	1296
Qy		401	LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp	420
Db		1297	CTATGTCGTGAGGAGTCCCTTCTCTGCCAGCCCCACGAGAGCTTGGGGGAAGTGATCGAC	1356
Qy		421	ArgIlealaargGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu	440
Db		1357	AGGATTGCTCGGGAGCGAGGTACACAGGCTGGTGTGTAGTGACGAGACCCAGCATCTCTTG	1416
Qy		441	GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp	460
Db		1417	GGCGTGTCTCCCTCTCCGACATCCTTCAGGCACCTGGTGCTCAGCCCTGCTGGCATCGAT	1476
Qy		461	AlaLeuGlyAla	464
Db		1477	GCCCTCGGGGCC	1488

Search completed: January 26, 2006, 06:57:49  
Job time : 7377.54 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2006, 22:01:17 ; Search time 136.967 Seconds  
(without alignments)  
2390.094 Million cell updates/sec

Title: US-10-070-794a-30  
Perfect score: 2403  
Sequence: 1 MSFLEQNSSWPSPAVTSS.....LSDIQLVLSPAGIDALGA 464

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
\*score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2403	100.0	464	1 AAKG3_HUMAN	Q9ug19 homo sapien
2	2398	99.8	489	2 Q4V779_HUMAN	Q4V779 homo sapien
3	2390	99.5	489	2 Q4QCG8_HUMAN	Q4QCG8 homo sapien
4	2011	83.7	464	2 Q532T5_PIG	Q532T5 sus scrofa
5	2011	83.7	514	1 AAKG3_PIG	Q9my74 sus scrofa
6	2010	83.6	464	2 Q8CJ4I_MOUSE	Q8CJ4I mus musculus
7	2010	83.6	489	2 Q8BGW7_MOUSE	Q8BGW7 m amp-activ
8	2001.5	83.3	490	2 Q80WK8_MOUSE	Q80WK8 mus musculus
9	1988.5	82.8	465	2 Q4G3U3_BOVIN	Q4G3U3 bos taurus
10	1920	79.9	447	2 Q6TEH8_HORSE	Q6TEH8 equus caball
11	1888	78.6	440	2 Q6U7S1_HORSE	Q6U7S1 equus caball
12	1280	53.3	363	2 Q4JK38_CHICK	Q4JK38 gallus gall
13	1280	53.3	382	2 Q4JK39_CHICK	Q4JK39 gallus gall
14	1213.5	50.5	337	2 Q7ZYL2_XENLA	Q7ZYL2 xenopus lae
15	1100.5	45.8	443	2 Q8BIQ9_MOUSE	Q8BIQ9 mus musculus
16	1093.5	45.5	524	2 Q5R4S0_PONPY	Q5R4S0 pongo pygma
17	1093	45.5	525	2 Q6NU10_HUMAN	Q6NU10 homo sapien
18	1093	45.5	569	1 AAKG2_HUMAN	Q9ug10 homo sapien
19	1092.5	45.5	558	2 Q6P6A0_XENLA	Q6P6A0 xenopus lae
20	1091.5	45.4	343	2 Q4RVG2_TETNG	Q4RVG2 tetraodon n
21	1084.5	45.1	328	2 Q5ZK07_CHICK	Q5ZK07 gallus gall
22	1084.5	45.1	566	2 Q91KG5_MOUSE	Q91KG5 mus musculus
23	1082.5	45.0	448	2 Q4QRB9_FAT	Q4QRB9 rattus norv
24	1080.5	45.0	328	2 Q53Y07_HUMAN	Q53Y07 homo sapien
25	1078	44.9	326	2 Q6V7V4_FAT	Q6V7V4 rattus norv
26	1078	44.9	326	2 Q6V7V5_MOUSE	Q6V7V5 mus musculus
27	1050	43.7	297	2 Q4RTT1_TETNG	Q4RTT1 tetraodon n
28	1040	43.3	330	2 Q6PCS7_BRARE	Q6PCS7 brachydanio
29	1028	42.8	330	1 AAKG1_FAT	P80385 rattus norv
30	1028	42.8	330	2 Q4QQW6_FAT	Q4QQW6 rattus norv
31	1027	42.7	323	2 Q4RXW4_TETNG	Q4RXW4 tetraodon n

32 1019 42.4 333 2 Q4S1Z9\_TETNG  
33 1018 42.4 330 2 Q5PRE8\_MOUSE  
34 1017 42.3 330 2 Q6X275\_PIG  
35 1017 42.3 331 1 AAKG1\_HUMAN  
36 1013 42.2 330 1 AAKG1\_BOVIN  
37 1003 41.7 299 2 Q4RSP4\_MACFA  
38 1002.5 41.7 340 2 Q8N7V9\_HUMAN  
39 1000 41.6 287 2 Q6U7I6\_FAT  
40 1000 41.5 334 2 Q6GN94\_XENLA  
41 997 41.5 330 1 AAKG1\_MOUSE  
42 960 40.0 329 2 Q4RY44\_TETNG  
43 899 37.4 267 2 Q8EM63\_MOUSE  
44 874.5 36.4 718 2 Q8I0K6\_DROME  
45 874.5 36.4 814 2 Q8I0A1\_DROME

#### ALIGNMENTS

RESULT 1  
AAKG3\_HUMAN  
ID AAKG3\_HUMAN STANDARD; PRT; 464 AA.  
AC Q9UG19; Q9NEL1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)  
DE (AMPK gamma3).  
GN Name=PRKAG3; Synonyms=AMPKG3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20164049; PubMed=10698692; DOI=10.1042/0264-6021:3460659;  
RA Cheung P.C.F., Salt I.P., Davies S.P., Hardie D.G., Carling D.;  
RT "Characterization of AMP-activated protein kinase gamma-subunit  
RT isoforms and their role in AMP binding.";  
RL Biochem. J. 346:659-669(2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Skeletal muscle;  
RX MEDLINE=20280150; PubMed=10818001; DOI=10.1126/science.288.5469.1248;  
RA Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M.,  
RA Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H.,  
RA Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,  
RA Andersson L.;  
RT "A mutation in PRKAG3 associated with excess glycogen content in pig  
RT skeletal muscle.";  
RL Science 288:1248-1251(2000).  
CC -!- FUNCTION: AMPK is responsible for the regulation of fatty acid  
CC synthesis by phosphorylation of acetyl-CoA carboxylase. Also  
CC regulates cholesterol synthesis via phosphorylation and  
CC inactivation of hydroxymethylglutaryl-CoA reductase and hormone-  
CC sensitive lipase. This is a regulatory subunit. It may play a role  
CC in the regulation of energy metabolism in skeletal muscle.  
CC -!- SUBUNIT: Heterotrimer of an alpha catalytic subunit, a beta and a  
CC gamma non-catalytic regulatory subunits.  
CC -!- TISSUE SPECIFICITY: Skeletal muscle, with weak expression in heart  
CC and pancreas.  
CC -!- SIMILARITY: Belongs to the 5'-AMP-activated protein kinase gamma  
CC subunit family.  
CC -!- SIMILARITY: Contains 4 CBS domains.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC EMBL; AJ249977; CAB65117.1; ALT\_INIT; mRNA.

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DR EMBL; AF214519; AAF73987.1; -; mRNA.
DR Ensembl; ENSG00000115592; Homo sapiens.
DR HGNC; HGNC:9387; PRKAG3.
DR MTM; 604976; -.
DR GO; GO:0004679; F:AMP-activated protein kinase activity; TAS.
DR GO; GO:0007243; P:protein kinase cascade; TAS.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 4.
KW CBS domain; Fatty acid biosynthesis; Lipid synthesis; Repeat.
FT DOMAIN 147 201 CBS 1.
FT DOMAIN 228 282 CBS 2.
FT DOMAIN 303 356 CBS 3.
FT DOMAIN 375 428 CBS 4.
FT CONFLICT 58 58 T -> A (in Ref. 1).
FT CONFLICT 163 164 MQ -> IE (in Ref. 1).
FT CONFLICT 398 398 Q -> K (in Ref. 1).
FT CONFLICT 461 464 ALGA -> PSGPEKI (in Ref. 1).
SQ SEQUENCE 464 AA; 51514 MW; 53985C2C77003A63 CRC64;

Query Match 100.0%; Score 2403; DB 1; Length 464;
Best Local Similarity 100.0%; Pred. No. 3.1e-174;
Matches 464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFLEQNSSWSPSPAVTSSSIRGRKRAKALRWTRQKSVEEGPPGQGGPRSRPTAE 60
Db 1 MSFLEQNSSWSPSPAVTSSSIRGRKRAKALRWTRQKSVEEGPPGQGGPRSRPTAE 60
Qy 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDVDELATEPPATEAW 120
Db 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDVDELATEPPATEAW 120
Qy 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLELRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 180
Db 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLELRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 180
Qy 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLITDILVHLHYRSPVLQIYEIE 240
Db 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLITDILVHLHYRSPVLQIYEIE 240
Qy 241 QHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300
Db 241 QHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300
Qy 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRRVSAALPV 360
Db 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRRVSAALPV 360
Qy 361 VNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHESLGEVID 420
Db 361 VNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHESLGEVID 420
Qy 421 RIAREQVHRLVLVDVETQHLGLVSVSLDILQALVLSPPAGIDALGA 464
Db 421 RIAREQVHRLVLVDVETQHLGLVSVSLDILQALVLSPPAGIDALGA 464

RESULT 2
Q4V779_HUMAN PRELIMINARY; PRT; 489 AA.
AC Q4V779;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE AMP-activated protein kinase, non-catalytic gamma-3 subunit.
GN Name=PRKAG3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE AMP-activated protein kinase, non-catalytic gamma-3 subunit.  
 GN Name=PRKAG3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=PCR rescued clones;  
 RA MDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ugin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Schmutz J., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Green E.D., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=PCR rescued clones;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC098306; AAH98306.1; -; mRNA.  
 DR EMBL; BC098255; AAH98255.1; -; mRNA.  
 KW Kinase.  
 SQ SEQUENCE 489 AA; 54232 MW; A67D9DEAB76BFC9 CRC64;  
 Query Match 99.5%; Score 2390; DB 2; Length 489;  
 Best Local Similarity 99.6%; Pred. No. 3.2e-173;  
 Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MSFLEQENSSWSPSPAVTSSSRIRGKRAKALRWTRQKSVGEPPGQGGPRSPRTAE 60  
 DB 26 MSFLEQENSSWSPSPAVTSSSRIRGKRAKALRWTRQKSVGEAPGQGGPRSPAAE 85  
 QY 61 STGLEATFPKTTPLAQAADPAGVGTPTGWDCLPSDCTASAGSSTDDELATEFPATEAW 120  
 DB 86 STGLEATFPKTTPLAQAADPAGVGTPTGWDCLPSDCTASAGSSTDDELATEFPATEAW 145  
 QY 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKPAQIYMRFMQHTCYDAMATSSKLVI 180  
 DB 146 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKPAQIYMRFMQHTCYDAMATSSKLVI 205  
 QY 181 FDTMLEIKKAFPAALVANGVRAAPLWDSKKQSFVGMLTITDFILVLRHYRSPVLQIYEI 240  
 DB 206 FDTMLEIKKAFPAALVANGVRAAPLWDSKKQSFVGMLTITDFILVLRHYRSPVLQIYEI 265  
 QY 241 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHLTHK 300  
 DB 266 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHLTHK 325  
 QY 301 RLKLFHLIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRSALPV 360  
 DB 326 RLKLFHLIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRSALPV 385  
 QY 361 VNECGQVGLYSRFDVHILAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPESLGEVID 420

DB 386 VNECGQVGLYSRFDVHILAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPESLGEVID 445  
 QY 421 RIAREQVHRLVLDVDETHLLGVVSLSDILOALVLSFAGIDALGA 464  
 DB 446 RIAREQVHRLVLDVDETHLLGVVSLSDILOALVLSFAGIDALGA 489  
 RESULT 4  
 Q53ZT5\_PIG  
 ID Q53ZT5\_PIG PRELIMINARY; PRT; 464 AA.  
 AC Q53ZT5\_PIG  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE AMP-activated protein kinase gamma subunit.  
 GN Name=PRKAG3;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 OC Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC PubMed=14970697; DOI=10.1159/000075743;  
 RA Anarger V., Erlanson R., Pielberg G., Jeon J.T., Andersson L.;  
 RT "Comparative sequence analysis of the PRKAG3 region between human and  
 RT pig: evolution of repetitive sequences and potential new exons.";  
 RL Cytogenet. Genome Res. 102:163-172(2003).  
 DR EMBL; AY264345; AAP12533.1; -; mRNA.  
 KW Kinase.  
 SQ SEQUENCE 464 AA; 51308 MW; 17638CB12A2BA9DF CRC64;  
 Query Match 83.7%; Score 2011; DB 2; Length 464;  
 Best Local Similarity 86.0%; Pred. No. 2.1e-144;  
 Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;  
 QY 1 MSFLEQENSSWSPSPAVTSSSRIRGKRAKALRWTRQKSVGEPPGQGGPRSPRTAE 60  
 DB 1 MSFLEQENSSWSPSPAVTSSSRIRGKRAKALRWTRQKSVGEPPGQGGPRSPVAE 60  
 QY 61 STGLEATFPKTTPLAQAADPAGVGTPTGWDCLPSDCTASAGSSTDDELATEFPATEA 119  
 DB 61 STGLEATFPKTTPLAQAADPAGVGTPTGWDCLPSDCTASAGSSTDDELATEFPATEA 120  
 QY 120 WECELEGLLEERPALCLSPQAPFPKLGWDDLRKPAQIYMRFMQHTCYDAMATSSKLVI 179  
 DB 121 SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDLRKPAQIYMRFMQHTCYDAMATSSKLVI 179  
 QY 180 IFDTMLEIKKAFPAALVANGVRAAPLWDSKKQSFVGMLTITDFILVLRHYRSPVLQIYEI 239  
 DB 180 IFDTMLEIKKAFPAALVANGVRAAPLWDSKKQSFVGMLTITDFILVLRHYRSPVLQIYEI 239  
 QY 240 EQHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHLTH 299  
 DB 240 EQHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHLTH 299  
 QY 300 KRLKLFHLIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRSALPV 359  
 DB 300 KRLKLFHLIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRSALPV 359  
 QY 360 VNECGQVGLYSRFDVHILAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPESLGEVI 419  
 DB 360 VNECGQVGLYSRFDVHILAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPESLGEVI 419  
 QY 420 DRIAREQVHRLVLDVDETHLLGVVSLSDILOALVLSFAGIDALGA 464  
 DB 420 DRIAREQVHRLVLDVDETHLLGVVSLSDILOALVLSFAGIDALGA 464  
 RESULT 5  
 AAKG3\_PIG  
 ID AAKG3\_PIG STANDARD; PRT; 514 AA.

AC QMYP4; Q6WZ89;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)  
 DE (AMPK gamma3).  
 GN Name=PRKAG3;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 OC SUB TaxID=9823;  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANT RN(-) GIN-250.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=20280150; PubMed=10818001; DOI=10.1126/science.288.5469.1248;  
 RA Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M.,  
 RA Rogel-Gallard C., Paul S., Iannuccelli N., Rask L., Ronne H.,  
 RA Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,  
 RA Andersson L.;  
 RA "A mutation in PRKAG3 associated with excess glycogen content in pig  
 skeletal muscle.";  
 RT Science 288:1248-1251 (2000).  
 RL [2]  
 RN NUCLEOTIDE SEQUENCE (ISOFORM 2).  
 RP TISSUE=Skeletal muscle;  
 RC Milan D., Jeon J.-T., Looft C., Amarger V., Robic A.,  
 RA Rogel-Gallard C., Paul S., Gellin J., Lundstrom K., Reinsch N.,  
 RA Kalm E., Le Roy P., Chardon P., Andersson L.;  
 RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 RL [3]  
 RN NUCLEOTIDE SEQUENCE (ISOFORM 1).  
 RP PubMed=14970697; DOI=10.1159/000075743;  
 RX Amarger V., Bralandsson R., Pielberg G., Jeon J.-T., Andersson L.;  
 RA "Comparative sequence analysis of the PRKAG3 region between human and  
 pig: evolution of repetitive sequences and potential new exons.";  
 RT Cytogenet. Genome Res. 102:163-172 (2003).  
 CC -!- FUNCTION: AMPK is responsible for the regulation of fatty acid  
 synthesis by phosphorylation of acetyl-CoA carboxylase. Also  
 regulates cholesterol synthesis via phosphorylation and  
 inactivation of hydroxymethylglutaryl-CoA reductase and hormone-  
 sensitive lipase. This is a regulatory subunit. It may play a role  
 in the regulation of energy metabolism in skeletal muscle.  
 CC -!- SUBUNIT: Heterotrimer of an alpha catalytic subunit, a beta and a  
 gamma non-catalytic regulatory subunits.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=2;  
 CC IsoId=Q9MYP4-1; Sequence=Displayed;  
 CC Name=1;  
 CC IsoId=Q9MYP4-2; Sequence=VSP\_008059;  
 CC -!- TISSUE SPECIFICITY: Muscle.  
 CC -!- DISEASE: Defects in PRKAG3 are the cause of the RN- phenotype  
 which is associated with excess glycogen content (about 70%) in  
 skeletal muscle. This mutation originated in the Hampshire breed  
 pigs and has beneficial effects on meat content but detrimental  
 effects on processing yield. Thus, this mutation is of  
 considerable economic significance in the pig breeding industry.  
 CC -!- SIMILARITY: Belongs to the 5'-AMP-activated protein kinase gamma  
 subunit family.  
 CC -!- SIMILARITY: Contains 4 CBS domains.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC EMBL; AF2144520; AAF73988.2; -; mRNA.  
 DR EMBL; AF2144521; AAF73989.1; -; Genomic DNA.  
 DR EMBL; AY263454; AAP14907.1; -; Genomic DNA.  
 DR InterPro; IPR000644; CBS.  
 DR Pfam; PF00571; CBS; 2.

KW Alternative splicing; CBS domain; Disease mutation;  
 KW Fatty acid biosynthesis; Lipid synthesis; Repeat.  
 FT DOMAIN 222 276 CBS 1.  
 FT DOMAIN 303 357 CBS 2.  
 FT DOMAIN 378 431 CBS 3.  
 FT DOMAIN 450 503 CBS 4.  
 FT VARSPLIC 1 50 Missing (in isoform 1).  
 FT VARIANT 250 250 R -> Q (in RN-).  
 FT CONFLICT 418 418 V -> E (in Ref. 3).  
 FT CONFLICT 441 441 N -> S (in Ref. 3).  
 SQ SEQUENCE 514 AA; 56790 MW; 8CE025FBBF93E4AE CRC64;  
 Query Match 83.7%; Score 2011; DB 1; Length 514;  
 Best Local Similarity 86.0%; Pred. No. 2.4e-144;  
 Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;  
 QY 1 MSFLEQENSSWPSPAVTSSSIRGRKRAKALRWTRQKSVSEGEPPGQGEGRSRPTAE 60  
 DB 51 MSFLEQESRSWFSRAVTTSSRSRSHGDNKASRWTQEDVESGGPPGREGQSRPAE 110  
 QY 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGWDCLPSCDCTASAGSSTDDVELATEFPATEA 119  
 DB 111 STGQEAFFPKATPLAQAAPLAEVDNPTERDILPSCDCAASASDNTDHLDLGIEFSAA 170  
 QY 120 WECELEGLLEERPALCLSPQAPFKLGWDDDELKPGQAIYMRFMORHTCYDAMATSKLV 179  
 DB 171 SGDEL-GLVEEKAPCPSPVLLPRIGWDDDELQPGCAQVYMHFMQEHCTYDAMATSKLV 229  
 QY 180 IFDTMLEIKKAFALVANGRAAPLWDSKKQSFVGMLTITDFILVLRHYRSLVQIYEI 239  
 DB 230 IFDTMLEIKKAFALVANGRAAPLWDSKKQSFVGMLTITDFILVLRHYRSLVQIYEI 289  
 QY 240 EQHKIETWREIYLGQCFKPLVSPNDLSPEAVYTLIKNRIHRLPVLDPVSGNVHLHLTH 299  
 DB 290 EEHKIETWREIYLGQCFKPLVSPNDLSPEAVYTLIKNRIHRLPVLDPVSGNVHLHLTH 349  
 QY 300 KRLLKFLHIHFGTLPRPSFLYRTIQDIGTFERDLAVVLETPALTALDIFVDRRVSAALP 359  
 DB 350 KRLLKFLHIHFGTLPRPSFLYRTIQDIGTFERDLAVVLETPALTALDIFVDRRVSAALP 409  
 QY 360 VVNECGVGLYRFDVIHLAAQTYNHLDMVSGEALRQRTLCLEGLVSCOPHSLGEVI 419  
 DB 410 VVNETGVGLYRFDVIHLAAQTYNHLDMVSGEALRQRTLCLEGLVSCOPHSLGEVI 469  
 QY 420 DRIAREQVHRLVLVDETHQLHGVVSLDILQALVLSAPAGIDALGA 464  
 DB 470 DRIAREQVHRLVLVDETHQLHGVVSLDILQALVLSAPAGIDALGA 514  
 RESULT 6  
 Q8CJ41 MOUSE PRELIMINARY; PRT; 464 AA.  
 AC Q8CJ41;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE AMP-activated protein kinase gamma 3 subunit short form.  
 GN Name=Prkg3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RP [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALB/c; TISSUE=Skeletal muscle;  
 RX PubMed=14512293; DOI=10.1152/ajpcell.00319.2003; Goodyear L.J.;  
 RA Yu H., Fujii N., Hirschman M.F., Pomerleau J.M., Goodyear L.J.;  
 RT "Cloning and characterization of mouse 5'-AMP-activated protein kinase  
 gamma3 subunit.";  
 RL Am. J. Physiol. Cell Physiol. 286:C283-C292 (2004).  
 DR EMBL; AF525501; AAN47138.1; -; mRNA.



RC STRAIN=C57BL/6J; TISSUE=Bone;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama S., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kigawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Soabe Y., Tagami M.,  
RA Tegawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AF525500; AA047137.1; -; mRNA.  
DR ENBL; AK036585; BAC29492.1; -; mRNA.  
DR MG1; MGI:1891343; Prkg3.  
DR GO; GO:0016301; P:kinase activity; IEA.  
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
DR InterPro; IPR006644; CBS.  
DR Pfam; PF00571; CBS; 2.  
DR SMART; SM00116; CBS; 4.  
DR KW Kinase.  
SQ SEQUENCE 489 AA; 53848 MW; 85C9F71D8BDBDASD CRC64;  
Query Match 83.6%; Score 2010; DB 2; Length 489;  
Best Local Similarity 85.8%; Pred. No. 2.7e-144;  
Matches 399; Conservative 16; Mismatches 48; Indels 2; Gaps 2;  
Qy 1 MSFLEQENSSWSPAVTSSTSSIRGKRRKALRWTRQKSVSEEGEPGQGGPRSRPTAE 60  
Db 26 MDFLEQ-GENSWSPAVATSSERTCAIRGVKASRWTRQEAEEAEPPGLGEGAQSRPAE 84  
Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTGWDCLPSCDTASAAGSSTDDELATEFPATEA 119  
Db 85 STROEATFPKATPLAQAVPLAEATSPGTGWDLLLPDCAASAGGSTGDLTIEFPAPEA 144  
Qy 120 WECELEGLEERPALCLSPQAPFPKLGWDELKPGAIYMRFMQHTCYDAMATSSKLV 179  
Db 145 WDCELEGIGKDRPRPGSPQAPLGLSWDELQKGAQVYMHFMQHTCYDAMATSSKLV 204  
Qy 180 IFDTMLETIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDILVLRHYRSPVLQIYEI 239  
Db 205 IFDTTLEIKKAPFANVANGVRAAPLWDSKQSFVGMLTITDILVLRHYRSPVLQIYEI 264  
Qy 240 EQHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNRHRLPVLDPVSGNVHLIHTH 299  
Db 265 EEHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNRHRLPVLDPVSGTVLYILTH 324  
Qy 300 KRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRVVSALP 359  
Db 325 KRLKFLHIFGALLPRPSFLCRTIQDLGIGTFRDLAVVLETAPVLTALDIFVDRVVSALP 384  
Qy 360 VVNECGQVVGYSRFDVTHLAAQQTYNHLDMSVGEALQRITCLLEGVLSQCPHESLGEVI 419  
Db 385 VVNECGQVVGYSRFDVTHLAAQQTYNHLDMSVGEALQRITCLLEGVLSQCPHESLGEVI 444  
Qy 420 DRIAREQVHRLVLDVETQHLGVVSLSDILQALVLSPAGIDALSA 464

Db 445 DRIAREQVHRLVLDVETQHLGVVSLSDILQALVLSPAGIDALSA 489  
RESULT 8  
Q80WK8 MOUSE PRELIMINARY; PRT; 490 AA.  
ID Q80WK8\_MOUSE PRELIMINARY; PRT; 490 AA.  
AC Q80WK8\_MOUSE PRELIMINARY; PRT; 490 AA.  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE AMP-activated protein kinase gamma subunit.  
GN Name=Prkg3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=14970697; DOI=10.1159/000075743;  
RA Anarger V., Erlandsson R., Pielberg G., Jeon J.T., Andersson L.;  
RT "Comparative sequence analysis of the PRKG3 region between human and  
RT pig: evolution of repetitive sequences and potential new exons.";  
RL Cytochrome. Genome Res. 102:163-172(2003).  
DR ENBL; AY263402; AAP22981.1; -; Genomic DNA.  
DR GO; GO:0016301; P:kinase activity; IEA.  
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
DR InterPro; IPR006644; CBS.  
DR Pfam; PF00571; CBS; 2.  
DR SMART; SM00116; CBS; 4.  
DR KW Kinase.  
SQ SEQUENCE 490 AA; 53948 MW; DBFEF917B67D4CDS CRC64;  
Query Match 83.3%; Score 2001.5; DB 2; Length 490;  
Best Local Similarity 85.6%; Pred. No. 1.2e-143;  
Matches 399; Conservative 16; Mismatches 48; Indels 3; Gaps 3;  
Qy 1 MSFLEQENSSWSPAVTSSTSSIRGKRRKALRWTRQKSVSEEGEPGQGGPRSRPTAE 60  
Db 26 MDFLEQ-GENSWSPAVATSSERTCAIRGVKASRWTRQEAEEAEPPGLGEGAQSRPAE 84  
Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTGWDCLPSCDTASAAGSSTDDELATEFPATEA 119  
Db 85 STROEATFPKATPLAQAVPLAEATSPGTGWDLLLPDCAASAGGSTGDLTIEFPAPEA 144  
Qy 120 WECELEGLEERPALCLSPQAPFPKLGWDELKPGAIYMRFMQHTCYDAMATSSKLV 179  
Db 145 WDCELEGIGKDRPRPGSPQAPLGLSWDELQKGAQVYMHFMQHTCYDAMATSSKLV 204  
Qy 180 IFDTMLETIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDILVLRHYRSPVLQIYEI 239  
Db 205 IFDTTLEIKKAPFANVANGVRAAPLWDSKQSFVGMLTITDILVLRHYRSPVLQIYEI 264  
Qy 240 EQHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNRHRLPVLDPVSGNVHLIHTH 299  
Db 265 EEHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNRHRLPVLDPVSGTVLYILTH 324  
Qy 300 KRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRVVSALP 359  
Db 325 KRLKFLHIFGALLPRPSFLCRTIQDLGIGTFRDLAVVLETAPVLTALDIFVDRVVSALP 384  
Qy 360 VVNECG-QVVGYSRFDVTHLAAQQTYNHLDMSVGEALQRITCLLEGVLSQCPHESLGEV 418  
Db 385 VVNECGQVVGYSRFDVTHLAAQQTYNHLDMSVGEALQRITCLLEGVLSQCPHESLGEV 444  
Qy 419 IDRIAREQVHRLVLDVETQHLGVVSLSDILQALVLSPAGIDALGA 464  
Db 445 IDRIAREQVHRLVLDVETQHLGVVSLSDILQALVLSPAGIDALSA 490  
RESULT 9  
Q4G3U3\_BOVIN PRELIMINARY; PRT; 465 AA.  
ID Q4G3U3\_BOVIN PRELIMINARY; PRT; 465 AA.

AC Q4G3U3;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DE AMP-activated protein kinase gamma subunit (update)  
 DE AMP-activated protein kinase gamma subunit.  
 GN Name=PRKAG3;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skeletal muscle;  
 RA Yu S.L., Kim J.E., Jung K.C., Lee J.H., Choi I.H., Yoon D.H.,  
 RA San B.C.;  
 RT "Cloning and characterization of bovine AMP-activated protein kinase  
 gamma subunit (PRKAG3) gene."  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY692035; AAU67666.1; -; Genomic\_DNA.  
 KW Kinase.  
 SQ SEQUENCE 465 AA; 51523 MW; 35C8BC32C901D565 CRC64;  
 Query Match 82.8%; Score 1988.5; DB 2; Length 465;  
 Best Local Similarity 85.0%; Pred. No. 1.1e-142;  
 Matches 396; Conservative 24; Mismatches 43; Indels 3; Gaps 3;  
 Qy 1 MSFLEQSSSWPSPAVTSSSRIRGKRAKALRWTRQKSVSEGEPPGQGGPRSRPTAE 60  
 Db 1 MSFLEQSDTSWSPSPAMTSAEISLGQRTKVSWKQEDVEERELPGLGEGPQSRRAAE 60  
 Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGWDCLPSCDCTASAGSSTDDELATEFPATEA 119  
 Db 61 STGLEATFPKATPLAQATPLSAVGTPTTTERDSLPSDCTASAGSSTDDELQIEFSAPAA 120  
 Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHCTCDAMATSSKLV 179  
 Db 121 WGDEL-GLVERPACQSPQVFLURLGWDDDELKPKGAQVYMHFMQEHCTCDAMATSSKLV 179  
 Qy 180 IFDTMLIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEI 239  
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 Qy 240 EQHKIETWRIYLGQCFKPLVISPNDLSLFEAVVTILKNRIHRLPVLDPVSGVNLHLTH 299  
 Db 240 EEHKIETWRIYLGQCFKPLVISPNDLSLFEAVVTILKNRIHRLPVLDPVSGVNLHLTH 299  
 Qy 300 KRLLKFLHIF-GSLPPSPFLYRTIQDLGIGTFEDLAVVLETAPILTALDIFVDRRVSA 358  
 Db 300 KRLLKFLHIFQRTLLPPSPFLYRTIQDLGIGTFEDLAVVLETAPILTALDIFVDRRVSA 359  
 Qy 359 PVNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEV 418  
 Db 360 PVINEAGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEV 419  
 Qy 419 IDRIAREQVHRLVLVDTEQHLGLVVSLSLQALVLSFAGIDALGA 464  
 Db 420 IDRIAREQVHRLVLVDTEQHLGLVVSLSLQALVLSFAGIDALGA 465  
 RESULT 10  
 Q6TEH8 HORSE  
 ID Q6TEH8 HORSE PRELIMINARY; PRT; 447 AA.  
 AC Q6TEH8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE AMP-activated protein kinase gamma subunit (update)  
 DE AMP-activated protein kinase gamma subunit 3 (Fragment).  
 GN Name=prkag3;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skeletal muscle;  
 RA Yu S.L., Kim J.E., Jung K.C., Lee J.H., Choi I.H., Yoon D.H.,  
 RA San B.C.;  
 RT "Cloning and characterization of bovine AMP-activated protein kinase  
 gamma subunit (PRKAG3) gene."  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY692035; AAU67666.1; -; Genomic\_DNA.  
 KW Kinase.  
 SQ SEQUENCE 465 AA; 51523 MW; 35C8BC32C901D565 CRC64;  
 Query Match 82.8%; Score 1988.5; DB 2; Length 465;  
 Best Local Similarity 85.0%; Pred. No. 1.1e-142;  
 Matches 396; Conservative 24; Mismatches 43; Indels 3; Gaps 3;  
 Qy 1 MSFLEQSSSWPSPAVTSSSRIRGKRAKALRWTRQKSVSEGEPPGQGGPRSRPTAE 60  
 Db 1 MSFLEQSDTSWSPSPAMTSAEISLGQRTKVSWKQEDVEERELPGLGEGPQSRRAAE 60  
 Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGWDCLPSCDCTASAGSSTDDELATEFPATEA 119  
 Db 61 STGLEATFPKATPLAQATPLSAVGTPTTTERDSLPSDCTASAGSSTDDELQIEFSAPAA 120  
 Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHCTCDAMATSSKLV 179  
 Db 121 WGDEL-GLVERPACQSPQVFLURLGWDDDELKPKGAQVYMHFMQEHCTCDAMATSSKLV 179  
 Qy 180 IFDTMLIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEI 239  
 Db 180 IFDTMLQIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEI 239  
 Qy 240 EQHKIETWRIYLGQCFKPLVISPNDLSLFEAVVTILKNRIHRLPVLDPVSGVNLHLTH 299  
 Db 240 EEHKIETWRIYLGQCFKPLVISPNDLSLFEAVVTILKNRIHRLPVLDPVSGVNLHLTH 299  
 Qy 300 KRLLKFLHIF-GSLPPSPFLYRTIQDLGIGTFEDLAVVLETAPILTALDIFVDRRVSA 358  
 Db 300 KRLLKFLHIFQRTLLPPSPFLYRTIQDLGIGTFEDLAVVLETAPILTALDIFVDRRVSA 359  
 Qy 359 PVNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEV 418  
 Db 360 PVINEAGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEV 419  
 Qy 419 IDRIAREQVHRLVLVDTEQHLGLVVSLSLQALVLSFAGIDALGA 464  
 Db 420 IDRIAREQVHRLVLVDTEQHLGLVVSLSLQALVLSFAGIDALGA 465

Q6U7S1 HORSE  
 ID Q6U7S1 HORSE PRELIMINARY; PRT; 440 AA.  
 AC Q6U7S1;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE AMP-activated protein kinase gamma subunit (update)  
 DE AMP-activated protein kinase gamma subunit 3 (Fragment).  
 GN Name=Prkag3;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skeletal muscle;  
 RA Park H.B., Marklund S., Jeon J.T., Mickelson J.R., Valberg S.J.,  
 RA Sandberg K., Andersson L.;  
 RT "Molecular characterization and mutational screening of the PRKAG3  
 gene in the horse."  
 RL Cytogenet. Genome Res. 102:211-216(2003).  
 DR EMBL; AY423273; AAR03832.1; -; Genomic\_DNA.  
 DR EMBL; AY423271; AAR03832.1; JOINED; Genomic\_DNA.  
 DR EMBL; AY423272; AAR03832.1; JOINED; Genomic\_DNA.  
 DR GO; GO:0016301; P:kinase activity; IEA.  
 DR InterPro; IPR000644; CBS.  
 DR Pfam; PF00571; CBS; 2.  
 DR SMART; SM00116; CBS; 4.  
 KW Kinase.  
 FT NON TER 447 447  
 SQ SEQUENCE 447 AA; 49219 MW; 3BB4E70BA6F93C3E CRC64;  
 Query Match 79.9%; Score 1920; DB 2; Length 447;  
 Best Local Similarity 84.6%; Pred. No. 1.7e-137;  
 Matches 379; Conservative 25; Mismatches 42; Indels 2; Gaps 2;  
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 Db 1 MSFLEQSDTSWSPSPAMTSAEISLGQRTKVSWKQEDVEERELPGLGEGPQSRRAAE 60  
 Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGWDCLPSCDCTASAGSSTDDELATEFPATEA 119  
 Db 61 STGLEATFPATPLAQAPLAGVDTTPPERGILPSCDCASSSTGSSSTDDELQIEFSATAG 120  
 Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHCTCDAMATSSKLV 179  
 Db 121 WGCEL-GLVETPARVPSPRALLPRLGWDDDELKPKGAQVYMHFMQEHCTCDAMATSSKLV 179  
 Qy 180 IFDTMLIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEI 239  
 Db 180 IFDTTLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEI 239  
 Qy 240 EQHKIETWRIYLGQCFKPLVISPNDLSLFEAVVTILKNRIHRLPVLDPVSGVNLHLTH 299  
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 Db 300 KRLLKFLHIFGTLPPSPFLSRTIQDLGIGTFEDLAVVLETAPILTALDIFVDRRVSA 359  
 Qy 360 PVNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEV 419  
 Db 360 PVNEEGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEV 419  
 Qy 420 DRIAREQVHRLVLVDTEQHLGLVVSLSLSD 447  
 Db 420 DRIAREQVHRLVLVDTEQHLGLVVSLSLSD 447  
 RESULT 11  
 Q6U7S1 HORSE  
 ID Q6U7S1 HORSE PRELIMINARY; PRT; 440 AA.  
 AC Q6U7S1;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE AMP-activated protein kinase gamma subunit (update)  
 DE AMP-activated protein kinase gamma subunit 3 (Fragment).  
 GN Name=Prkag3;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skeletal muscle;  
 RA Park H.B., Marklund S., Jeon J.T., Mickelson J.R., Valberg S.J.,  
 RA Sandberg K., Andersson L.;  
 RT "Molecular characterization and mutational screening of the PRKAG3  
 gene in the horse."  
 RL Cytogenet. Genome Res. 102:211-216(2003).  
 DR EMBL; AY423273; AAR03832.1; -; Genomic\_DNA.  
 DR EMBL; AY423271; AAR03832.1; JOINED; Genomic\_DNA.  
 DR EMBL; AY423272; AAR03832.1; JOINED; Genomic\_DNA.  
 DR GO; GO:0016301; P:kinase activity; IEA.  
 DR InterPro; IPR000644; CBS.  
 DR Pfam; PF00571; CBS; 2.  
 DR SMART; SM00116; CBS; 4.  
 KW Kinase.  
 FT NON TER 447 447  
 SQ SEQUENCE 447 AA; 49219 MW; 3BB4E70BA6F93C3E CRC64;  
 Query Match 79.9%; Score 1920; DB 2; Length 447;  
 Best Local Similarity 84.6%; Pred. No. 1.7e-137;  
 Matches 379; Conservative 25; Mismatches 42; Indels 2; Gaps 2;  
 Qy 1 MSFLEQSSSWPSPAVTSSSRIRGKRAKALRWTRQKSVSEGEPPGQGGPRSRPTAE 60  
 Db 1 MSFLEQSDTSWSPSPAMTSAEISLGQRTKVSWKQEDVEERELPGLGEGPQSRRAAE 60  
 Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGWDCLPSCDCTASAGSSTDDELATEFPATEA 119  
 Db 61 STGLEATFPATPLAQAPLAGVDTTPPERGILPSCDCASSSTGSSSTDDELQIEFSATAG 120  
 Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHCTCDAMATSSKLV 179  
 Db 121 WGCEL-GLVETPARVPSPRALLPRLGWDDDELKPKGAQVYMHFMQEHCTCDAMATSSKLV 179  
 Qy 180 IFDTMLIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEI 239  
 Db 180 IFDTTLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEI 239  
 Qy 240 EQHKIETWRIYLGQCFKPLVISPNDLSLFEAVVTILKNRIHRLPVLDPVSGVNLHLTH 299  
 Db 240 EEHKIETWRIYLGQCFKPLVISPNDLSLFEAVVTILKNRIHRLPVLDPVSGVNLHLTH 299  
 Qy 300 KRLLKFLHIFGSLPPSPFLYRTIQDLGIGTFEDLAVVLETAPILTALDIFVDRRVSA 359  
 Db 300 KRLLKFLHIFGTLPPSPFLSRTIQDLGIGTFEDLAVVLETAPILTALDIFVDRRVSA 359  
 Qy 360 PVNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEV 419  
 Db 360 PVNEEGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEV 419  
 Qy 420 DRIAREQVHRLVLVDTEQHLGLVVSLSLSD 447  
 Db 420 DRIAREQVHRLVLVDTEQHLGLVVSLSLSD 447



RA	Sandberg K., Andersson L.;
RT	"Molecular characterization and mutational screening of the PRKAG3 gene in the horse.";
RL	Cytogenet. Genomes. 102:211-216 (2003).
RL	EMBL: AY376689; AAQ83583.1; -; mRNA.
DR	GO: 0016301; F-kinase activity; IEA.
DR	InterPro: IPR000644; CBS.
DR	Pfam: PF00571; CBS; 2.
DR	SMART: SM00116; CBS; 3.
FT	NON TER 440 440
FT	SEQUENCE 440 AA; 48561 MW; CB6C706D98E4A66A CRC64;
QY	1 MSFLEQNSSSWPSPAVTSSSRTRGKRRAKALRWTRQKSVVEEGEPQCGGPPSRPTAE 60
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QY	61 STGLEATFPKTTPLAQADP-AGVGTPTGMDCLPSDCTASAGSSTDDVELATEFPATEA 119
DB	61 STGLEATFPENTPLAQAPLAGVTTPPERGILFSDCASSSTGSTDLDLGIFFSATAG 120
QY	120 WECLEGLLEERPALCISPOAPFPKLGWDDDELKPGAGIYNRFMOEHTCYDAMATSSKLV 179
DB	121 WGCEL-GLVEETPARYSPRALLPRLGWDDDELQKPGAQVYMHFMOEHTCYDAMATSSKLV 179
QY	180 IFDTWLEIKKAFVALVANGVTAAPLWDSKKQSFVGMLTITDTFILVHRYRSPVQIYEI 239
DB	180 IFDFTTLEIKKAFVALVANGVRAAPLWDSKKQSFVGMLTITDTFILVHRYRSPVQIYEI 239
QY	240 EOKIETWREIYLOGCFKPLVSIISPNDSLPAVYTLIKNRHRLPVLDPVSGNVLHLTH 299
DB	240 EEHKIETWREIYLOGCFKPLVSIISPSDSLPAVYTLIKNRHRLPVLDPVSGNVLHLTH 299
QY	300 KRLKLFHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPLITALDIFVDRRVSAIP 359
DB	300 KRLKLFHIFGTLPPQPSFLSKTIQDLGIGTFRDLAVVLETAPLITALDIFVDRRVSAIP 359
QY	360 VVNEGGQVGLYSRFDVTHLAAQTYNHLDMSVGENLRQRTLCLEGVLSQCPHESLGEVI 419
DB	360 VVNEGGQVGLYSRFDVTHLAAQTYNHLDSVGEALFQRTVCLGVLSQCPHESLGEVI 419
QY	420 DRIAREQVHRLVLVDQTHLL 440
DB	420 DRIAREQVHRLVLVDQTHLL 440
RESULT 12	
Q4JK38_CHICK	
ID	Q4JK38_CHICK PRELIMINARY; PRT; 363 AA.
AC	Q4JK38;
DT	13-SEP-2005 (TRENBLrel. 31, Created)
DT	13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT	13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE	5'-AMP-activated protein kinase gamma-3 non-catalytic subunit short form.
DE	form.
GN	Name=PRKAG3;
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OX	NCBI_TaxID=9031;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Skeletal muscle;
RL	Proezkowicz-Węglarz M., Richards M.P., Poch S.M.;
RA	Submitted (MAY-2005) to the EMBL/GenBank/DBSJ databases.
DR	EMBL; DQ079815; AAY86042.1; -; mRNA.
KW	Kinase.
SQ	SEQUENCE 363 AA; 41151 MW; 06FCDD94FCC3AEDC CRC64;



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Qy 388 LDMVSGRALRRTICLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLGVLSLD 447
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Db 306 LDISVREALRRTVCLGVLTCYPHETMEDIIDRTIEEQVHRLVLDENRYPRGIVSLSD 365
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Qy 448 ILQALVLSPPAGIDALGA 464
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 366 ILQALVLTTPAGIDALNS 382
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RESULT 14
Q7ZYL2_XENLA
ID Q7ZYL2_XENLA PRELIMINARY; PRT; 337 AA.
AC Q7ZYL2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prkag1-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Fellings E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043738; AA043738.1; -; mRNA.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 4.
SQ SEQUENCE 337 AA; 3825 MW; EFF4AE102D6FD4 CRC64;

Query Match 50.5%; Score 1213.5; DB 2; Length 337;
Best Local Similarity 73.3%; Pred. No. 7e-84;
Matches 233; Conservative 40; Mismatches 38; Indels 7; Gaps 1;

Qy 143 PKLGWDELKPKGAIYWRMQEHTCYDMATSKLVIFDTMLEIKAFALVANGVRAA 202
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Db 23 PDIGED-----ASYMEFMKNCNNAIPTSKLVVFTTTQIKKAFALVANGVRAA 75
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    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 PLWDSKKQSGVGMLTITDFINILHRYKAPLVQIYEIEEKKIETWRDVLQSSFKPLIYI 135
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Qy 263 SPNDSLPEAVYTLIKRIHRLPVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRT 322
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 136 SPADSLFQAVYSLTKNKHRLPVMQPVSGNHLHILTHKRLKFLHIFGDLTPRQFLQKT 195
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 323 IQDLGIGTFRDLAVLETPALTALDIFVDRRYSALPVNVECGQVGLYSRFDVHLAAQ 382
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 196 ILELGIGTFRDIAVQVDTSSVNALEIFVRRYSALPVNVECGQVGLYSRFDVHLAAQ 255
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 383 QTYNHLDMSVGEALRQTLCLGVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLGV 442
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Db 256 KIYNLDISVLDAIRLSLCIEGVMCYPHESLEWIDRIVREQIHRVLVDEERRPLGI 315
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Qy 443 VLSLDILQALVLSPPAGID 460
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Db 316 VLSLDILQALVLTTPAGID 333
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RESULT 15
Q8BIQ9_MOUSE
ID Q8BIQ9_MOUSE PRELIMINARY; PRT; 443 AA.
AC Q8BIQ9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:6430509K05 product:similar to AMP ACTIVATED
DE PROTEIN KINASE GAMMA 1.
GN Name=Prkag2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: January 24, 2006, 22:04:33 ; Search time 38.6164 Seconds  
(without alignments)  
993.400 Million cell updates/sec

Title: US-10-070-794A-30  
Perfect score: 2403  
Sequence: 1 MSFLEQNSSSWSPAVTSS.....LSDIQLQVLSPAGIDALGA 464

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pap:\*
- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pap:\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pap:\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pap:\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pap:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2013	83.8	464	2	US-09-950-022A-4
2	2011	83.7	464	2	US-09-950-022A-2
3	2010	83.6	464	2	US-09-950-022A-8
4	2007	83.5	464	2	US-09-950-022A-10
5	2005	83.4	464	2	US-09-950-022A-6
6	1088.5	45.3	413	2	US-09-949-016-8261
7	1080.5	45.0	328	1	US-08-878-989-7
8	1080.5	45.0	328	2	US-09-272-796-7
9	1028	42.8	330	2	US-09-359-161-6
10	1017	42.3	331	1	US-08-878-989-21
11	1017	42.3	331	2	US-09-101-146-64
12	1017	42.3	331	2	US-09-272-796-21
13	1017	42.3	331	2	US-09-538-092-1211
14	1017	42.3	336	2	US-09-949-016-10881
15	457	19.0	322	2	US-09-359-161-7
16	457	19.0	322	2	US-09-538-092-297
17	312	13.0	101	2	US-09-513-999C-5736
18	258	10.7	254	2	US-09-248-796A-18872
19	214	8.9	379	2	US-09-359-161-5
20	205.5	8.6	629	2	US-09-248-796A-14535
21	190	7.9	373	2	US-09-359-161-3
22	117	4.9	776	2	US-09-252-991A-30380
23	114.5	4.8	490	2	US-09-252-991A-30355
24	106.5	4.4	272	2	US-09-252-991A-18313
25	104.5	4.3	375	2	US-09-328-352-6078
26	101	4.2	187	2	US-09-199-637A-287
27	101	4.2	187	2	US-09-252-991A-21454

28	100.5	4.2	622	2	US-09-605-703B-2098	Sequence 2098, Ap
29	100	4.2	419	2	US-09-270-767-46031	Sequence 46031, A
30	100	4.2	2766	2	US-09-964-956-62	Sequence 62, Appl
31	99.5	4.1	701	2	US-10-052-092-12	Sequence 12, Appl
32	99	4.1	676	2	US-09-248-796A-14898	Sequence 14898, A
33	98.5	4.1	375	2	US-09-634-238-260	Sequence 260, App
34	98.5	4.1	680	2	US-09-949-016-10770	Sequence 10770, A
35	97.5	4.1	510	2	US-09-489-039A-11778	Sequence 11778, A
36	97	4.0	752	2	US-09-919-039-235	Sequence 235, App
37	97	4.0	852	1	US-09-070-060-3	Sequence 3, Appli
38	97	4.0	852	2	US-09-357-746-3	Sequence 3, Appli
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40	96.5	4.0	481	2	US-09-252-991A-31708	Sequence 31708, A
41	96.5	4.0	736	2	US-09-949-016-8855	Sequence 8855, Ap
42	96	4.0	405	2	US-09-198-452A-301	Sequence 301, App
43	96	4.0	405	2	US-09-438-185A-290	Sequence 290, App
44	95.5	4.0	180	2	US-09-252-991A-18269	Sequence 18269, A
45	95.5	4.0	307	2	US-09-949-016-8453	Sequence 8453, Ap

## ALIGNMENTS

### RESULT 1

US-09-950-022A-4  
; Sequence 4, Application US/09950022A  
; Patent No. 6919177  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Clobanui, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark.  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950, 022A  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-09-950-022A-4

Query Match	83.8%;	Score	2013;	DB	2;	Length	464;
Best Local Similarity	86.0%;	Pred. No.	8.1e-218;				
Mismatches	400;	Conservative	19;	Mismatches	44;	Indels	2;
Gaps	2;						
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Db	61	STGQEAFFPKATPLAQAAPLAEDVNPFTERDILPSCAASASDNTDHLDLGIEFSAA	120				
QY	120	WECELEGLLEERPALCLSPQAPFKLGWDELKPGCAQIYMRPMOEHCTYDANATSKLV	179				
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Qy 360 VVNECGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEVI 419  
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Qy 420 DRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSGIDALGA 464  
Db 420 DRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSGIDALGA 464

## RESULT 2

US-09-950-022A-2  
; Sequence 2, Application US/09950022A  
; Patent No. 6919177  
; GENERAL INFORMATION:  
; APPLICANT: Rothechild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950,022A  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-09-950-022A-2

Query Match 83.7%; Score 2011; DB 2; Length 464;  
Best Local Similarity 86.0%; Pred. No. 1.4e-217;  
Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;  
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Db 1 MSFLEQESRSWSPSAVTSSEIRIGKRAKALRWTRQKSVVEEGEPGQGGPRSRPTAE 60  
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Db 61 STGLEATFPKTTPLAQAADP-AGVGTPTGMDCLPSDCTASAGSSTDVDELATFPATEA 119  
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Db 240 EHKIETWREIYLQGCCKPLVSPNDLSFEAVYALIKNRIHRLPVLDPVSGAVLHILTH 299  
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Db 300 KRLLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALP 359

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Db 360 VVNETGVVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEVI 419  
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Db 420 DRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSGIDALGA 464  
RESULT 3  
US-09-950-022A-8  
; Sequence 8, Application US/09950022A  
; Patent No. 6919177  
; GENERAL INFORMATION:  
; APPLICANT: Rothechild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950,022A  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-09-950-022A-8

Query Match 83.6%; Score 2010; DB 2; Length 464;  
Best Local Similarity 85.8%; Pred. No. 1.8e-217;  
Matches 399; Conservative 20; Mismatches 44; Indels 2; Gaps 2;  
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Db 1 MSFLEQESRSWSPSAVTSSEIRIGKRAKALRWTRQKSVVEEGEPGQGGPRSRPTAE 60  
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Db 120 WECELEGILBERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHTCYDAMATSSKLV 179  
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Db 121 SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDDELKPKGAQIYMRFMQEHTCYDAMATSSKLV 179  
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Db 240 EHKIETWREIYLQGCCKPLVSPNDLSFEAVYALIKNRIHRLPVLDPVSGAVLHILTH 299  
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Db 300 KRLLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALP 359  
Qy 360 VVNECGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEVI 419  
Db 360 VVNETGVVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQRTLCLEGLVSCQPHELSGEVI 419  
Qy 420 DRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSGIDALGA 464  
Db 420 DRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSGIDALGA 464

## RESULT 4

US-09-950-022A-10  
; Sequence 10, Application US/09950022A

; Patent No. 6919177

; GENERAL INFORMATION:

; APPLICANT: Rothschild, Max

; APPLICANT: Ciobanu, Dan

; APPLICANT: Malek, Massoud

; APPLICANT: Plastow, Graham

; TITLE OF INVENTION: Reproductive

; TITLE OF INVENTION: and Meat Quality Traits

; FILE REFERENCE: P04668US3

; CURRENT APPLICATION NUMBER: US/09/950,022A

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231045

; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: 60/260,239

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/299,111

; PRIOR FILING DATE: 2001-06-18

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 464

; TYPE: PRT

; ORGANISM: Sus scrofa

US-09-950-022A-10

; Query Match

Best Local Similarity 83.5%; Score 2007; DB 2; Length 464;

Matches 399; Conservative 20; Mismatches 44; Indels 2; Gaps 2;

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Db 1 MSFLEQESRSWPSRAVTTSSRSHGQGNKASRWTRQEDVEEGPPGQCGEGRSRPTAE 60

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Db 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGWDCLPSCDTASAAGSSTDVDELATEFPATEA 120

Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHCTYDAMATSSKLV 179

Db 121 SGDEL-GLVEEKAPCPSPVLLPRLGWDDDELKPKGAQVYMHFMQEHCTYDAMATSSKLV 179

Qy 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDFFILVLRHYRSPVQIYEI 239

Db 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDFFILVLRHYRSPVQIYEI 239

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Db 360 VVNETGVGLYSRFDVIHLAAQOQYVNLHDMVGEALRQRTLCLEGLVSCOPHETLGEVI 419

Qy 420 DRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSFAGIDALGA 464

Db 420 DRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSFAGIDALGA 464

## RESULT 5

US-09-950-022A-6

; Sequence 6, Application US/09950022A

; Patent No. 6919177

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; APPLICANT: Rothschild, Max

; APPLICANT: Ciobanu, Dan

; APPLICANT: Malek, Massoud

; APPLICANT: Plastow, Graham

; TITLE OF INVENTION: Reproductive

; TITLE OF INVENTION: and Meat Quality Traits

; FILE REFERENCE: P04668US3

; CURRENT APPLICATION NUMBER: US/09/950,022A

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231045

; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: 60/260,239

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/299,111

; PRIOR FILING DATE: 2001-06-18

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 464

; TYPE: PRT

; ORGANISM: Sus scrofa

US-09-950-022A-6

; Query Match

Best Local Similarity 83.4%; Score 2005; DB 2; Length 464;

Matches 399; Conservative 19; Mismatches 45; Indels 2; Gaps 2;

Qy 1 MSFLEQENSSWSPATVSSSRIRGKRRAKALRWTRQKSVGEPPGQCGEGRSRPTAE 60

Db 1 MSFLEQESRSWPSRAVTTSSRSHGQGNKASRWTRQEDVEEGPPGQCGEGRSRPTAE 60

Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGWDCLPSCDTASAAGSSTDVDELATEFPATEA 119

Db 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGWDCLPSCDTASAAGSSTDVDELATEFPATEA 120

Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHCTYDAMATSSKLV 179

Db 121 SGDEL-GLVEEKAPCPSPVLLPRLGWDDDELKPKGAQVYMHFMQEHCTYDAMATSSKLV 179

Qy 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDFFILVLRHYRSPVQIYEI 239

Db 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDFFILVLRHYRSPVQIYEI 239

Qy 240 EOHKIETWREIYLGQCFKPLVSPNDLSLFEAVVTLIKNRIHRLPVLDPVSGNVHLHILTH 299

Db 240 EOHKIETWREIYLGQCFKPLVSPNDLSLFEAVVTLIKNRIHRLPVLDPVSGNVHLHILTH 299

Qy 300 KRLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALP 359

Db 300 KRLLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALP 359

Qy 360 VVNECGVGLYSRFDVIHLAAQOQYVNLHDMVGEALRQRTLCLEGLVSCOPHESLGEVI 419

Db 360 VVNETGVGLYSRFDVIHLAAQOQYVNLHDMVGEALRQRTLCLEGLVSCOPHETLGEVI 419

Qy 420 DRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSFAGIDALGA 464

Db 420 DRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSFAGIDALGA 464

## RESULT 6

US-09-949-016-8261

; Sequence 8261, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

```

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8261
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8261

Query Match      45.3%; Score 1088.5; DB 2; Length 413;
Best Local Similarity 53.9%; Pred. No. 1.5e-113;
Matches 223; Conservative 73; Mismatches 67; Indels 51; Gaps 9;

Qy 46 PPGGEGPRSEPTAESTGLETFKTPLAQADPAGVGTPTGWDCLPSCDTASAAGSST 105
Db 41 PPDTGQ--RCPSPFQS-----PTRPPLAS-----PTHY--APSKAALAAALG- 80
Qy 106 DDVELATEFPATEAWECELEGLLEERPALCILSPQAPFPKLGWDDE-LRKFGAQIYMRPMQ 164
Db 81 -----PA-EA-----GMLE-----KLEFEDEAVEDSDSGVYMRFR 110
Qy 165 EHTCYDAMATSSKLVIPDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDILV 224
Db 111 SHKCYDIVPTSSKLVVFTTLQVKKAPFALVANGVRAAPLWESKQSFVGMLTITDIFNI 170
Qy 225 LHRYYRSPVOIYEIOHKIETWREIYLGQCFKPLVSPNDLSLFEAVYTLIKNRIHRLP 284
Db 171 LHRYYRSPVOIYEIEEHKIEHWRELYQETFKPLVNSPDASLFDVYSLIKNRIHRLP 230
Qy 285 VLDPSGNGVLHILTHKRLLKELHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETA 344
Db 231 VIDPISGNALYILTHKRILKFLQFMSDMPKPAFMKQNLDELGIGTYVHIAFIHPDPII 290
Qy 345 TALDIFDVRVSALPVNVECGQVGLYSRFDVHIAAQOTNHLDMVSVEALRORTLCLE 404
Db 291 KALNIFERRISALPVNDESGKVDIYSKFDVINLAEKTYNNLDITVTQALQHSQYFE 350
Qy 405 GVLSQPHSEIGEVDIARISQVHRLVLDVETQHLGVVSLSDILOALVLSLSPAG 458
Db 351 GVVKCNKLEILETIVDRIVRAEVRHRLVVVNEADSIIVGIIISLDILOALILTPAG 404

RESULT 7
US-08-878-989-7
; Sequence 7, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PENITUT01
; CLONE: 1452972
; US-08-878-989-7

Query Match      45.0%; Score 1080.5; DB 1; Length 328;
Best Local Similarity 63.3%; Pred. No. 8.1e-113;
Matches 200; Conservative 67; Mismatches 48; Indels 1; Gaps 1;

Qy 144 KLGWDEHT-LRKPGAQIYMRFWQHEITCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAA 202
Db 4 KLEFEDEAVEDSDSGVYMRFWRSKCYDIVPTSSKLVVFTTLQVKKAPFALVANGVRAA 63
Qy 203 PLWDSKQSFVGMLTITDIFILHRYRSPVLSQIYEIEIOHKIETWREIYLGQCFKPLVSI 262
Db 64 PLWESKQSFVGMLTITDIFINILHRYKSPMVQIYEIEEHKIEHWRELYQETFKPLVNI 123
Qy 263 SPNDLSLFEAVYTLIKNRIHRLPVLDVPSGNVHLTHKRLLKFLHIFGSLPRPSFLYRT 322
Db 124 SPDASLFDVYSLIKNRIHRLPVLDIPISGNALYILTHKRILKFLQFMSDMPKPAFMKQ 183
Qy 323 IQDLGIGTFRDLAVVLETAIPILTALDIFDVRVSALPVNVECGQVGLYSRFDVHIAAQ 382
Db 184 LDELGIGTYVHIAFIHPDTPILKALNIFERRISALPVNDESGKVDIYSKFDVINLAE 243
Qy 383 QTYNHLDMVSVEALRORTLCLEGLVLSQPHSEIGEVDIARISQVHRLVLDVETQHLGV 442
Db 244 KTYNNLDITVTQALQHSQYFEGVVKCNKLEILETIVDRIVRAEVRHRLVVVNEADSI 303
Qy 443 VLSLDILOALVLSLSPAG 458
Db 304 ISLSLDILOALILTPAG 319

RESULT 8
US-09-272-796-7
; Sequence 7, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive

```

;; CITY: Palo Alto  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/272,796  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/878,989  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J J  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0321 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-855-0555  
;; TELEFAX: 415-845-4166  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 328 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: PENITUT01  
;; CLONE: 1452972  
;; US-09-272-796-7

Query Match 45.0%; Score 1080.5; DB 2; Length 328;  
Best Local Similarity 63.3%; Pred. No. 8.1e-113;  
Matches 200; Conservative 67; Mismatches 48; Indels 1; Gaps 1;

Qy 144 KLGWDE-LRKPQAQIYMRFMQHTCYDAMATSSKLVIFDTMLIKKAFKAFVANGVRAA 202  
Db 4 KLEPDEAEDSESGVYMRFMRSKCYDVTSSKLVVFDITLQVKKAFKAFVANGVRAA 63

Qy 203 PLWDSKKQSFVGMLTITDFILVLRHYRSPVQIYEIEQHKIETWREIYLOGCFKPLVSI 262  
Db 64 PLWESKKQSFVGMLTITDFINILHRYKSPVQIYEIEEHHKIEIETWRELYLQETFKPLVNI 123

Qy 263 SPNDLSFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLKFLHIFGSLLPSPFLYRT 322  
Db 124 SPASLFDVYSLIKNRIHRLPVLDPISGNALYILTHKRLKFLQFLPMSDMPKPAFMQN 183

Qy 323 IQDLGIGTFRDLAVVLETAIPALTALDIFVDRRVSALPVNVECGVGLYSRFDVVIHAAQ 382  
Db 184 LDELIGTYHNIAPHDPTPIKALNIFVERRISALPVNDESGKVDIYKFDVINLAAE 243

Qy 383 QTNHLDMSVGEALRQRTLCLEGVLSQPHESIGEVIDRIAREQVHRLVLDVDETOHL 442  
Db 244 KTYNNLDITVQALQHRSQYFEGVVKCNKLEILETIVDRIVRAEVHRLVVNDEADSVGI 303

Qy 443 VLSLDILOALVLPAG 458  
Db 304 ISLSLDILOALILTPAG 319

RESULT 9  
US-09-359-161-6  
; Sequence 6, Application US/09359161A  
; Patent No. 6342656  
; GENERAL INFORMATION:  
; APPLICANT: Bradford, Kent J.  
; APPLICANT: Dahal, Peetambar  
; APPLICANT: Yang, Hong  
; APPLICANT: Cooley, Michael

;; APPLICANT: Downie, Bruce  
;; APPLICANT: Gee, Oliver  
;; APPLICANT: The Regents of the University of California  
;; TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses  
;; FILE REFERENCE: 023070-095900US  
;; CURRENT APPLICATION NUMBER: US/09/359,161A  
;; CURRENT FILING DATE: 1999-07-21  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 6  
;; LENGTH: 330  
;; TYPE: PRT  
;; ORGANISM: Rattus norvegicus  
;; FEATURE:  
;; OTHER INFORMATION: gamma subunit of AMP-activated protein kinase  
;; OTHER INFORMATION: (AMPK-gamma)  
US-09-359-161-6

Query Match 42.8%; Score 1028; DB 2; Length 330;  
Best Local Similarity 62.3%; Pred. No. 6.9e-107;  
Matches 197; Conservative 56; Mismatches 63; Indels 0; Gaps 0;

Qy 140 APPKLGWDELRKPGAQIYMRFMQHTCYDAMATSSKLVIFDTMLIKKAFKAFVANGV 199  
Db 9 APAPENHSQETPESNSSVYITFMKSHRCYDLIPTSSKLVVFDITLQVKKAFKAFVANGV 68

Qy 200 RAAPLWDSKKQSFVGMLTITDFILVLRHYRSPVQIYEIEQHKIETWREIYLOGCFKPL 259  
Db 69 RAAPLWDSKKQSFVGMLTITDFINILHRYKSPVQIYEIEEHHKIEIETWRELYLQDSFKPL 128

Qy 260 VSISPNDLSFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLKFLHIFGSLLPSPFL 319  
Db 129 VCISPNASLFDVSSLIKRIHRLPVIDPESGNTLYILTHKRLKFLKFLTFTEFPKPEFM 188

Qy 320 YRTIQDLGIGTFRDLAVVLETAIPALTALDIFVDRRVSALPVNVECGVGLYSRFDVHL 379  
Db 189 SKSLEELQIGTYANIAMVTRITTPVYVALGIFVQHRVSALPVNDEKGRVDIYKFDVINL 248

Qy 380 AAQOTYNNHLDMSVGEALRQRTLCLEGVLSQPHESIGEVIDRIAREQVHRLVLDVDETOHL 439  
Db 249 AAEKTYNNLDVSVTKALQHRSHYFEGVVKCYLHETLEAIINRLVRAEVHRLVVVDEHDVV 308

Qy 440 LGVVSLSLDILOALVLS 455  
Db 309 KGIVSLSLDILOALVLT 324

RESULT 10  
US-08-878-989-21  
; Sequence 21, Application US/08878989  
; Patent No. 5885803  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; TITLE OF INVENTION: KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible

Thu Jan 26 09:20:51 2006

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; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 435
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1335856
; US-08-878-989-21

Query Match 42.3%; Score 1017; DB 1; Length 331;
Best Local Similarity 64.8%; Pred. No. 1.2e-105;
Matches 193; Conservative 53; Mismatches 52; Indels 0; Gaps 0;

Qy 158 IYMFQMHCTCYDAMATSSKLVIFDTMLEIKKAFKAFVANGVRAAPLWDSKKQSFVGMLT 217
Db 28 VYTFMKSHRCYDLIPTSSKLVFDTSLQVKKAFKAFVANGVRAAPLWDSKKQSFVGMLT 87

Qy 218 ITDFILVHRYRSPVQIYIEQHKIETWREIYLGCCFKPLVSPNDSLFEAVYTLIK 277
Db 88 ITDFINILHRYYSKALVQIYELEHKIETWREIYLGCCFKPLVSPNDSLFEAVYTLIK 147

Qy 278 NRIHRLPVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSLYRTIOGLGTGTRDLAV 337
Db 148 NKIHLRPVDPESGNTLYLTHKRLKFLHIFGSLPRPSLYRTIOGLGTGTRDLAV 207

Qy 338 LETAPILTALDIFVDRRVSAFPVNECGVGLYSRFDVIHLAAQOTVNHLDMSVGEALR 397
Db 208 RTTTPVYVALGIFVQHRVSALPVVDEKGRVVDIYSKFDVINLAAEKTNNLDVSVTKALQ 267

Qy 398 QRTLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLDILQALVLS 455
Db 268 HRSHYFEGVLKCYLHETLETTIINRLVEAEVHRLVVVDENVVKGIVSLSDILQALVLT 325

RESULT 11
US-09-101-146-64
; Sequence 64, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincent's Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95

; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-101-146-64

Query Match 42.3%; Score 1017; DB 2; Length 331;
Best Local Similarity 64.8%; Pred. No. 1.2e-105;
Matches 193; Conservative 53; Mismatches 52; Indels 0; Gaps 0;

Qy 158 IYMFQMHCTCYDAMATSSKLVIFDTMLEIKKAFKAFVANGVRAAPLWDSKKQSFVGMLT 217
Db 28 VYTFMKSHRCYDLIPTSSKLVFDTSLQVKKAFKAFVANGVRAAPLWDSKKQSFVGMLT 87

Qy 218 ITDFILVHRYRSPVQIYIEQHKIETWREIYLGCCFKPLVSPNDSLFEAVYTLIK 277
Db 88 ITDFINILHRYYSKALVQIYELEHKIETWREIYLGCCFKPLVSPNDSLFEAVYTLIK 147

Qy 278 NRIHRLPVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSLYRTIOGLGTGTRDLAV 337
Db 148 NKIHLRPVDPESGNTLYLTHKRLKFLHIFGSLPRPSLYRTIOGLGTGTRDLAV 207

Qy 338 LETAPILTALDIFVDRRVSAFPVNECGVGLYSRFDVIHLAAQOTVNHLDMSVGEALR 397
Db 208 RTTTPVYVALGIFVQHRVSALPVVDEKGRVVDIYSKFDVINLAAEKTNNLDVSVTKALQ 267

Qy 398 QRTLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLDILQALVLS 455
Db 268 HRSHYFEGVLKCYLHETLETTIINRLVEAEVHRLVVVDENVVKGIVSLSDILQALVLT 325

RESULT 12
US-09-272-796-21
; Sequence 21, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lai, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PE-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1335856
;
US-09-272-796-21

Query Match 42.3%; Score 1017; DB 2; Length 331;
Best Local Similarity 64.8%; Pred. No. 1.2e-105;
Matches 193; Conservative 53; Mismatches 52; Indels 0; Gaps 0;

Qy 158 IYRMFQEHCTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMILT 217
Db 28 VYTSFMKSHRCYDLIPTSSKLVVFDTSLOVKKAFALVTNGVRAAPLWDSKKQSFVGMILT 87
Qy 218 ITDFILVLRHYRSPVQIYEIHOHKIETWREIYLOGCFFKPLVSIISNDLSLFEAVYTLIK 277
Db 88 ITDFINILHRYKSAVQIYELEHKEIETWREYVLOQSFKPLVCISPNASLFDVSSLR 147
Qy 278 NRHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVV 337
Db 148 NKIHLRPVIDPESGNTLYLTHKRLKFLKLFITEFPKPFMSKLEELQIGTYANIAMV 207
Qy 338 LETAPILTALDIFVDRRVSAIPVNVCGQVGLYSRFDVIHLAAQOQTYNHLDMVSGEALR 397
Db 208 RTTPVTVVAGIFVQHRVSALPVVDEKGRVVDIYSKFDVINLAAEKTNNLDVSVTKALQ 267
Qy 398 QRTLCLEGVLSQCPHESIGEVIDRIAREQVHRLVLDVDETHLLGVVSLDILQALVLS 455
Db 268 HRSHYFEGVLKCYLHETLEIINRLVEAEVHRLVVVDENVVKGIVSLDILQALVLT 325

RESULT 13
US-09-538-092-1211
; Sequence 1211, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqformat Version 0.9
; SEQ ID NO 1211
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P54619
US-09-538-092-1211

Query Match 42.3%; Score 1017; DB 2; Length 331;
Best Local Similarity 64.8%; Pred. No. 1.2e-105;
Matches 193; Conservative 53; Mismatches 52; Indels 0; Gaps 0;

Qy 158 IYRMFQEHCTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMILT 217
Db 28 VYTSFMKSHRCYDLIPTSSKLVVFDTSLOVKKAFALVTNGVRAAPLWDSKKQSFVGMILT 87
Qy 218 ITDFILVLRHYRSPVQIYEIHOHKIETWREIYLOGCFFKPLVSIISNDLSLFEAVYTLIK 277
Db 88 ITDFINILHRYKSAVQIYELEHKEIETWREYVLOQSFKPLVCISPNASLFDVSSLR 147
Qy 278 NRHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVV 337
Db 148 NKIHLRPVIDPESGNTLYLTHKRLKFLKLFITEFPKPFMSKLEELQIGTYANIAMV 207
Qy 338 LETAPILTALDIFVDRRVSAIPVNVCGQVGLYSRFDVIHLAAQOQTYNHLDMVSGEALR 397
Db 208 RTTPVTVVAGIFVQHRVSALPVVDEKGRVVDIYSKFDVINLAAEKTNNLDVSVTKALQ 267
Qy 398 QRTLCLEGVLSQCPHESIGEVIDRIAREQVHRLVLDVDETHLLGVVSLDILQALVLS 455
Db 268 HRSHYFEGVLKCYLHETLEIINRLVEAEVHRLVVVDENVVKGIVSLDILQALVLT 325

RESULT 14
US-09-949-016-10881
; Sequence 10881, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10881
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10881

Query Match 42.3%; Score 1017; DB 2; Length 336;
Best Local Similarity 64.8%; Pred. No. 1.2e-105;
Matches 193; Conservative 53; Mismatches 52; Indels 0; Gaps 0;

Qy 158 IYRMFQEHCTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMILT 217
Db 33 VYTSFMKSHRCYDLIPTSSKLVVFDTSLOVKKAFALVTNGVRAAPLWDSKKQSFVGMILT 92
Qy 218 ITDFILVLRHYRSPVQIYEIHOHKIETWREIYLOGCFFKPLVSIISNDLSLFEAVYTLIK 277
Db 93 ITDFINILHRYKSAVQIYELEHKEIETWREYVLOQSFKPLVCISPNASLFDVSSLR 152
Qy 278 NRHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVV 337
Db 153 NKIHLRPVIDPESGNTLYLTHKRLKFLKLFITEFPKPFMSKLEELQIGTYANIAMV 212
Qy 338 LETAPILTALDIFVDRRVSAIPVNVCGQVGLYSRFDVIHLAAQOQTYNHLDMVSGEALR 397
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Db 213 RTTPVVALGIFVQHRVSALPVVDEKGRVVDIYSKFDVINLAAEKTNNLDVSVTKALQ 272  
Qy 398 QRTLCLEGVLSQOPHESIGEVIDRIAREQVHRVLVLDVETQHLGVSVLSLQALVLS 455  
Db 273 HRSHYFEGVLKCYLHETLETTINRLVEAEVHRVLVVVDENDVVKGIVSLSDILOALVLT 330

RESULT 15  
US-09-359-161-7  
; Sequence 7, Application US/093359161A  
; Patent No. 6342656  
; GENERAL INFORMATION:  
; APPLICANT: Bradford, Kent J.  
; APPLICANT: Dahal, Peetambar  
; APPLICANT: Yang, Hong  
; APPLICANT: Cooley, Michael  
; APPLICANT: Downie, Bruce  
; APPLICANT: Gee, Oliver  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses  
; FILE OF INVENTION: to Stress Conditions in Plants  
; FILE REFERENCE: 023070-095900US  
; CURRENT APPLICATION NUMBER: US/09/359,161A  
; CURRENT FILING DATE: 1999-07-21  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; OTHER INFORMATION: Yeast sucrose nonfermenting protein kinase 1  
; OTHER INFORMATION: kinase subunit (SNF1)  
US-09-359-161-7

Query Match 19.0%; Score 457; DB 2; Length 322;  
Best Local Similarity 34.2%; Pred. No. 1.9e-42;  
Matches 106; Conservative 66; Mismatches 108; Indels 30; Gaps 6;  
Qy 161 RFMOBHTCYDAMATSKSLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITD 220  
Db 24 KFLNSKTSYDVLVPSYRLVLDTSLLVKSLNVLQNSIVSAPLWDSKTSRFAGLLTTTD 83  
Qy 221 FILVLRHYRSPLOIYEIOHKIETWREIYLCQCFKL-----VSIENDSL 269  
Db 84 FINVIQYFNSP-----DKFELVDKQLDGL-KDIERALGVGDQDLDTSIHPSRELF 133  
Qy 270 EAVYTLIKNRIHRLPVLDPVSGN----VLHILTKRLKLFHIFGSLAPRPS-FLYRTIQ 324  
Db 134 EACLKMLESRGRIPLIDQDETHREIVSVLTQYRIKLFV-----ALNCRETHFLKIFIG 189  
Qy 325 DLIGITFRDLAVLTAPILTALDIFVDRRVSAFPVNECGQVGVLYSRFDFVIHLAAQOT 384  
Db 190 DLNIITQDNMKSQMTFVIDIQLMTQGRVSSVPIIDENGVLINVEAYDVLGIKGGI 249  
Qy 385 YNHLDMSVGEALRQRTLCLEGVLSQOPHESIGEVIDRIAREQVHRVLVLDVETQHLGVLS 444  
Db 250 YNDLSLSVGEALMRRSDDFEGVYCTCKNDKLTIMDNIRKARVHRFFVVDVGVRLGVLT 309  
Qy 445 LSDILOALVL 454  
Db 310 LSDILKYILL 319

Search completed: January 24, 2006, 22:16:25  
Job time : 39.6164 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:14:24 ; Search time 102.575 Seconds  
(without alignments)  
1890.063 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403

Sequence: 1 MSFLEQENSSWPSPAVTSS.....LSDILOALVLPAGIDALGA 464

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_Main.\*

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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*

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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2403	100.0	489	5	US-10-503-175-2
2	2398	99.8	489	3	US-09-826-581-6
3	2398	99.8	489	4	US-10-473-670-15
4	2398	99.8	489	4	US-10-705-137-6
5	2376	98.9	489	5	US-10-503-039-2
6	2376	98.9	489	5	US-10-503-175-6
7	2372	98.7	492	5	US-10-756-149-5028
8	2013	83.8	464	3	US-09-950-022-4
9	2013	83.8	464	6	US-11-075-134-4
10	2011	83.7	464	3	US-09-950-022-2
11	2011	83.7	464	6	US-11-075-134-2
12	2010	83.6	464	3	US-09-950-022-8
13	2010	83.5	464	6	US-11-075-134-8
14	2007	83.5	464	3	US-09-950-022-10
15	2007	83.5	464	6	US-11-075-134-10
16	2005	83.4	464	3	US-09-950-022-6
17	2005	83.4	464	6	US-11-075-134-6
18	2000	83.2	489	5	US-10-503-175-4
19	1082.5	45.0	352	5	US-10-466-162-12
20	1080.5	45.0	328	3	US-09-769-970-7
21	1080.5	45.0	328	5	US-10-466-162-14
22	1017	42.3	331	3	US-09-769-970-21
23	1017	42.3	331	5	US-10-473-127-923
24	1017	42.3	331	5	US-10-473-127-924
25	1017	42.3	331	5	US-10-473-127-927
26	1017	42.3	331	5	US-10-473-127-928
27	1017	42.3	331	5	US-10-466-162-16

28	1017	42.3	344	3	US-09-925-297-461	Sequence 461, App
29	1017	42.3	344	5	US-10-473-127-925	Sequence 925, App
30	886	36.9	488	5	US-10-450-763-50437	Sequence 50437, A
31	874.5	36.4	1207	4	US-10-108-605-71	Sequence 71, Appl
32	869.5	36.2	634	6	US-11-097-143-25527	Sequence 25527, A
33	845.5	35.2	383	5	US-10-450-763-50439	Sequence 50439, A
34	759	31.5	181	4	US-10-276-774-1611	Sequence 1611, Ap
35	494	20.6	180	4	US-10-106-698-6572	Sequence 6572, Ap
36	396	16.5	149	4	US-10-264-237-1653	Sequence 1653, Ap
37	374.5	15.6	487	5	US-10-739-930-6722	Sequence 6722, Ap
38	362	15.1	477	4	US-10-425-114-50302	Sequence 50302, A
39	357	14.9	448	4	US-10-425-115-187601	Sequence 187601, A
40	355	14.8	451	4	US-10-437-963-168583	Sequence 168583, A
41	352.5	14.7	368	4	US-10-425-114-54796	Sequence 54796, A
42	352.5	14.7	493	4	US-10-424-599-187700	Sequence 187700, A
43	352	14.6	461	4	US-10-424-599-22531	Sequence 22531, A
44	350.5	14.6	365	4	US-10-425-114-69679	Sequence 69679, A
45	347.5	14.5	497	4	US-10-425-115-274759	Sequence 274759, A

ALIGNMENTS

RESULT 1

US-10-503-175-2  
; Sequence 2, Application US/10503175  
; Publication No. US20050172348A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersson, Leif  
; APPLICANT: Marklund, Stefan  
; TITLE OF INVENTION: Transgenic animals expressing prkg3  
; FILE REFERENCE: 11145-020US1  
; CURRENT APPLICATION NUMBER: US/10/503,175  
; CURRENT FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: PCT/IB03/00912  
; PRIOR FILING DATE: 2003-01-31  
; PRIOR APPLICATION NUMBER: US 60/353,430  
; PRIOR FILING DATE: 2002-02-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 489  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-503-175-2

Query Match	100.0%	Score	2403	DB	5	Length	489
Best Local Similarity	100.0%	Pred. No.	2.6e-217				
Matches	464	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MSFLEQENSSWPSPAVTSSSRIRGKRAKALRWTRQKSVGEPPGQEGPGRSRPTAE	60				
Db	26	MSFLEQENSSWPSPAVTSSSRIRGKRAKALRWTRQKSVGEPPGQEGPGRSRPTAE	85				
Qy	61	STGLEATFPKTTPLAQADPAGVCTPTGMDCLPDSCTASAGSSTDVDELATFPATEAW	120				
Db	86	STGLEATFPKTTPLAQADPAGVCTPTGMDCLPDSCTASAGSSTDVDELATFPATEAW	145				
Qy	121	ECELEGLERPALCLSPQAPPKLGDDELKPKGQIYMRFMQHTCYDAMATSSKLVI	180				
Db	146	ECELEGLERPALCLSPQAPPKLGDDELKPKGQIYMRFMQHTCYDAMATSSKLVI	205				
Qy	181	FTMLIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVLQIYEIE	240				
Db	206	FTMLIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVLQIYEIE	265				
Qy	241	QHKIETWREIYLOGCFKPLVSPNDSLFEAVVTLTKNRIHRLPVLDPVSGNVLHLTHK	300				
Db	266	QHKIETWREIYLOGCFKPLVSPNDSLFEAVVTLTKNRIHRLPVLDPVSGNVLHLTHK	325				
Qy	301	RLIKFLHFGSLPRPSFLYRTIQDGICTFRDLAVLETAITLTDIFVDRVRSALPV	360				
Db	326	RLIKFLHFGSLPRPSFLYRTIQDGICTFRDLAVLETAITLTDIFVDRVRSALPV	385				

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Qy 361 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQPHESLGEVID 420
Db 386 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQPHESLGEVID 445
Qy 421 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPPAGIDALGA 464
Db 446 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPPAGIDALGA 489

RESULT 2
US-09-826-581-6
; Sequence 6, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Lelf
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-581-6

Query Match 99.8%; Score 2398; DB 3; Length 489;
Best Local Similarity 99.8%; Pred. No. 7.8e-217;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGPPQGEGPSRPTAE 60
Db 26 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGPPQGEGPSRPAAE 85
Qy 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 120
Db 86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 145
Qy 121 ECEGLELEERPALCLSPQAPFPKLGWDDLELRKPCAQIYMERFMOEHTCYDAMATSSKLVI 180
Db 146 ECEGLELEERPALCLSPQAPFPKLGWDDLELRKPCAQIYMERFMOEHTCYDAMATSSKLVI 205
Qy 181 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMGLTTTDFILVLRHYRSPVQIYEIE 240
Db 206 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMGLTTTDFILVLRHYRSPVQIYEIE 265
Qy 241 QHKTETWREIYLOGCFKPLVSI PNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300
Db 266 QHKTETWREIYLOGCFKPLVSI PNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 325
Qy 301 RLLKFLHIFGLSPRLPSFLYRTIQDLGIGTFRDLAVVLETPALITDIFVDRRVSALPV 360
Db 336 RLLKFLHIFGLSPRLPSFLYRTIQDLGIGTFRDLAVVLETPALITDIFVDRRVSALPV 385
Qy 361 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQPHESLGEVID 420
Db 386 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQPHESLGEVID 445
Qy 421 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPPAGIDALGA 464
Db 446 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPPAGIDALGA 489

RESULT 3
US-10-473-670-15
; Sequence 15, Application US/10473670
; Publication No. US20040110180A1

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; GENERAL INFORMATION:
; APPLICANT: RECIPON, Shirley A.; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: TANG, Y. Tom; THORNTON, Michael;
; APPLICANT: BOROWSKY, Mark L.; BAUGHN, Mariah R.;
; APPLICANT: BURFORD, Neil; LEE, Soo Yeun;
; APPLICANT: BANDMAN, Olga; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; RAMKUMAR, Jayalaxmi;
; APPLICANT: CHAWLA, Narinder K.; LU, Dying Aina M.;
; APPLICANT: ARVIZU, Chandra S.; ISON, Craig H.;
; APPLICANT: DING, Li; LU, Yan;
; APPLICANT: GURURAJAN, Rajagopal; WALSH, Roderick T.;
; APPLICANT: GANDHI, Ameena R.; SWARNAKAR, Anita;
; APPLICANT: FORSTIHE, Ian J.; YUE, Henry;
; APPLICANT: AU-YOUNG, Janice K.; ELLIOTT, Vicki S.;
; APPLICANT: LEE, Sally
; TITLE OF INVENTION: KINASES AND PHOSPHATASES
; FILE REFERENCE: PI-0398 USN
; CURRENT APPLICATION NUMBER: US/10/473,670
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/10818
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/282,119
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/283,588
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,759
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/285,589
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/287,037
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/287,036
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/288,608
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/288,712
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/289,909
; PRIOR FILING DATE: 2001-05-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474666CD1
US-10-473-670-15

Query Match 99.8%; Score 2398; DB 4; Length 489;
Best Local Similarity 99.8%; Pred. No. 7.8e-217;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGPPQGEGPSRPTAE 60
Db 26 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGPPQGEGPSRPAAE 85
Qy 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 120
Db 86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 145
Qy 121 ECEGLELEERPALCLSPQAPFPKLGWDDLELRKPCAQIYMERFMOEHTCYDAMATSSKLVI 180
Db 146 ECEGLELEERPALCLSPQAPFPKLGWDDLELRKPCAQIYMERFMOEHTCYDAMATSSKLVI 205
Qy 181 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMGLTTTDFILVLRHYRSPVQIYEIE 240
Db 206 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMGLTTTDFILVLRHYRSPVQIYEIE 265
Qy 241 QHKTETWREIYLOGCFKPLVSI PNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300

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; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00912
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,430
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-175-6

Query Match      98.9%; Score 2376; DB 5; Length 489;
Best Local Similarity 98.9%; Pred. No. 9.2e-215;
Matches 459; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPRSRPTAE 60
Db      26 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPRSRPAE 85

Qy      61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 120
Db      86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 145

Qy      121 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRPMQEHCTCYDAMATSSKLVI 180
Db      146 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRPMQEHCTCYDAMATSSKLVI 205

Qy      181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEIE 240
Db      206 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEIE 265

Qy      241 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300
Db      266 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 325

Qy      301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 360
Db      326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 385

Qy      361 VNECGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRORTLCLEGLVSCQPHESLGEVID 420
Db      386 VNECGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRORTLCLEGLVSCQPHESLGEVID 445

Qy      421 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAPAGIDALGA 464
Db      446 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAPAGIDALGA 489

RESULT 7
US-10-756-149-5028
; Sequence 5028, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5028
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5028

Query Match      98.7%; Score 2372; DB 5; Length 492;
Best Local Similarity 98.7%; Pred. No. 2.2e-214;
Matches 457; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPRSRPTAE 60
Db      26 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPRSRPAE 85

Qy      61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 120
Db      86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 145

Qy      121 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRPMQEHCTCYDAMATSSKLVI 180
Db      146 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRPMQEHCTCYDAMATSSKLVI 205

Qy      181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEIE 240
Db      206 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEIE 265

Qy      241 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300
Db      266 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 325

Qy      301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 360
Db      326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 385

Qy      361 VNECGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRORTLCLEGLVSCQPHESLGEVID 420
Db      386 VNECGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRORTLCLEGLVSCQPHESLGEVID 445

Qy      421 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAPAGIDALGA 464
Db      446 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAPAGIDALGA 489

RESULT 8
US-09-950-022-4
; Sequence 4, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRK33 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022-4

Query Match      83.8%; Score 2013; DB 3; Length 464;
Best Local Similarity 86.0%; Pred. No. 1.5e-180;
Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;

Qy      1 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPRSRPTAE 60
Db      1 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPRSRPAE 60

Qy      61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 119
Db      61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 120
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Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKRPKGAQIYMRFMQEHCTYDAMATSSKLV 179
Db 121 SGDEL-GLVEKPAKPSPEVLLPRLGWDDDELKRPKGAQVYMHFMQEHCTYDAMATSSKLV 179
Qy 180 IFDTMLEIKKAFKAFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLHRYRSPVLQIYEI 239
Db 180 IFDTMLEIKKAFKAFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLHRYRSPVLQIYEI 239
Qy 240 BOHKIETWREIYLOGCFKPLVISPNDLSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Db 240 BEHKIETWREIYLOGCFKPLVISPNDLSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Qy 300 KRLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPALTALDIFVDRRVSAALP 359
Db 300 KRLLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETPALTALDIFVDRRVSAALP 359
Qy 360 VVNECGVGLYSRFDVHILAAQOTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVI 419
Db 360 VVNETGVVGLYSRFDVHILAAQOTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVI 419
Qy 420 DRIAREOVHRLVLVDETOHLLGVVSLSDILOALVLSFAGIDALGA 464
Db 420 DRIVEQVHRLVLVDETOHLLGVVSLSDILOALVLSFAGIDALGA 464

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## RESULT 9

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US-11-075-134-4
; Sequence 4, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-075-134-4

```

```

Query Match 83.8%; Score 2013; DB 6; Length 464;
Best Local Similarity 86.0%; Pred. No. 1.5e-180;
Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;
Qy 1 MSFLEQENSSSWPSPAVTSSSRIKRRKAKALRWTRQKSVEEGEPGQGGPRSRPTAE 60
Db 1 MSFLEQESRSWPSRAVTTSSSRHGDGKTSRWTRQEDVEEGPPGPGQSRPVAE 60
Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTGWDCLPSCDTASAGSSTDVLEATEFPATEA 119
Db 61 STGQEAFFPKATPLAQAPLAEVNDPPTERDILPSCDAASDSNTDHLDLGIEFSAAA 120
Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKRPKGAQIYMRFMQEHCTYDAMATSSKLV 179
Db 121 SGDEL-GLVEKPAKPSPEVLLPRLGWDDDELKRPKGAQVYMHFMQEHCTYDAMATSSKLV 179

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Qy 180 IFDTMLEIKKAFKAFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLHRYRSPVLQIYEI 239
Db 180 IFDTMLEIKKAFKAFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLHRYRSPVLQIYEI 239
Qy 240 BOHKIETWREIYLOGCFKPLVISPNDLSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Db 240 BEHKIETWREIYLOGCFKPLVISPNDLSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Qy 300 KRLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPALTALDIFVDRRVSAALP 359
Db 300 KRLLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETPALTALDIFVDRRVSAALP 359
Qy 360 VVNECGVGLYSRFDVHILAAQOTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVI 419
Db 360 VVNETGVVGLYSRFDVHILAAQOTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVI 419
Qy 420 DRIAREOVHRLVLVDETOHLLGVVSLSDILOALVLSFAGIDALGA 464
Db 420 DRIVEQVHRLVLVDETOHLLGVVSLSDILOALVLSFAGIDALGA 464

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## RESULT 10

```

US-09-950-022-2
; Sequence 2, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022-2

```

```

Query Match 83.7%; Score 2011; DB 3; Length 464;
Best Local Similarity 86.0%; Pred. No. 2.3e-180;
Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;
Qy 1 MSFLEQENSSSWPSPAVTSSSRIKRRKAKALRWTRQKSVEEGEPGQGGPRSRPTAE 60
Db 1 MSFLEQESRSWPSRAVTTSSSRHGDGKTSRWTRQEDVEEGPPGPGQSRPVAE 60
Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTGWDCLPSCDTASAGSSTDVLEATEFPATEA 119
Db 61 STGQEAFFPKATPLAQAPLAEVNDPPTERDILPSCDAASDSNTDHLDLGIEFSAAA 120
Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKRPKGAQIYMRFMQEHCTYDAMATSSKLV 179
Db 121 SGDEL-GLVEKPAKPSPEVLLPRLGWDDDELKRPKGAQVYMHFMQEHCTYDAMATSSKLV 179
Qy 180 IFDTMLEIKKAFKAFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLHRYRSPVLQIYEI 239
Db 180 IFDTMLEIKKAFKAFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLHRYRSPVLQIYEI 239
Qy 240 BOHKIETWREIYLOGCFKPLVISPNDLSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Db 240 BEHKIETWREIYLOGCFKPLVISPNDLSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299

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Qy 300 KRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
Db 300 KRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
Qy 360 VVNECGVVGGLYSRFDVIHLAAQOQTYNHLDMVSGEALRQRTCLCEGLVSCOPHESLGEVI 419
Db 360 VVNETGVVGLYSRFDVIHLAAQOQTYNHLDMVSGEALRQRTCLCEGLVSCOPHETLGEVI 419
Qy 420 DRIAREQVHRLVLVDETOHLLGVVSLSDILOALVLSLSPAGIDALGA 464
Db 420 DRIAREQVHRLVLVDETOHLLGVVSLSDILOALVLSLSPAGIDALGA 464

RESULT 11
US-11-075-134-2
; Sequence 2, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PKAG3 Alleles and Use to the Same as Genetic Markers for
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-075-134-2

Query Match 83.7%; Score 2011; DB 6; Length 464;
Best Local Similarity 86.0%; Pred. No. 2.3e-180;
Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MSFLEQENSSWSPSPAVTSSSIRIGKRAKALRWTRKSVSEEGPPGQGGPRSRPTAE 60
Db 1 MSFLEQGESRSWSPSRAVTTSSERSHGQGNKASRWTRQEDVEEGPPGPRGQSRPVAE 60
Qy 61 STGLEATFPKTTPLAQADP-AGVCTPPTGWDCLPSCDCTASAAGSSTDVLELATEFPATEA 119
Db 61 STGQEAATPKATPLAQAPLAEVNDPPTERDILPSDCAASASDSNTDHLDLGIEFSASAA 120
Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQHTCYDAMATSSKLV 179
Db 121 SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDDELQKFGAQVYMHFMQHTCYDAMATSSKLV 179
Qy 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDPIVLVHRYRSPVQIYEI 239
Db 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDPIVLVHRYRSPVQIYEI 239
Qy 240 EHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Db 240 EHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Qy 300 KRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
Db 300 KRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
Qy 360 VVNECGVVGGLYSRFDVIHLAAQOQTYNHLDMVSGEALRQRTCLCEGLVSCOPHESLGEVI 419
Db 360 VVNETGVVGLYSRFDVIHLAAQOQTYNHLDMVSGEALRQRTCLCEGLVSCOPHETLGEVI 419
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Db 360 VVNETGVVGLYSRFDVIHLAAQOQTYNHLDMVSGEALRQRTCLCEGLVSCOPHETLGEVI 419
Qy 420 DRIAREQVHRLVLVDETOHLLGVVSLSDILOALVLSLSPAGIDALGA 464
Db 420 DRIAREQVHRLVLVDETOHLLGVVSLSDILOALVLSLSPAGIDALGA 464

RESULT 12
US-09-950-022-8
; Sequence 8, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PKAG3 Alleles and Use to the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022-8

Query Match 83.6%; Score 2010; DB 3; Length 464;
Best Local Similarity 85.8%; Pred. No. 2.8e-180;
Matches 399; Conservative 20; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MSFLEQENSSWSPSPAVTSSSIRIGKRAKALRWTRKSVSEEGPPGQGGPRSRPTAE 60
Db 1 MSFLEQGESRSWSPSRAVTTSSERSHGQGNKASRWTRQEDVEEGPPGPRGQSRPVAE 60
Qy 61 STGLEATFPKTTPLAQADP-AGVCTPPTGWDCLPSCDCTASAAGSSTDVLELATEFPATEA 119
Db 61 STGQEAATPKATPLAQAPLAEVNDPPTERDILPSDCAASASDSNTDHLDLGIEFSASAA 120
Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQHTCYDAMATSSKLV 179
Db 121 SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDDELQKFGAQVYMHFMQHTCYDAMATSSKLV 179
Qy 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDPIVLVHRYRSPVQIYEI 239
Db 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDPIVLVHRYRSPVQIYEI 239
Qy 240 EHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Db 240 EHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Qy 300 KRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
Db 300 KRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
Qy 360 VVNECGVVGGLYSRFDVIHLAAQOQTYNHLDMVSGEALRQRTCLCEGLVSCOPHESLGEVI 419
Db 360 VVNETGVVGLYSRFDVIHLAAQOQTYNHLDMVSGEALRQRTCLCEGLVSCOPHETLGEVI 419
Qy 420 DRIAREQVHRLVLVDETOHLLGVVSLSDILOALVLSLSPAGIDALGA 464
Db 420 DRIAREQVHRLVLVDETOHLLGVVSLSDILOALVLSLSPAGIDALGA 464
```



## RESULT 13

US-11-075-134-8

; Sequence 8, Application US/11075134

; Publication No. US20050208551A1

; GENERAL INFORMATION:

; APPLICANT: Rothchild, Max

; APPLICANT: Ciobanu, Dan

; APPLICANT: Malek, Massoud

; APPLICANT: Plastow, Graham

; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for

; TITLE OF INVENTION: Reproductive and Meat Quality Traits

; FILE REFERENCE: P04668US3

; CURRENT APPLICATION NUMBER: US/11/075,134

; CURRENT FILING DATE: 2005-03-08

; PRIOR APPLICATION NUMBER: US/09/950,022

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231045

; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: 60/260,239

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/299,111

; PRIOR FILING DATE: 2001-06-18

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 464

; TYPE: PRT

; ORGANISM: Sus scrofa

US-11-075-134-8

## Query Match

Best Local Similarity 83.6%; Score 2010; DB 6; Length 464;

Best Local Similarity 85.8%; Pred. No. 2.8e-180;

Matches 399; Conservative 20; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MSFLEQENSSSWPSPATVSSSRIRGKRAKALRWTRQKSVGEPPGQGGPRSRPTAE 60

Db 1 MSFLEQESRSWSPRAVTTSSSRSHGQGNKASRWTRQEDVEEGPPGQGGPRSPVAE 60

Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGWDCLPSPDCTASAGSSTDVLEATEFPATEA 119

Db 61 STGQEAFFPKATPLAQAPLAEDVNPPTERDILPSCDCAASDSNTDHLGIEFSASAA 120

Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHCTYDAMATSSKLV 179

Db 121 SGDEL-GLVEEKAPCPSPVLLPRLGWDDDELQKPGAQVYMHFMQEHCTYDAMATSSKLV 179

Qy 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFTLVLRHYRSPVLQIYEI 239

Db 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFTLVLRHYRSPVLQIYEI 239

Qy 240 EOHKIETWREIYLGQCFKPLVSPNDLSLFEAVYTLIKNRIHRLPVLDPVSGVNLHILTH 299

Db 240 EHKIETWREIYLGQCFKPLVSPNDLSLFEAVYTLIKNRIHRLPVLDPVSGVNLHILTH 299

Qy 300 KRLLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETAFTALTALDIFVDRRVSAALP 359

Db 300 KRLLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETAFTALTALDIFVDRRVSAALP 359

Qy 360 VVNECGQVGLYSRFDVIHLAAQOQTYNHLDMVSVEALRQRTLCLEGVLSQPHESLGEVI 419

Db 360 VVNETGVVGLYSRFDVIHLAAQOQTYNHLDMVSVEALRQRTLCLEGVLSQPHETLGEVI 419

Qy 420 DRIAREQVHRLVLVDVETQHLGVVLSLSDIILQALVLSGIDALGA 464

Db 420 DRIAREQVHRLVLVDVETQHLGVVLSLSDIILQALVLSGIDALGA 464

## RESULT 14

US-09-950-022-10

; Sequence 10, Application US/09950022

; Publication No. US20030017470A1

; GENERAL INFORMATION:

; APPLICANT: Rothchild, Max

; APPLICANT: Ciobanu, Dan

; APPLICANT: Malek, Massoud

; APPLICANT: Plastow, Graham

; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for

; TITLE OF INVENTION: Reproductive and Meat Quality Traits

; FILE REFERENCE: P04668US3

/ CURRENT APPLICATION NUMBER: US/11/075,134	
/ CURRENT FILING DATE: 2005-03-08	
/ PRIOR APPLICATION NUMBER: US/09/950,022	
/ PRIOR FILING DATE: 2001-09-10	
/ PRIOR APPLICATION NUMBER: 60/231045	
/ PRIOR FILING DATE: 2000-09-08	
/ PRIOR APPLICATION NUMBER: 60/260,239	
/ PRIOR FILING DATE: 2001-01-08	
/ PRIOR APPLICATION NUMBER: 60/299,111	
/ PRIOR FILING DATE: 2001-06-18	
/ NUMBER OF SEQ ID NOS: 21	
/ SOFTWARE: Patentin version 3.1	
/ SEQ ID NO 10	
/ LENGTH: 464	
/ TYPE: PRT	
/ ORGANISM: Sus scrofa	
US-11-075-134-10	
Query Match	
Best Local Similarity 83.5%; Score 2007; DB 6; Length 464;	
Matches 399; Conservative 20; Mismatches 44; Indels 2; Gaps 2;	
Qy	1 MSFLEQENSSWPSPAVTSSSRTRGKRRAKALRWTRQKSVVEEGPPQGGGPRSRPTAE 60
Db	1 MSFLEQGESWSPRAVTTSSRSHGQGNKASRWTRQEDVEEGGPGPREGQSRPVAE 60
Qy	61 STGLEATFPKTTPLQAADP - AGVCTPPTGMDCLPDCSTASAGSSTDDELATFPATEA 119
Db	61 STGQEAFTPKATPLQAAPLAEAVDNPPTERDILPSCDAASDSNTDHLDLGIFBSAA 120
Qy	120 WECELEGLLEERPALCLSPQAPPFKLGHWDDELKPGAQIYNRFMQEHTCYDAMATSSKLV 179
Db	121 SGDEL - GLVEEKPAFCPSPEVLLPRLGLWDDDELQKPGAQVYMHFQEHTCYDAMATSSKLV 179
Qy	180 IFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLRHYRSPVQIYEI 239
Db	180 IFDTMLEIKKAFFALVANGVQAAPLWDSKKQSFVGMLTITDFILVLRHYRSPVQIYEI 239
Qy	240 EQHKIETWREIYLQCGFKPLVSI SPNDSLFEAVYTLIKNRTHRLPVLDPVSGNVHLIHTH 299
Db	240 EEHKIETWREIYLQCGFKPLVSI SPNDSLFEAVYALIKNRTHRLPVLDPVSGAVHLIHTH 299
Qy	300 KRLLKFLHI FGSILPRPSFLYRTTQDLGIGTFRDLAVVLETAPILTALDIFVDRKVSALP 359
Db	300 KRLLKFLHIFGTLPRPSFLYRTTQDLGIGTFRDLAVVLETAPILTALDIFVDRKVSALP 359
Qy	360 VVNECGOVGLYSRFDVTHLAAQOTYNHLDMSVGEALRQRTLCLEGLVSLSCOPHESLGEVI 419
Db	360 VVNETGVVGLYSRFDVTHLAAQOTYNHLDNMVGEALRQRTLCLEGLVSLSCOPHETLGEVI 419
Qy	420 DRIAREQVHRLVLVDETHLLGVVSLSDIILQALVLSPAGIDALGA 464
Db	420 DRIVREOVHRLVLVDETHLLGVVSLSDIILQALVLSPAGIDALGA 464

Search completed: January 24, 2006, 22:30:58  
Job time : 103.575 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2006, 22:15:19 ; Search time 20.515 Seconds  
(without alignments)  
229.213 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403

Sequence: 1 MSFLEQNSSSPSPAVTSS.....LSDILQALVLSPPAGIDALGA 464

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70609 seqs, 10134256 residues

Total number of hits satisfying chosen parameters: 70609

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:\*  
1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppaa/US03\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
\* score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	4.6	466	7	US-11-156-084-26
2	111	4.6	466	7	US-11-156-084-33
3	111	4.6	494	7	US-11-156-084-34
4	107.5	4.5	498	6	US-10-467-657-5006
5	107.5	4.5	829	6	US-10-821-234-1179
6	102	4.2	461	7	US-11-156-084-35
7	100.5	4.2	495	7	US-11-156-084-36
8	99	4.1	330	7	US-11-156-084-230
9	92.5	3.8	529	6	US-10-632-150-44
10	92.5	3.8	529	7	US-11-073-457-44
11	92.5	3.8	529	7	US-11-073-460-44
12	92.5	3.8	554	6	US-10-467-657-8240
13	91	3.8	4374	7	US-11-128-572-2
14	90.5	3.8	909	7	US-11-076-187-4
15	90.5	3.8	1137	7	US-11-012-762-70
16	89.5	3.7	488	6	US-10-793-626-2308
17	89.5	3.7	1311	6	US-10-509-422-5
18	88.5	3.7	643	7	US-11-137-465-54
19	88	3.7	653	7	US-11-137-465-55
20	87.5	3.6	1618	6	US-10-984-645-2
21	87	3.6	619	7	US-11-052-554A-229
22	87	3.6	1251	7	US-11-043-889-22
23	86.5	3.6	506	7	US-11-055-822-946
24	86.5	3.6	867	6	US-10-467-657-2208
25	86	3.6	1225	7	US-11-053-100-50

26	85.5	3.6	158	7	US-11-055-822-948	Sequence 948, App
27	85.5	3.6	644	6	US-10-509-121-39	Sequence 39, Appl
28	85.5	3.6	7968	7	US-11-143-980-49	Sequence 49, Appl
29	85	3.5	1023	6	US-10-131-826A-200	Sequence 200, App
30	82	3.4	1005	7	US-11-080-991-90	Sequence 90, Appl
31	81.5	3.4	1841	7	US-11-057-058-63	Sequence 63, Appl
32	81	3.4	412	7	US-11-093-808-1	Sequence 1, Appl
33	81	3.4	412	7	US-11-093-808-7	Sequence 7, Appl
34	81	3.4	412	6	US-11-093-808-8	Sequence 8, Appl
35	81	3.4	621	6	US-10-632-150-28	Sequence 28, Appl
36	81	3.4	621	7	US-11-073-457-28	Sequence 28, Appl
37	81	3.4	621	7	US-11-073-460-28	Sequence 28, Appl
38	81	3.4	712	6	US-10-770-726-66	Sequence 66, Appl
39	81	3.4	761	6	US-10-453-372-126	Sequence 126, App
40	81	3.4	823	6	US-10-453-372-122	Sequence 122, App
41	81	3.4	823	6	US-10-453-372-124	Sequence 124, App
42	81	3.4	826	6	US-10-453-372-118	Sequence 118, App
43	81	3.4	826	6	US-10-453-372-156	Sequence 156, App
44	81	3.4	826	6	US-10-453-372-166	Sequence 166, App
45	81	3.4	826	6	US-10-453-372-172	Sequence 172, App

#### ALIGNMENTS

##### RESULT 1

US-11-156-084-26  
; Sequence 26, Application US/11156084  
; Publication No. US20060010515A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology LLC  
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to  
; FILE OF INVENTION: agronomically interesting phenotypes  
; FILE REFERENCE: (38-21)  
; CURRENT APPLICATION NUMBER: US/11/156,084  
; CURRENT FILING DATE: 2005-06-17  
; NUMBER OF SEQ ID NOS: 364  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26  
; LENGTH: 466  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-11-156-084-26

Query Match 4.6%; Score 111; DB 7; Length 466;

Best Local Similarity 23.2%; Pred. No. 0.017;

Matches 68; Conservative 45; Mismatches 90; Indels 90; Gaps 16;

Qy	228	YYSPLVQIYEIQHKIETWREIYLOGCFKPLVSISPNDSLFEAV-----YTLIKN	278
Db	120	YIQAQVSVKELDDAAEDT-----ECCADVASVVDQDMVSVFGRDDLHGVELLKE	173
Qy	279	RIHRLPVLDPVSGNVLHILTHKLLKELHIFGSLPPSPFLY--RTIQDLG-IGTFR-DL	334
Db	174	-----LDPAANRHPNNHKKINQYLSLHSGRGLPSKLYQGTAKNMGGINASRPDY	226
Qy	335	AVV-----LETAPILTALDIFVDRVRSALPVVNECQVGVLY-----S	372
Db	227	CLICMDAETA-----VLDRYVEQRVDAMVDAGLDEVVDIYKPGADYTRGLRQSGVREFE	282
Qy	373	RFDVHILAAQOTYNHL-----DMSVGEALRQRTLCLEGLVSCQPHES-----LGEVIDRI	422
Db	283	DFLKIHLL-SETCAGHLTSLSDNDKWKENLRK-----ILNPPKDKLRIMLESEIDRV	334
Qy	423	-----ARQVHRLVLY-----DETQHLGLVSLSDILQALVLSPPA	457
Db	335	KLNTRLLRRQRKRRVSRLETVFGNTHIYDAITYILS--KSEESWNAQVVKPA	385

##### RESULT 2

US-11-156-084-33  
; Sequence 33, Application US/11156084  
; Publication No. US20060010515A1

```

; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; TITLE OF INVENTION: agronomically interesting phenotypes
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-156-084-33

Query Match          4.6%; Score 111; DB 7; Length 466;
Best Local Similarity 23.2%; Pred. No. 0.017;
Matches 68; Conservative 45; Mismatches 90; Indels 90; Gaps 16;

Qy 228 YRSLPVLQVIEIOHKIETWREIYLOGCFKPLVSPNDSLFEAV-----YTLIKN 278
Db 120 YIIQAVVSKFLDDAAEDT-----EECCADVSVVDQMVVESVFGRRDLSHGVELLKE 173

Qy 279 RIHRLPVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLY--RTIQDLG-IGTFR-DL 334
Db 174 -----LDPVAANRIHPNHRKINQVLSLHASRGVLPKLYQKTAENWGCINASRFDY 226

Qy 335 AVV-----LETAPILTALDIFVDRRSALPVVNECGQVGLY-----S 372
Db 227 CLICMDAETA---VLDRYVEQVRDAMVDAGLLDEVYDIKPGADYTRGLRQSIGVREFE 282

Qy 373 RFDVHILAAQTYNHL-----DMSVGEALRQRTLCLEGVLSQCPHES----LGEVIDRI 422
Db 283 DFLKIHL-SETCAGHLTSLSDKVKMKENLRK-----ILNFPKDDKRLIMLEEAIDRV 334

Qy 423 -----AREQVHRLVLV-----DETQHLGLVWSLSDIQLQALVSPA 457
Db 335 KLNTRLLRRQKRRVSRLETFVGNHIIHYIDATEVILS--KSEESWNAQVVKPA 385

; QUERY MATCH
; BEST LOCAL SIMILARITY 4.6%; SCORE 107.5; DB 6; LENGTH 498;
; BEST LOCAL SIMILARITY 26.3%; PRED. NO. 0.04;
; MATCHES 36; CONSERVATIVE 31; MISMATCHES 57; INDELS 13; GAPS 4;

Qy 329 GTFRDLAVLLETAPILTALDIFVD--RRVSALPVVNECGQVGLYSRFDVHLHAAQTYN 386
Db 102 GVWKDPVTVAPTTLIREVLEMRQAKRKMSGLPVV-ENGKVGIVTNRDL-----RPN 154

Qy 387 HLDMSVGEALRQRTLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLVDETQHLGLVWSLS 446
Db 155 RVDLPVSAIMTPR-----ERLVTVPGETSIDARELMHTYKVERVLNKEDELKGLITIK 210

Qy 447 DILQALVLSAPAGIDALG 463
Db 211 DILKTTEFPNANKDSEG 227

; RESULT 5
US-10-821-234-1179
; Sequence 1179, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pf SEQ_genes Version 1.0
; SEQ ID NO 1179
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Homo sapiens

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```

; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; TITLE OF INVENTION: agronomically interesting phenotypes
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-156-084-33

Query Match          4.6%; Score 111; DB 7; Length 466;
Best Local Similarity 23.2%; Pred. No. 0.017;
Matches 68; Conservative 45; Mismatches 90; Indels 90; Gaps 16;

Qy 228 YRSLPVLQVIEIOHKIETWREIYLOGCFKPLVSPNDSLFEAV-----YTLIKN 278
Db 120 YIIQAVVSKFLDDAAEDT-----EECCADVSVVDQMVVESVFGRRDLSHGVELLKE 173

Qy 279 RIHRLPVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLY--RTIQDLG-IGTFR-DL 334
Db 174 -----LDPVAANRIHPNHRKINQVLSLHASRGVLPKLYQKTAENWGCINASRFDY 226

Qy 335 AVV-----LETAPILTALDIFVDRRSALPVVNECGQVGLY-----S 372
Db 227 CLICMDAETA---VLDRYVEQVRDAMVDAGLLDEVYDIKPGADYTRGLRQSIGVREFE 282

Qy 373 RFDVHILAAQTYNHL-----DMSVGEALRQRTLCLEGVLSQCPHES----LGEVIDRI 422
Db 283 DFLKIHL-SETCAGHLTSLSDKVKMKENLRK-----ILNFPKDDKRLIMLEEAIDRV 334

Qy 423 -----AREQVHRLVLV-----DETQHLGLVWSLSDIQLQALVSPA 457
Db 335 KLNTRLLRRQKRRVSRLETFVGNHIIHYIDATEVILS--KSEESWNAQVVKPA 385

; QUERY MATCH
; BEST LOCAL SIMILARITY 4.6%; SCORE 111; DB 7; LENGTH 494;
; BEST LOCAL SIMILARITY 23.2%; PRED. NO. 0.019;
; MATCHES 68; CONSERVATIVE 45; MISMATCHES 90; INDELS 90; GAPS 16;

Qy 228 YRSLPVLQVIEIOHKIETWREIYLOGCFKPLVSPNDSLFEAV-----YTLIKN 278
Db 120 YIIQAVVSKFLDDAAEDT-----EECCADVSVVDQMVVESVFGRRDLSHGVELLKE 173

Qy 279 RIHRLPVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLY--RTIQDLG-IGTFR-DL 334
Db 174 -----LDPVAANRIHPNHRKINQVLSLHASRGVLPKLYQKTAENWGCINASRFDY 226

Qy 335 AVV-----LETAPILTALDIFVDRRSALPVVNECGQVGLY-----S 372

```

US-10-821-234-1179

Query Match 4.5%; Score 107.5; DB 6; Length 829;  
Best Local Similarity 20.5%; Pred. No. 0.084;  
Matches 107; Conservative 72; Mismatches 191; Indels 151; Gaps 26;

QY 4 LEQNSSWSPSPATVSSSRIRGRRAKALRWTRQKSVESGEPGQCGPRSRRTAESTG 63  
DB 6 LRSLSAPAWNTAAVLGL-LSSRRGPAAPACAVRSVSDGPDGY-----50

QY 64 LEATFPKTPAQADPAGVGPPTGWDCLE-PSDCTASAGSSTDDVELATEFPATEA 119  
DB 51 -----RPLARCSPA-QTRPQWRLAINTDTWAEVARAPRHPVTKLGAREAVA 100

QY 120 WECELEGLLEBPALCISQAPFPKLGWDDELKPGAQIYMRFMQEHCTYDAMATSKLV 179  
DB 101 ECEEEAVC---VIMCASVKY-----NIRGPA-LIPRMKTKHRY-----YIT 139

QY 180 IFDTML--EIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIY 237  
DB 140 LFSIVLGLIATGMFQWPHSIESNDWNVEKRS-----IRD-VPVRLPADSPIPERG 192

QY 238 EIEQKJETWREIYLOGCFKLVSISPNDSLFEAVYTL-INKRIHR-----282  
DB 193 DL-SCRMTCEDVYRCG-----FNPXNKIKVYIYALKKVDVDFGVSNTISREYNEL 244

QY 283 -----LPVLDPVSGNVHLHTHKKRLKFL-----HIFGSLLP 314  
DB 245 LMAISDSYVTTDDINRACLFVPSIDVLNQLTRIKETAQAMAQLSRWDRGTNHLLENLP 304

QY 315 RPSFLYTIQDL-----GIG-----TFR---DLAVVLETAPILTALDIFVDRRVSLP 359  
DB 305 GGPDPYNTALDVPDRDALLAGG3FSTWYRQYDVS-----PVYSPLSAEVD-----LP 354

QY 360 VVNECGVGVLYSRFVHLAAQOYTNHLDMSVGEALRQRTLC---EGVLS---COPH 412  
DB 355 EKGPGQYFLLSQVGLHPEYRDEALQVKGESVILVDKCNLSEGLSVKRCCHKH 414

QY 413 ELSGEVID--RIAREQVHRLVLDVETQHLGWSLSDLQA 451  
DB 415 ----QVFDYPOVLQEAFTCVLRGAR---LQAVLSDLVLA 448

## RESULT 6

US-11-156-084-35  
; Sequence 35, Application US/11156084  
; Publication No. US20060010515A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology LLC  
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to  
; FILE REFERENCE: (38-21)  
; CURRENT APPLICATION NUMBER: US/11/156,084  
; CURRENT FILING DATE: 2005-06-17  
; NUMBER OF SEQ ID NOS: 364  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 35  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-11-156-084-35

Query Match 4.2%; Score 102; DB 7; Length 461;  
Best Local Similarity 22.4%; Pred. No. 0.11;  
Matches 68; Conservative 45; Mismatches 90; Indels 100; Gaps 16;

QY 228 YRSPVQIYIEIOHKIETWREIYLOGCFKLVSISPNDSLFEAV-----YTLIKN 278  
DB 105 YVQVAVVSKFLDDAAEDT-----EECCADVASVVDQDMVSVFGRDDLHSHGYELKE 158

QY 279 RIHRLPVLDPVSGNVHLHTHKKRLKFLHIFGSLLPSPSELYR-----TIQDL 326  
DB 159 -----LDPVANRIHPNNHNRKINQYLSLHSGVLPKLYQKTAEVDSFFLTSRQNW 211

QY 327 G-IGTFR-DLAVV---LETAPILTALDIFVDRRVVSALPVVNECGQVGVLY-----371  
DB 212 GCINASRFDYCLICMDAETA---VLDRYVEQRVDMVMDAGLLDEVYDIYKPGADYTRGL 267

QY 372 -----SRFDVIHLAAQOYTNHL-----DMSVGEALRQRTLCLEGVLSQCPHES--414  
DB 268 RQSIGVREFEDFKIHL-SETCAGHLTSLNDDKVMKENLRK-----ILNFPKDDKLR 319

QY 415 --LGEVIDRI-----AREQVHRLV---DETQHLGWSLSDLQALVL 454  
DB 320 IMLEEAIDRVKLNTRLLRQKRVSRLETVFGWNIHYDATEYILS--KSEESWNAQVV 377

QY 455 SPA 457  
DB 378 KPA 380

## RESULT 7

US-11-156-084-36  
; Sequence 36, Application US/11156084  
; Publication No. US20060010515A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology LLC  
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to  
; FILE REFERENCE: (38-21)  
; CURRENT APPLICATION NUMBER: US/11/156,084  
; CURRENT FILING DATE: 2005-06-17  
; NUMBER OF SEQ ID NOS: 364  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 36  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-11-156-084-36

Query Match 4.2%; Score 100.5; DB 7; Length 495;  
Best Local Similarity 21.8%; Pred. No. 0.17;  
Matches 69; Conservative 47; Mismatches 93; Indels 107; Gaps 16;

QY 222 ILVLRHYRSPVQIYIEIOHKIETWREIYLOGCFKLVSISPNDSLFEAV-----272  
DB 113 VLVGGTHYIYQVVSXFLDDAAEDT-----EECCADVASVVDQDMVSVVDQDMVSVES 166

QY 273 -----YTLIKNRIHRLPVLDPVSGNVHLHTHKKRLKFLHIFGSLLPSPSELY--320  
DB 167 VFGRDDLSHGYELKE-----LDPVANRIHPNNHNRKINQYLSLHSGVLPKLYQG 219

QY 321 RTIQDLG-IGTFR-DLAVV---LETAPILTALDIFVDRRVVSALPVVNECGQVGVLY----371  
DB 220 KTAENWGCINASRFDYCLICMDAETA---VLDRYVEQRVDMVMDAGLLDEVYDIYKPGA 275

QY 372 -----SRFDVIHLAAQOYTNHL-----DMSVGEALRQRTLCLEGVLSQ 410  
DB 276 DYTRGLRQSIGVREFEDFKIHL-SETCAGHLTSLNDDKVMKENLRK-----ILNFP 327

QY 411 PHES---LGEVIDRI-----AREQVHRLV---DETQHLG 441  
DB 328 KDKLRIMLEEAIDRVKLNTRLLRQKRVSRLETVFGWNIHYDATEYILS 387

QY 442 VVLSLSDILQALVLSA 457  
DB 388 --KSEESWNAQVVKPA 401

## RESULT 8

US-11-156-084-230  
; Sequence 230, Application US/11156084  
; Publication No. US20060010515A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology LLC  
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to

;; TITLE OF INVENTION: agronomically interesting phenotypes

;; FILE REFERENCE: (38-21)  
;; CURRENT APPLICATION NUMBER: US/11/156.084  
;; CURRENT FILING DATE: 2005-06-17  
;; NUMBER OF SEQ ID NOS: 364  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 230  
;; LENGTH: 330  
;; TYPE: PRT  
;; ORGANISM: Arabidopsis thaliana  
US-11-156-084-230

Query Match 4.1%; Score 99; DB 7; Length 330;

Best Local Similarity 23.9%; Pred. No. 0.13;  
Matches 63; Conservative 40; Mismatches 77; Indels 84; Gaps 15;

QY 257 KPLVISPNDSLEAV-----YTLKNRIHRLPVLDPVSGNVLIHILTHKRLKFLH 307  
DB 7 RSVQMLLDQMVESVFGRRDLSHGVELKE-----LDPVAANRHPNNHRKINQYLS 59  
QY 308 IFGSLPRPSFLY--RTIQDILG-IGTFR-DLAVV---LETAPILTALDIFVDRRVLSALPV 360  
DB 60 LHASRGVLPKLYQKTAENWGCINASRFDYCLICMDAETA---VLDRYVEQVRDAMDV 115  
QY 361 VNECGQVVGLY-----SRFDVIHLAAQOITYNHL-----DMSVGEA 395  
DB 116 AGLLEVDVYIKPGADYTRGLRQSIGVREFEDFLKIHL-SETCAGHLTSLSNDDKVMKEN 174  
QY 396 LRQRTLCLEGLVSCOPHES-----LGEVIDRI-----ARQVHRLVLV----- 433  
DB 175 LRK-----ILNPKDDKLRIIMEEALDRVKLNTRLLRRQKRVSRSELTVFCGNIHYI 227  
QY 434 DETQHLGLVWSLSILQALVLSPA 457  
DB 228 DATEVILS--KSESSNAQVVKPA 249

RESULT 9

US-10-632-150-44  
;; Sequence 44, Application US/10632150  
;; Publication No. US20050251871A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Chiaux, D.  
;; APPLICANT: Pagano, M.  
;; APPLICANT: Latres, E.  
;; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS  
;; FILE REFERENCE: 5914-081  
;; CURRENT APPLICATION NUMBER: US/10/632,150  
;; CURRENT FILING DATE: 2003-07-30  
;; PRIOR APPLICATION NUMBER: US/09/385,219  
;; PRIOR FILING DATE: 1999-08-27  
;; PRIOR APPLICATION NUMBER: 60/098,355  
;; PRIOR FILING DATE: 1998-08-28  
;; PRIOR APPLICATION NUMBER: 60/118,568  
;; PRIOR FILING DATE: 1999-02-03  
;; PRIOR APPLICATION NUMBER: 60/124,449  
;; PRIOR FILING DATE: 1999-03-15  
;; NUMBER OF SEQ ID NOS: 90  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 44  
;; LENGTH: 529  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-632-150-44

Query Match 3.8%; Score 92.5; DB 6; Length 529;

Best Local Similarity 18.7%; Pred. No. 1;  
Matches 89; Conservative 66; Mismatches 175; Indels 145; Gaps 19;

QY 22 ERIRGKRRAKAL--RWTRQKSVEEGPPQGEGSPRSPTAESTGLEATFPKTTPLAQADP 79  
DB 13 KGARGARRKXQGGREARAAADGEGSGFGABAGARTPREAEGGSGVEEGARGIIKGD 72

QY 80 AGVGTPTPTG-----WDCLPSPDCTASAAGSSTD 107  
DB 73 GSVGAGKEAQGRKYKEEWRVRRREGARPRVQGGQVWAYIPTGGAAMAAAREEE 132  
QY 108 VELATEFPATEAWCELEGLLEERPALCLSPQAPFPKLGWDDDELKPG--AQIYMRMQE 165  
DB 133 EEAARESA-----CPAAG-----PALWRLPEVILLHMC SYLDMRALGRLAQVY--RWLWH 181  
QY 166 HTCYDAMATSSKLVI FDTMLEIKKAFPA LVANGVRAAPLWDSKKQSFVGM LTTITDFILVL 225  
DB 182 FTNCDLLRRQI-----AWASLNSGFTRLGNLMTSVPV----- 214  
QY 226 HRYRSPLVQIYEIOHQKIETWREIYVLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPV 285  
DB 215 -----KVSON-----WIVGCC-----EGI--LLKWRCSQMPW 240  
QY 286 LDPVSGNVLIHILTHKRLKFLHIFGSLPRPSFLYRTIQDILGIGTFRDLAV---VLETP 342  
DB 241 MQ-LEDDALYISQANFILAYQF-----RFDGASLNROQLGVSGAGHEDVCHVFLATSH 292  
QY 343 ILTALDIFVDRRVLSALPVNVECGQVGLYSRFDVIHLAAQOITYNHLDM SVGEALRQRTLC 402  
DB 293 IVSAGG--DGKIG-----LGKI-----HSTFAAKYWAHQEVNCDV-----C 327  
QY 403 LEGVLSCOPHESLGEVIDRIAREQVHRLVLVDETQHLGLVWSLSDIILQALVLSPA 457  
DB 328 KGGIISPGSRDRTAKWP--LASGOLGQCLTYIQTEDQIWSVAIRPLLSFTGTGTA 381

RESULT 10

US-11-073-457-44  
;; Sequence 44, Application US/11073457  
;; Publication No. US20050260556A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Pagano, M.  
;; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS  
;; FILE REFERENCE: 5914-090-999  
;; CURRENT APPLICATION NUMBER: US/11/073,457  
;; CURRENT FILING DATE: 2005-03-04  
;; PRIOR APPLICATION NUMBER: 10/042,417  
;; PRIOR FILING DATE: 2002-01-07  
;; PRIOR APPLICATION NUMBER: 60/260,179  
;; PRIOR FILING DATE: 2001-01-05  
;; NUMBER OF SEQ ID NOS: 92  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 44  
;; LENGTH: 529  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-073-457-44

Query Match 3.8%; Score 92.5; DB 7; Length 529;

Best Local Similarity 18.7%; Pred. No. 1;  
Matches 89; Conservative 66; Mismatches 175; Indels 145; Gaps 19;

QY 22 ERIRGKRRAKAL--RWTRQKSVEEGPPQGEGSPRSPTAESTGLEATFPKTTPLAQADP 79  
DB 13 KGARGARRKXQGGREARAAADGEGSGFGABAGARTPREAEGGSGVEEGARGIIKGD 72  
QY 80 AGVGTPTPTG-----WDCLPSPDCTASAAGSSTD 107  
DB 73 GSVGAGKEAQGRKYKEEWRVRRREGARPRVQGGQVWAYIPTGGAAMAAAREEE 132  
QY 108 VELATEFPATEAWCELEGLLEERPALCLSPQAPFPKLGWDDDELKPG--AQIYMRMQE 165  
DB 133 EEAARESA-----CPAAG-----PALWRLPEVILLHMC SYLDMRALGRLAQVY--RWLWH 181  
QY 166 HTCYDAMATSSKLVI FDTMLEIKKAFPA LVANGVRAAPLWDSKKQSFVGM LTTITDFILVL 225  
DB 182 FTNCDLLRRQI-----AWASLNSGFTRLGNLMTSVPV----- 214  
QY 226 HRYRSPLVQIYEIOHQKIETWREIYVLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPV 285

Db 215 -----KVSQN-----WIVGCC-----EGI-----LKWRCQMPW 240

Qy 286 LDPVSGNVLHILTHKRLKFLHIFGSLPRFLYRTIQDIGITFRDLAV---VLETAP 342

Db 241 MQ-LEDDALYISQANFILAYOF-----RDGASLNRPQLGVSGAGHDEVDCHVFLATSH 292

Qy 343 ILTALDIFVDRRVGALPVVNECGQVGLYRFDVIHLAAQQTYNHLDMSVGEALRQRTLC 402

Db 293 IVSAGG---DGKIG-----LGKI---HSTFAAKYWAHEQEVNCDV-----C 327

Qy 403 LEGVLSCOPHESLGEVIDRIAREQVHRLVLVDETHLLGVVLSLSDILQALVLSA 457

Db 328 KGGIISFGSRDRTAKVWP-LASGOLGQCLYTIQTEDQIWSVAIRPLSSFTGTGTA 381

RESULT 11

US-11-073-460-44

; Sequence 44, Application US/11073460

; Publication No. US20050272066A1

; GENERAL INFORMATION:

; APPLICANT: Pagano, M.

; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATION AND DIFFERENTIATIVE DISORDERS

; FILE REFERENCE: S914-090-999

; CURRENT APPLICATION NUMBER: US/11/073.460

; PRIOR FILING DATE: 2005-03-04

; PRIOR FILING DATE: 2005-03-04

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: 60/260,179

; PRIOR FILING DATE: 2001-01-05

; NUMBER OF SEQ ID NOS: 92

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 44

; LENGTH: 529

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-073-460-44

Query Match 3.8%; Score 92.5; DB 7; Length 529;

Best Local Similarity 18.7%; Pred. No. 1;

Matches 89; Conservative 66; Mismatches 175; Indels 145; Gaps 19;

Qy 22 ERIGKRRAKAL--RWTRQKSVERGEPGQGGPRPTAESTGLEATFPKTTPLAQADP 79

Db 13 KRARGARRKQGGREARADGEGSGPAGAGARTPREAEAGGSGVEEGARGIIGKDE 72

Qy 80 AGVGTPTG-----WDCLPSDCTASAAGSSTD 107

Db 73 GSVGAGKEAQGRKYGKEWRVRRRREGARGRVQGGQGVWAYIPGTGAAMAAAREEE 132

Qy 108 VELATEFPATBWECELEGLLEERPALCLSPQAPFPKLGWDELKPG--AQIYWRFMQE 165

Db 133 EEAARESA-----CPAAG-----PALWRLDEVLLHMCVSLDMRALGRLAQVY-RWLWH 181

Qy 166 HTCYDAMATSKLVIFDTMLKKAFFALVANGRAAPLWDSKQSFVGMILTITDFILVL 225

Db 182 FTNCDLLRRQI-----AWASLNSGFTRLGNLMTSPV-----214

Qy 226 HRYRSPVLQIYEYEQHKIETWRIYLOQCFKPLVISPNDLSLFEAVYTLKRIHLPLV 285

Db 215 -----KVSQN-----WIVGCC-----EGI-----LKWRCQMPW 240

Qy 286 LDPVSGNVLHILTHKRLKFLHIFGSLPRFLYRTIQDIGITFRDLAV---VLETAP 342

Db 241 MQ-LEDDALYISQANFILAYOF-----RDGASLNRPQLGVSGAGHDEVDCHVFLATSH 292

Qy 343 ILTALDIFVDRRVGALPVVNECGQVGLYRFDVIHLAAQQTYNHLDMSVGEALRQRTLC 402

Db 293 IVSAGG---DGKIG-----LGKI---HSTFAAKYWAHEQEVNCDV-----C 327

Qy 403 LEGVLSCOPHESLGEVIDRIAREQVHRLVLVDETHLLGVVLSLSDILQALVLSA 457

Db 328 KGGIISFGSRDRTAKVWP-LASGOLGQCLYTIQTEDQIWSVAIRPLSSFTGTGTA 381

RESULT 12

US-10-467-657-8240

; Sequence 8240, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SpA

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 8240

; LENGTH: 554

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-8240

Query Match 3.8%; Score 92.5; DB 6; Length 554;

Best Local Similarity 26.1%; Pred. No. 1.1;

Matches 54; Conservative 27; Mismatches 71; Indels 55; Gaps 13;

Qy 138 POAPFPKLGWDELKKEGAQIYMRPMOEHTCYDAMATSKLVIFDTMLKKAFFALVAN 197

Db 234 PAIQIPRL-----LRMIGLHI-RRYAIRFCYRRRLCNKKISVQIIFE-TLAFFSIVET 286

Qy 198 GVRAPLWDSKKQSFVGMILTID-----FILVLH---RYRSPVLQIYEIE 240

Db 287 PI-----DFLRQT---VRIADHKTVRLHPPGQHPHILKHIARVRCNPVALFAEVP 337

Qy 241 Q-----HKIETWRIYLOQCFK-----LVSIISPNDLSLFEAVYTLKRIHLPL-----284

Db 338 NLLLVTRDIPVFQIYVGLHITPEAMLINIFPD---FPAP-RRIKYTVRLPNNPIFSCR 393

Qy 285 -VLDPSVGNVLHILTHKRLKFLHIFG 310

Db 394 FIIFPVSRSAHVIV-RKRTIVPIQIFG 419

RESULT 13

US-11-128-572-2

; Sequence 2, Application US/11128572

; Publication No. US20050266513A1

; GENERAL INFORMATION:

; APPLICANT: Boehringer Ingelheim International GmbH

; TITLE OF INVENTION: Method for identifying compounds that have the potential to inhibit the activity of Myc

; FILE REFERENCE: Case 12-0231-PCT

; CURRENT APPLICATION NUMBER: US/11/128,572

; CURRENT FILING DATE: 2005-05-13

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 4374

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-128-572-2

Query Match 3.8%; Score 91; DB 7; Length 4374;

Best Local Similarity 21.1%; Pred. No. 32;

Matches 76; Conservative 53; Mismatches 142; Indels 90; Gaps 16;

Qy 14 SPATSSSEIRK--RRAKALRWTRKSVBEPPQGGPRPRPTAESTGLEATFPKT 71

Db 2842 SDALTAVSSQLEGSFMDTSSILASCTLEAEVCDTSAAGSSBQPR- --GSSTPGDAPPAVA 2898  
Qy 72 TPLAQADPAGVGTPTGWDCLPSPDCT--ASAGSSTDDVELATEFPATEAWECELEGLLE 129  
Db 2899 EVQGRSDGSGESAQP-----PEDSSPPASSESSSTRDSAVAIS-----GADSRGILE 2945  
Qy 130 ERPALCLSPQAPFPKLGWDDDELKPGAQIYMRFMQEHCTCYDAMATSSKLVIFDTMLEIKK 189  
Db 2946 E-----PLFSTSEEB--DPLAGISLPEGVDFSLAALPDDIRREVLOLQOLGIRP 2993  
Qy 190 AFFALVANGVRAAPLWDSKKQSFVGMLTIT----DFILVLRHYRSPVLQVIYEIOHQIE 245  
Db 2994 P-----TETASTNSAPAVNGVTEVSFEFLAAL-----PRAIQEEVLAQORAE 3040  
Qy 246 TWREIYQGCCKPLVSPNDLSFEAVVTLKRIHRLPVLDPVSGNVHLIFG----- 297  
Db 3041 QORRELAQNA-----SSDTPMDPV-TFIQTLPSDL--RRSVLEDMEDSVLAVMPDIAAEA 3093  
Qy 298 -----THKRLKFLHIFG-----SLLPRPSFLYRTIQDLGI-----GTF 331  
Db 3094 QALRREQEARQQLMHERLFCHSSTLSALSAILRSPAFSTRLSGNRGVOYTRLAVORGTF 3153  
Qy 332 R 332  
Db 3154 Q 3154

RESULT 14  
US-11-076-187-4  
; Sequence 4, Application US/11076187  
; Publication No. US20050244857A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Pan, James G  
; APPLICANT: Gentz, Reiner L  
; APPLICANT: Dixit, Vishva M  
; TITLE OF INVENTION: Death Domain Containing Receptor-4  
; FILE REFERENCE: PF355P3  
; CURRENT APPLICATION NUMBER: US/11/076,187  
; CURRENT FILING DATE: 2005-03-10  
; PRIOR APPLICATION NUMBER: 60/035,722  
; PRIOR FILING DATE: 1997-01-28  
; PRIOR APPLICATION NUMBER: 60/037,829  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 60/013,895  
; PRIOR FILING DATE: 1998-01-27  
; PRIOR APPLICATION NUMBER: 60/132,922  
; PRIOR FILING DATE: 1999-05-06  
; PRIOR APPLICATION NUMBER: 09/565,918  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/406,922  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: 60/413,861  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: 10/648,786  
; PRIOR FILING DATE: 2003-08-27  
; PRIOR APPLICATION NUMBER: 60/551,768  
; PRIOR FILING DATE: 2004-03-11  
; PRIOR APPLICATION NUMBER: 60/608,469  
; PRIOR FILING DATE: 2004-09-10  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 4  
; LENGTH: 909  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-076-187-4

Query Match 3.8%; Score 90.5; DB 7; Length 909;  
Best Local Similarity 20.2%; Pred. No. 3.5;  
Matches 80; Conservative 47; Mismatches 114; Indels 155; Gaps 22;

Qy 34 RWTRO-----KSVEEGEPGOGEGRSRPTAESTGLEATFPKTTPLAQADPAGVGTTP 86  
Db 236 RWKSKLYIVCGKSTPEK--GELEGTTTFLAPNPSFPT-PGFTTFLGFSFVPSSTFT 292  
Qy 87 TGWDCLPDSCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC--LSQAPFP 143  
Db 293 SSSTYTPGDCPNFAAPRR---EVAPPYQAD-----PILATALASDPPIPNP 335  
Qy 144 KLGWDDDELKPGAQIYMRFMQEHCTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAP 203  
Db 336 LQWEDSAHKPOS-----LDT--DDPATLYAVVEN---VPP 366  
Qy 204 L-WDSKKQSFVGMLTITDFILVLRHYRSPVLQVIYEIOHQIETWREIYQGCCKPLVSI 262  
Db 367 LRW-----KEFVRLGLSD-----HEIDRLQLNGR-----CLR----- 395  
Qy 263 SPNDSLFEAVVTLKRIHRLPVLDPVSGNVHLIHLTHKRLKFLHIFG----- 310  
Db 396 -----EAQYSMLATWRRRTPRREA---TLELL--GRVLRMDMLGLCLEDEEALCGP 442  
Qy 311 -SLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVLSALPVNCEGOWVG 369  
Db 443 AALPPAPESLL-----RMGLSTVPDLLPL-----VLELLLVGIYP-----SGVIG 482  
Qy 370 LYSRFDVHIAAQOQTYNHLDMVSVEALRQRTCLLEG 405  
Db 483 L-----VPHL-----GDREKRDVSVCQG 500

RESULT 15  
US-11-012-762-70  
; Sequence 70, Application US/11012762  
; Publication No. US20050244815A1  
; GENERAL INFORMATION:  
; APPLICANT: Georgia State University Research Foundation, Inc.  
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes  
; FILE REFERENCE: GSU1.PCT  
; CURRENT APPLICATION NUMBER: US/11/012,762  
; CURRENT FILING DATE: 2004-12-15  
; PRIOR APPLICATION NUMBER: PCT/US03/19300  
; PRIOR FILING DATE: 2003-06-19  
; PRIOR APPLICATION NUMBER: US 60/390,046  
; PRIOR FILING DATE: 2002-06-19  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 70  
; LENGTH: 1137  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-11-012-762-70

Query Match 3.8%; Score 90.5; DB 7; Length 1137;  
Best Local Similarity 21.2%; Pred. No. 4.9;  
Matches 77; Conservative 30; Mismatches 135; Indels 121; Gaps 16;

Qy 13 PSPAVTSSSERIRG-----KRAKALRWTRQKSVBERGEPGQGEGRSPRPTAESTGLE 65  
Db 21 PAPEPTAAVRALGSLDNVLRKNGAGGLQRPVIRIKG-----GAHARGTALRGSTD 73  
Qy 66 ATFPKTTPLAQADPAGVGTPTGWDCLPDSCTASAGSSTDDVELATEFPFA-TEAWEC-- 122  
Db 74 VEL-----VIFLDCLSRSGDQKTCHTEILGAIQALLESWCNP 111  
Qy 123 -----ELEGLEERPA-----LCLSPQAPFKLGWDDDELKPGAQIYMRFMQ 164  
Db 112 GPGLTFEFGPKASGILQFRLASVDQENWIDVSLVPAPDALGQLHSEVKPTPNVYSSLLS 171  
Qy 165 EHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFILV 224  
Db 172 SH-CQAG-----EHSACFTELKRNKFNIRP-----VKLKNLILL 204  
Qy 225 LHRYRSPVLQI-----YEIOHQIETWREIYQGCCKPLVSIKNDLSLFEAVYTLI 276



Db 205 VKHYRQVQTOVRATLPPSYALSLITIFAW-----QCCRKDAFSLAQG---LRTVLALI 257  
Qy 277 KNRIH-----RLFVLDPVSGNVLIHILTHKRLLKFLHIFGSLIPRPSFL--YRTIQDLG 327  
Db 258 QRNKHLCIFWTENYGFEDPAVGFEF-----RRQLK-----RPRPVILDPADPTWDLG 304  
Qy 328 IGT 330  
Db 305 NGT 307

Search completed: January 24, 2006, 22:31:44  
Job time : 21.515 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 25, 2006, 20:40:11 ; Search time 713.8 Seconds  
(without alignments)  
4332.332 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403

Sequence: 1 MSFLEGNSSWSPAVTSS.....LSDILQVLVSPAGIDALGA 464

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool.p/US10070794/runat\_24012006\_164414\_8779/app.query.fasta\_1.1102  
-DB=N Geneseq -QFWT=fastap -SUPFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10070794 @CGN 1.1359 @runat\_24012006\_164414\_8779 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2403	100.0	1470	10 ADF50309	Adf50309 Human prk
2	2403	100.0	2115	4 AAD03320	Aad03320 Human AMP
3	2403	100.0	2115	12 ADP43247	Adp43247 Human AMP
4	2398	99.8	1647	5 AAH43685	Aah43685 PRKAG3 CD

5	2398	99.8	1647	12	ADP87616	Adp87616 Human NOV
6	2398	99.8	2781	8	AAD49456	Aad49456 Human kin
7	2394	99.6	2109	4	AAD03296	Aad03296 Human AMP
8	2391	99.5	2314	6	ABQ61173	Abq61173 AMP kinas
9	2372	98.7	2290	12	ADP87618	Adp87618 Human NOV
10	2372	98.7	2290	14	AE869127	Ae869127 Human mod
11	2013	83.8	1873	6	AAD36457	Aad36457 Pig PRKAG
12	2011	83.7	1873	4	AAD03319	Aad03319 Pig AMPK
13	2011	83.7	1873	6	AAD36456	Aad36456 Pig wild-
14	2011	83.7	2022	4	AAD03321	Aad03321 Sus scrof
15	2010	83.6	1873	6	AAD36459	Aad36459 Pig PRKAG
16	2007	83.5	1873	6	AAD36460	Aad36460 Pig PRKAG
17	2005	83.4	1873	6	AAD36458	Aad36458 Pig PRKAG
18	2002	83.3	1867	4	AAD03295	Aad03295 Pig AMPK
19	2000	83.2	1518	10	ADF50311	Adf50311 Murine pr
20	1276	53.1	9100	10	ADF50313	Adf50313 Human prk
21	1276	53.1	26000	9	AAD58250	Aad58250 Human Prk
22	1101.5	45.8	1846	14	AD280781	Ad280781 Nucleotid
23	1094	45.5	2223	4	AAH14839	Aah14839 Human CDN
24	1094	45.5	2223	6	AAH148615	Aah148615 Human ins
25	1094	45.5	2223	12	ADP87610	Adp87610 Human NOV
26	1094	45.5	2223	12	ADP87693	Adp87693 Human AMP
27	1094	45.5	2223	12	ADP87612	Adp87612 Human NOV
28	1093	45.5	2062	12	ADP43248	Adp43248 Human AMP
29	1093	45.5	2062	12	ADP21388	Adp21388 Gene PRKA
30	1093	45.5	2062	14	AE869126	Ae869126 Human mod
31	1089	45.3	2223	12	ADP87614	Adp87614 Human NOV
32	1088	45.3	1435	2	AAx06882	Aax06882 Disease a
33	1082.5	45.0	1157	6	AAH48614	Aah48614 Human ins
34	1059.5	44.1	2024	13	ACN42072	Acn42072 Human dia
35	1028	42.8	1328	13	ADV40979	Adv40979 Rat card1
36	1022.5	42.6	1578	6	AAH48616	Aah48616 Human ins
37	1022.5	42.6	1578	6	ABK84324	Abk84324 Human CDN
38	1022.5	42.6	1578	10	ACA56515	Acas56515 Human sig
39	1022.5	42.6	1578	10	ADK61237	Adk61237 Ovarian c
40	1022.5	42.6	1578	12	ADP56311	Adp56311 Human pol
41	1022.5	42.6	1578	12	ADP43250	Adp43250 Human AMP
42	1022.5	42.6	1578	12	ADP87691	Adp87691 Human AMP
43	1022.5	42.6	1578	12	ADP87606	Adp87606 Human NOV
44	1022.5	42.6	1578	13	ACN39423	Acn39423 Tumour-as
45	1022.5	42.6	1578	14	AE869125	Ae869125 Human mod

ALIGNMENTS

RESULT 1	ADP50309	ADP50309 standard; cDNA; 1470 BP.
ID	ADP50309	
XX	XX	
AC	ADP50309;	
XX	XX	
DT	12-FEB-2004 (first entry)	
XX	XX	
DE	Human prkag3 cDNA encoding the AMPK-gamma3 subunit.	
XX	XX	
KW	human; gene; ss; transgenic;	
KW	AMP-activated protein kinase gamma 3 subunit; Prkag3; AMPK;	
KW	energy metabolism; obesity; dyslipidaemia; insulin resistance syndrome;	
KW	type 2 diabetes; antidiabetic; anorectic; antilipaemic.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	1..1470
FT	FT	/tag= a
FT	FT	/product= "AMPK-gamma 3 protein"
XX	XX	
PN	WO2003063586-A1.	
XX	XX	
PD	07-AUG-2003.	
XX	XX	
PF	31-JAN-2003; 2003WO-IB000912.	
XX	XX	

PR 01-FEB-2002; 2002US-0353430P.  
 XX (AREXIS-) AREXIS AB.  
 XX PA  
 XX PI Andersson L, Marklund S;  
 XX DR WPI; 2003-663404/62.  
 XX DR P-PSDB; ADF50310.  
 XX PT New transgenic non-human animals expressing an AMP-activated protein  
 PT kinase gamma 3 subunit, useful as models for improving treatment,  
 PT prevention or diagnosis of diseases related to energy metabolism, e.g.  
 PT obesity or type 2 diabetes.  
 XX  
 XX Claim 4; SEQ ID NO 1; 46pp; English.  
 XX  
 CC This invention relates to novel transgenic non-human animals expressing  
 CC an AMP-activated protein kinase (AMPK) gamma 3 subunit. Specifically, it  
 CC relates to the transgene pRkgs3 gene that encodes the AMPK gamma3 subunit  
 CC or a variant thereof, where the nucleic acid is operably linked to a  
 CC regulatory element. AMPK is involved in the regulation of energy  
 CC metabolism in eukaryotic cells, and is recognised as a major regulator of  
 CC lipid biosynthetic pathways due to its role in the phosphorylation and  
 CC inactivation of key enzymes such as acetyl-CoA carboxylase. The present  
 CC invention describes transgenic animals expressing AMPK-gamma 3 to be used  
 CC as models for energy metabolism diseases and also methods for the  
 CC development of drugs for the treatment or prevention of obesity,  
 CC dyslipidaemia, insulin resistance syndrome or type 2 diabetes.  
 CC Accordingly, the compositions of this invention have various activities  
 CC including anidiabetic, anorectic and antilipemic. This polynucleotide  
 CC sequence is the human pRkgs3 cDNA of the invention.  
 XX  
 SQ Sequence 1470 BP; 310 A; 444 C; 420 G; 296 T; 0 U; 0 Other;  
 XX

Alignment Scores:  
 Pred. No.: 3.89e-174 Length: 1470  
 Score: 2403.00 Matches: 464  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-10-070-794A-30 (1-464) x ADF50309 (1-1470)

QY 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
 Db 76 ATGAGCTTCTTAGACCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGCACAGCAGC 135  
 QY 21 SerGluArgIleArgGlyIysArgArgAlaIysAlaLeuArgTrpThrArgGlnLysSer 40  
 Db 136 TCAGAAAGAATCCGTGGGAAACCGAGGGGCCAAAGCCTTTGAGATGGACAAAGGCAGAGTCG 195  
 QY 41 ValGluGluGlyGluProProGlyGlnGlyGlyGlyProArgSerArgProThrAlaGlu 60  
 Db 196 GTGAGAGGAAGGGAGCCACCAGCTCAGGGGGAAGGTCCCGGTCCAGGCCAACTGCTGAG 255  
 QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
 Db 256 TCCACCGGGCTGGAGGCCACATTCGCCAAGACCAACACCTTGGCTCAAGCTGATCCTGCC 315  
 QY 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100  
 Db 316 GGGGTGGGCACCTCCACCAACAGGGTGGGAGTCCCTCCCTCTGACTGTACAGCCTCAGCT 375  
 QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120  
 Db 376 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACCGAGTTCACGACGACAGAGCCCTGG 435  
 QY 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140  
 Db 436 GAGTGTGAGCTAGAAGGCTGTGGAAAGAGAGGCTGCGCTGTGCTGCTGCTGCTGCTGCTG 495  
 QY 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTrpMet 160

Db 496 CCAFTTCCCAAGCTGGGCTGGGATGACGAACTCGGGAACCCCGGCGCCAGATCTACATG 555  
 QY 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180  
 Db 556 CGCTTCATGCAGGAGCACACCTGCTACGATGCCATGCAACTAGCTCCAAGCTAGTATCATC 615  
 QY 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
 Db 616 TTCGACACCATGCTGGAGATCAAGAAGGCCCTCTTTGCTCTGGTGGCAACGGTGTGCGG 675  
 QY 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
 Db 676 GCAGCCCTCTATGGGACACCAAGACGACAGCTTTGTGGGATGCTGACCATCCTGAC 735  
 QY 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleLysGluIleGlu 240  
 Db 736 TTCATCTCTCTAATGATAGCTGTGTGAAGCTGTCTACACCTCATCAAGAACCGGATC 795  
 QY 241 GlnHisLysIleGluThrTrpArgGluIleLysGlnGlyCysPheLysProLeuVal 260  
 Db 796 CAACATAAAGATTGAGACTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTC 855  
 QY 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
 Db 856 TCCATCTCTCTAATGATAGCTGTGTGAAGCTGTCTACACCTCATCAAGAACCGGATC 915  
 QY 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
 Db 916 CATCGCTGCTGTCTTCTGACCCCGGTGTCAAGGCAACGTACTCCACATCTCCACACAAA 975  
 QY 301 ArgLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
 Db 976 GGCCTGTCTCAAGTTCCTGACATCTTTGGTTCCTGTGCTGCCCGGCCCTCTCTCTTAC 1035  
 QY 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340  
 Db 1036 CGCACTATCCAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTCTGGAGACA 1095  
 QY 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
 Db 1096 GCACCCATCTCTGACTGCACATCTTTGTGGACCGGCTGTGTCTGCACTGCTGTG 1155  
 QY 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380  
 Db 1156 GTCAACGAATGTGTGAGTGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1215  
 QY 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
 Db 1216 GCCCAGCAAACTACACCACCTCGACATGATGTGGGAGAAGCCCTGAGGCAGAGGACA 1275  
 QY 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420  
 Db 1276 CTATGTCTGGAGGAGTCTCTTTCCTGCCAGCCCCACGAGAGCTTTGGGGGAAGTGTGATC 1335  
 QY 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
 Db 1336 AGGATGTCTGGAGCAGGTACACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1395  
 QY 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuValLeuSerProAlaGlyIleAsp 460  
 Db 1396 GGGCTGGTCTCCCTCTCCGACATCTTCCAGGCACCTGGTGTGCTCAGCCCTGCTGGCATCGAT 1455  
 QY 461 AlaLeuGlyAla 464  
 Db 1456 GCCCTCGGGGCC 1467

RESULT 2  
 AAD03320  
 ID AAD03320 standard; cDNA; 2115 BP.  
 XX  
 AC AAD03320;  
 XX

DT 13-JUN-2001 (first entry)  
 XX Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.  
 XX  
 XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;  
 XX PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;  
 XX genetic testing; carbohydrate metabolism disorder; skeletal muscle;  
 XX cystathione beta synthase; CBS; cardiant; gene therapy; ss.  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 1..1395  
 XX /tag= a  
 XX /product= "Human complete Prkag3 protein"  
 XX  
 XX W0200120003-A2.  
 XX  
 XX 22-MAR-2001.  
 XX  
 XX 11-SEP-2000; 2000WO-EP009896.  
 XX  
 XX 10-SEP-1999; 99EP-00402236.  
 XX 18-MAY-2000; 2000EP-00401388.  
 XX  
 XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 XX (ANDE/) ANDERSSON L.  
 XX (LOOF/) LOOFT C.  
 XX (KALM/) KALM E.  
 XX  
 XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;  
 XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;  
 XX WPI: 2001-244810/25.  
 XX P-PSDB; AAE00223.  
 XX  
 XX New variants of the gamma subunit of vertebrate adenosine monophosphate-  
 XX activated kinase for diagnosis or treatment of disorders associated with  
 XX energy metabolism such as diabetes, obesity, and myopathy.  
 XX  
 XX Claim 12; Page 55-68; 71pp; English.  
 XX  
 XX The present sequence is a cDNA encoding human adenosine monophosphate  
 XX (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,  
 XX complete PRKAG3. Mutation in prkag3 results in an altered regulation of  
 XX carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is  
 XX useful as therapeutic for treating carbohydrate metabolism disorders such  
 XX as diabetes, obesity, and disorders associated with muscle metabolism  
 XX such as myopathy and cardiovascular diseases, to modulate AMPK activity,  
 XX and for restoring a normal AMPK function. PRKAG3 sequence and its  
 XX functionally altered mutants are useful for the diagnostic evaluation,  
 XX genetic testing and prognosis of a metabolic disorder, preferably a  
 XX carbohydrate metabolism disorder. Primers that can detect a genetic  
 XX polymorphic marker linked to a sequence encoding PRKAG3, are useful for  
 XX detecting a dysfunction of carbohydrate metabolism resulting from the  
 XX expression of a functionally altered allele of PRKAG3. Transgenic animal  
 XX and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting  
 XX of PRKAG3 or its mutant, are useful for screening compounds able to  
 XX modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for  
 XX detecting mutations in a PRKag3 gene, or in a sequence encoding the first  
 XX cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene  
 XX therapy  
 XX  
 XX SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 U; 0 Other;  
 XX  
 XX Alignment Scores:  
 XX Pred. No.: 6.2e-174 Length: 2115  
 XX Score: 2403.00 Matches: 464  
 XX Percent Similarity: 100.00% Conservative: 0  
 XX Best Local Similarity: 100.00% Mismatches: 0  
 XX Query Match: 100.00% Indels: 0  
 XX DB: 4 Gaps: 0

US-10-070-794A-30 (1-464) x AAD03320 (1-2115)  
 QY 1 MetSerPheLeuGluGlnGluAenSerSerSerTTPProSerProAlaValThrSerSer 20  
 DB 1 ATGAGCTTCTTAGAGCAAGAAACACAGCAGCTCATGGCCATCACCGCTGTGACCAAGCAGC 60  
 QY 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTTPThrArgGlnLysSer 40  
 DB 61 TCAGAAAGAAATCCGTGGAAACCGAGGGCCAAAGCCTTGAGATGGACAAAGCAAGAGTCG 120  
 QY 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
 DB 121 GTGGAGGAAGGGAGGCCACAGGTTCAGGGGAAAGGTCCCGGTCCAGGCCAACATGCTGAG 180  
 QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
 DB 181 TCCACCGGGCTGGAGGCCACATTCGCCACACACACACCTTGGCTCAAGCTGATCTCTGCC 240  
 QY 81 GlyValGlyThrProProThrGlyTTPAspCysLeuProSerAspCysThrAlaSerAla 100  
 DB 241 GGGGTGGGCACTCCACCAACAGGGTGGGACTGGCTCCCTCTGACTGTACAGCCTCAGCT 300  
 QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTTP 120  
 DB 301 GCAGGGCTCCAGACAGATGATGGAGCTGGCAGCGAGTTCGCCAGCCACAGAGGCTGG 360  
 QY 121 GluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAla 140  
 DB 361 GAGTGTGAGCTAGAGGCTCTGGAAAGAGAGGCTGCCCTGTGCTGTCTCCCGCAGGCC 420  
 QY 141 ProPheProLysLeuGlyTTPAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160  
 DB 421 CCATTTCCCAAGCTGGGCTGGGATGACGAATCGGAAACCCGCGGCCAGATCTACATG 480  
 QY 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180  
 DB 481 CGCTTTCATGAGGAGGACACCTCTGCTAGGATGCCAATCTAGCTCAAGTAGTATCATC 540  
 QY 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAenGlyValArg 200  
 DB 541 TTCGACACCATGCTGGAGATCAAGAGGCCCTCTTTGCTCTGGTGGCCAAAGGTGGCG 600  
 QY 201 AlaAlaProLeuTTPAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
 DB 601 GCAGCCCTCTATGGGACACCAAGAGCAGAGCTTTGTGGGATGCTGACCATCACTGAC 660  
 QY 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240  
 DB 661 TTCATCTGTGTGCTGCTGCTACTACAGGTCCCGCTGGTCCAGATCTATGAGATTGAA 720  
 QY 241 GlnHisLysIleGluThrTTPArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260  
 DB 721 CAACATAAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTCAAGCCTCTGGTC 780  
 QY 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
 DB 781 TCCATCTCTCTTAATGATGACCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 840  
 QY 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
 DB 841 CATCGCTGCTGCTGCTTCTTGAACCGGCTGTTCAGGCAACGTACTCCACATCTCCACACA 900  
 QY 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
 DB 901 CGCTGTCTCAAGTTCCTTGACATCTTTGGTTCCCTGTGCTCCCGGCCCTCTCTCTCTAC 960  
 QY 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340  
 DB 961 CGCACTATCCAAAGATTGGGCATCGGCACATTCGAGAGCTTGGCTGTGGTGGTGGACACA 1020  
 QY 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
 DB 1021 GCACCCATCTGACTGCACTGGACATCTTTTGTGGACCGGGTGTGTCTGCACTGCCTGTG 1080

CC modulator of the AMPK pathway to the subject is useful for treating or  
 CC preventing a disease or disorder in a subject, preferably a  
 CC cardiovascular disorder, a neoplastic disorder, a metabolic disorder, a  
 CC dermatological disorder, a geriatric disorder, an age-associated  
 CC disorder, or a geriatric disorder. A compound that alters the expression  
 CC or activity of an AMPK pathway component is useful for altering lifespan  
 CC regulation in a cell or organism. This sequence represents the DNA  
 CC sequence encoding one of the AMPK protein subunits.

XX  
 SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 U; 0 Other;

Alignment Scores: 6.2e-174 Length: 2115  
 Pred. No.: 2403.00 Matches: 464  
 Score: 2403.00 Conservations: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 12

US-10-070-794A-30 (1-464) x ADP43247 (1-2115)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20  
 Db 1 ATGAGCTTCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACAGCAGC 60

Qy 21 SerGluArgIleArgGlyLysArgAtqAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
 Db 61 TCAGAAAGAATCCGTGGGAAACCGAGGGCCAAAGCCCTTGAGATGGACAGCAGGATCG 120

Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
 Db 121 GTGGAGGAGGGAGGCCACACAGGTTCAGGGGAGAGTCCCGGTCCAGGCCAATGCTGAG 180

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
 Db 181 TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACCAACACCTTGGCTCAAGCTGATCCTGCC 240

Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100  
 Db 241 GGGGTGGGCTCCACCAACAGGGTGGAGTGGCTCCCTCTGACTGTACAGCTCAGCT 300

Qy 101 AlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120  
 Db 301 GCAGGCTCCAGCACAGATGATGTGGAGTGGCCACGGAGTTCCAGGCCACAGAGGCGCTGG 360

Qy 121 GluCysGluLeuGlyLeuLeuGluGluGluGluGluGluGluGluGluGluGluGlu 140  
 Db 361 GAGTGTGAGCTAGAAGGCCCTGCTGGAAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTrpMet 160  
 Db 421 CCATTTCCCAAGCTGGGCTGGGATGACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

Qy 161 ArgPheMetGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuValIle 180  
 Db 481 CGCTTCATGACAGGAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
 Db 541 TTCGACACCATGCTGGAGATCAAGAAGGCCCTTCTTGTCTGCTGCTGCTGCTGCTGCTGCTG 600

Qy 201 AlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
 Db 601 GCAGCCCTCTATGGGACAGCAAGCAGAGCTTTTGGGATGCTGACCATCATCTGCTGCTG 660

Qy 221 PheIleLeuValLeuHisArgTrpTrpArgSerProLeuValGlnIleTrpGluLeu 240  
 Db 661 TTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

Qy 241 GlnHisLysIleGluThrTrpArgGluIleTrpLeuGlnGlyCysPheLysProLeuVal 260  
 Db 721 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTGC 780

361 ValAsnGluCysGlyGlnValValGlyLeuTrpSerArgPheAspValIleHisLeuAla 380  
 1081 GTCAACGAATGTGTCAGGTGCTGGGCTCTATTCCCGCTTTTGATGTGATTCACCTGGCT 1140

381 AlaGlnGlnThrTrpAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
 1141 GCCCAGCAAACTTACACACCTGAGATGATGTGGAGAGCCCTTGAGGACAGGACA 1200

401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420  
 1201 CTATGCTCGAGGAGGCTCTTCTGCGACCCACAGAGCTTGGGGAGTGTATCGAC 1260

421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
 1261 AGGATTGCTCGGAGACAGGTACACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320

441 GlyValValSerLeuSerAspIleGluGlnAlaLeuValLeuSerProAlaGlyIleAsp 460  
 1321 GCGGTGGTCTCCCTCTCGCATCTCTCAGGCACTGTGTGCTCAGCCCTGCTGGCATCGAT 1380

461 AlaLeuGlyAla 464  
 1381 GCCCTCGGGGCC 1392

RESULT 3  
 ID ADP43247  
 ADP43247 standard; DNA; 2115 BP.

XX  
 AC ADP43247;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human AMP-activated protein kinase gamma subunit coding sequence.  
 XX  
 KW cardiovascular; neuroprotective; dermatological; cytostatic;  
 KW AMPK modulator; AMPK agonist; gene therapy;  
 KW adenosine monophosphate-activated protein kinase; AMPK;  
 KW cardiovascular disorder; neurological disorder; metabolic disorder;  
 KW dermatological disorder; neoplastic disorder; age-associated disorder;  
 KW geriatric disorder; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004050898-A2.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 04-DEC-2003; 2003WO-US038628.  
 XX  
 PR 04-DEC-2002; 2002US-0430804P.  
 PR 18-JUL-2003; 2003US-0488261P.  
 XX  
 PA (ELIX-) ELIXIR PHARM INC.  
 XX  
 PI Apfeld J, O'connor G;  
 XX  
 DR WPI; 2004-450740/42.  
 XX  
 PT Evaluating a compound, useful for treating e.g., age-related disorder,  
 PT comprises contacting a polypeptide at least 85% identical to e.g., alpha  
 PT adenosine monophosphate-activated protein kinase (AMPK) subunit with a  
 test compound.  
 XX  
 PS Disclosure; SEQ ID NO 50; 160pp; English.  
 XX  
 CC The invention relates to a method of evaluating a compound by contacting  
 CC a polypeptide comprising a sequence at least 85% identical to alpha, beta  
 CC or gamma adenosine monophosphate-activated protein kinase (AMPK) subunit  
 CC or a functional domain in vitro with a test compound, evaluating  
 CC interaction between compound and polypeptide, contacting a cell or  
 CC organism that produces the polypeptide with test compound, and evaluating  
 CC a rate of aging of the cell or organism. A method comprising providing a

Qy 261 SerIleSerProAsnAppSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
 Db 781 TCCATCTCTCCTAAATGATAGCTGTTTGAAGCTGTACACCTCATCAAGAACCGGATC 840  
 Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisIys 300  
 Db 841 CATCGCTGCTGTCTTGTAGCCCGGTGTAGGCAACGTACTCCACATCTCTCACACAAA 900  
 Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
 Db 901 CGCTGTCTCAAGTTCCTGCACATCTTGGTTCCTGTGCTGCCCGGCTCTCTTCTCTAC 960  
 Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340  
 Db 961 CGCATATCCAAAGATTGGGCATCGGCACATTCGGAGACTTGGCTGTGGTGTGGAGACA 1020  
 Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
 Db 1021 GCACCATCTCTGACTGGACATCTTGTGGACCGGTGTGTCTGCACCTGCCCTGTG 1080  
 Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380  
 Db 1081 GTCAACGAATGTGTCTAGTGTGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1140  
 Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
 Db 1141 GCCCAGCAAACTTCAACACCTGACATGATGTGGGAGAAGCCCTGAGCAGAGACA 1200  
 Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyValIleAsp 420  
 Db 1201 CTATGTCTGGAGGAGTCTTCTTCTGCGAGCCCTGAGAGAGCTTGGGGGAAGTATCGAC 1260  
 Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
 Db 1261 AGGATTCTCGGAGAGGTATACACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1320  
 Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460  
 Db 1321 GGCGTGTCTCCCTCTCCGACATCTTCTGAGCACTGTGTGTGTGTGTGTGTGTGTGTG 1380  
 Qy 461 AlaLeuGlyAla 464  
 Db 1381 GCCCTCGGGGCC 1392

AAH43685 standard; cDNA; 1647 BP.  
 AAH43685;  
 21-JAN-2002 (first entry)  
 PRKAG3 cDNA.

Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.  
 Homo sapiens.

Key Location/Qualifiers  
 CDS 20..1489  
 /tag= a  
 /product= "PRKAG3"  
 variation 230  
 /tag= b  
 /label= C230G  
 /note= "Causes P71A"  
 variation 559  
 /tag= c  
 /label= T559C  
 /note= "Silent variation"  
 variation 1037  
 /tag= d

/label= C1037T  
 /note= "Causes R340W"

W0200177305-A2.

18-OCT-2001.

06-APR-2001; 2001WO-SE000765.

07-APR-2000; 2000US-0195665P.

(AREX-) AREXIS AB.

Andersson L, Luthman H, Marklund S;

WPI; 2001-657170/75.

P-PSDB; Q0847679.

New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the variant.

Disclosure; Fig 5; 25pp; English.

This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame

SQ Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.09e-173 Length: 1647  
 Score: 2398.00 Matches: 463  
 Percent Similarity: 99.78% Conservative: 0  
 Best Local Similarity: 99.78% Mismatches: 1  
 Query Match: 99.79% Indels: 0  
 DB: 5 Gaps: 0

US-10-070-794A-30 (1-464) x AAH43685 (1-1647)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
 Db 95 ATGAGCTTCTTAGAGCAAGAAACAGAGCTCATGGCCATCAGCGCTGTGACGAGCAGC 154  
 Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40  
 Db 155 TCAGAAAGAATCCGTGGAAACCGAGGGCCAAAGCCTTGAGATGGACAGCAGAGTCG 214  
 Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
 Db 215 GTGGAGNAGGGGAGGCCACCGAGTCCAGGGGGAAGGTCCCGGTCCAGGCCAGCTGTGAG 274  
 Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
 Db 275 TCACCGGGCTGGAGGCCACATTCGCCAAGACCACACCCCTTGGCTCAAGCTGATCTCTGCC 334  
 Qy 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100  
 Db 335 GGGGTGGGCATCTCCACACAGGGTGGAGTGTCTCCCTCTGCTGCTACAGCTCAGCT 394  
 Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120  
 Db 395 GCAGGCTCCAGCACAGATGTGTGGAGTGGCCACGAGTTCCAGCAGCACAGAGGCTGTG 454





XX SQ Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 U; 0 Other;

Alignment Scores: 1.09e-173 Length: 1647  
Pred. No.: 2398.00 Matches: 463  
Score: 99.78% Conservations: 0  
Percent Similarity: 99.78% Mismatches: 1  
Best Local Similarity: 99.78% Indels: 0  
Query Match: 99.79% Gaps: 0  
DB: 12

US-10-070-794A-30 (1-464) x ADP87616 (1-1647)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20  
Db 95 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCGAGC 154

Qy 21 SerGluArgLeuArgGlyLeuArgArgAlaValAlaLeuArgTrpThrArgGlnLeuSer 40  
Db 155 TCAGAAAGAAATCCCTGGGAAACCGAGGGCCAAAGCCCTTGAGATGGACAGGCGAAGTCG 214

Qy 41 ValGluGluGluGluProGluGlnGlyGluGluGluGluGluGluGluGluGluGlu 60  
Db 215 GTGGAGAGAGGGAGCCACAGGTCAGGGGGAAGGTCCCGGTCCAGGCCAGCTGCTGAG 274

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
Db 275 TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACCACACCTTGGCTCAAGCTGATCTCTGCC 334

Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100  
Db 335 GGGGTGGGCCATCCACCAACAGGGTGGGACTGCCCTCCCTCTGACTGTACAGCCCTCAGCT 394

Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120  
Db 395 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGAGGTTCACGACCACAGAGCCCTGG 454

Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140  
Db 455 GAGTGTGAGCTAGAAGCCCTGTGGAAGAGAGGCTGCCCTGTGCTGCTGCCCGCAGGCC 514

Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnLeuTrpMet 160  
Db 515 CCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAAACCCCGGCCCGCATCATG 574

Qy 161 ArgPheMetGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuValLe 180  
Db 575 CGTTTCATGAGGAGCACACTGCTACATGCCATGCCAATGCTCAAGCTAGTATC 634

Qy 181 PheAspThrMetLeuGluLeuLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
Db 635 TTCGACACCATGCTGGAGATCAAGAAGCCCTTCTTCTGCTGGTGGCCAAAGGTGTGCG 694

Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrLeuThrAsp 220  
Db 695 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTTGTGGGATGCTGACCATCACTGAC 754

Qy 221 PheLeuValLeuHisArgTrpTrpArgSerProLeuValGlnLeuTrpGluLeuGlu 240  
Db 755 TTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 814

Qy 241 GlnHisLysLeuGluThrTrpArgGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 260  
Db 815 CAACATAAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTCAAGCTCTGCTC 874

Qy 261 SerLeuSerProAsnAspSerLeuPheGluAlaValThrThrLeuLeuLysAsnArgLe 280  
Db 875 TCCATCTCTCTATGATAGCTGCTTTTGAAGCTGCTTACACCTCTCATCAAGAACCGGATC 934

Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisLeuLeuThrHisLys 300  
Db 935 CATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 994

Qy 301 ArgLeuLeuLysPheLeuHisLeuPheGlySerLeuLeuProArgProSerPheLeuTrp 320  
Db 995 CGCCTGCTCAAGTTCTCTGCACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTCTAC 1054

Qy 321 ArgThrLeuGlnAspLeuGlyLeuGlyThrPheArgAspLeuAlaValLeuGluThr 340  
Db 1055 CGCATTATCCAAAGATTGGGCAATCGGCACATTCGAGACTTGGCTGTGGTCTGGAGACA 1114

Qy 341 AlaProLeuLeuThrAlaLeuAspLeuPheValAspArgArgValSerAlaLeuProVal 360  
Db 1115 GCACCATCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1174

Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTrpSerArgPheAspValLeuHisLeuAla 380  
Db 1175 GTCAACGAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1234

Qy 381 AlaGlnGlnThrTrpHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
Db 1235 GCCCAGCAACCTTACCAACCTTGGACATGAGTGTGGAGAACCCCTGAGGCGAGAGACA 1294

Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValLeuAsp 420  
Db 1295 CTATGCTGGAGGAGTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1354

Qy 421 ArgLeuAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
Db 1355 AGGATTGCTGGGAGCAGGTACACAGGCTGGTGTAGTGGACGAGACCCAGCATCTCTTG 1414

Qy 441 GlyValValSerLeuSerAspLeuGlnAlaLeuValLeuSerProAlaGlyLeuAsp 460  
Db 1415 GCGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1474

Qy 461 AlaLeuGlyAla 464  
Db 1475 GCCCTCGGGGCC 1486

RESULT 6  
AAD49456  
ID AAD49456 standard; cDNA; 2781 BP.  
XX  
AC AAD49456;  
XX  
XX 24-MAR-2003 (first entry)  
DT  
DE Human kinase and phosphatase (KPP) -15 cDNA.  
XX  
KW Human; kinase and phosphatase; KPP; cardiovascular; hypertension;  
KW myocardial infarction; angina pectoris; Alzheimer's disease; epilepsy;  
KW acquired immune deficiency syndrome; AIDS; Grave's disease; diabetes;  
KW neurological; Parkinson's disease; cirrhosis; psoriasis; gene therapy;  
KW hypercholesterolemia; anticonvulsant; hepatotropic; lipid myopathy;  
KW cell proliferative disorder; cancer; cardiac; neuroprotective; enzyme;  
KW neoptotic; ophthalmological; anorectic; cyrostatic; cataract; obesity;  
KW gene; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
Key Location/Qualifiers  
CDS 21..1500  
FT /\*tag= a  
FT /product= "Human KPP protein"  
FT  
PD WO200283709-A2.  
XX  
XX 24-OCT-2002.  
XX  
XX 05-APR-2002; 2002WO-US010818.  
XX  
XX 06-APR-2001; 2001US-0282119P.  
PR 13-APR-2001; 2001US-0283588P.  
PR 13-APR-2001; 2001US-0283759P.  
PR 20-APR-2001; 2001US-0285589P.  
PR 27-APR-2001; 2001US-0287036P.

PR 27-APR-2001; 2001US-0287037P.  
PR 04-MAY-2001; 2001US-0288608P.  
PR 04-MAY-2001; 2001US-0288712P.  
PR 09-MAY-2001; 2001US-0289909P.  
PR 17-MAY-2001; 2001US-0292246P.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Recipon SA, Burrill JD, Marcus GA, Zingler KA, Tang YT;  
XX Thornton M, Borowsky ML, Baughn MR, Lee SY, Bandman O;  
PI Hafalia AJA, Yao MG, Ramkumar J, Walia NK, Lu DAM, Arvizu CS;  
PI Ison CH, Ding L, Lu V, Gururajan R, Walsh RT, Gandhi AR;  
PI Swarnakar A, Forsythe IJ, Yue H, Au-Young JK, Elliott VS, Lee S;  
XX WPI; 2003-092995/08.  
DR P-PSDB; RAE32034.  
XX New human kinases and phosphatases (KPP), useful for diagnosing, treating  
PT and preventing diseases or conditions associated with the aberrant KPP  
PT expression, e.g. hypertension, cancer, AIDS, diabetes, cataract,  
XX psoriasis, obesity.  
PS Claim 5; Page 195-196; 195pp; English.  
XX The invention relates to human kinases and phosphatases (KPP), and their  
CC corresponding nucleic acids. The polypeptides and polynucleotides of the  
CC invention are useful in diagnosing, treating and preventing diseases or  
CC conditions associated with the decreased expression or overexpression of  
CC KPP, such as cardiovascular (e.g. hypertension, myocardial infarction,  
CC angina pectoris), immune (e.g. acquired immune deficiency syndrome  
CC (AIDS), Grave's disease, diabetes), neurological (e.g. Parkinson's  
CC disease, Alzheimer's disease, epilepsy), disorders affecting growth and  
CC development (e.g. cirrhosis, psoriasis, cataract), lipid (e.g.  
CC hypercholesterolaemia, obesity, lipid myopathies), cell proliferative  
CC disorders, or cancer. They are also useful in assessing the effects of  
CC exogenous compounds on the expression of nucleic acid and amino acid  
CC sequences of KPP. The KPP or its fragments are useful in screening  
CC compounds for effectiveness as agonist or antagonist of the polypeptides,  
CC or in altering the expression of the target polynucleotide and compounds  
CC that specifically bind to or modulate the activity of the polypeptide.  
CC The microarray is useful in monitoring and measuring protein-protein  
CC interactions, drug-target interactions, and gene expression profiles. KPP  
CC DNA is used in gene therapy. The present sequence is human KPP cDNA  
XX  
SQ Sequence 2781 BP; 628 A; 795 C; 714 G; 644 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 2,13e-173 Length: 2781  
Score: 2398.00 Matches: 463  
Percent Similarity: 99.78% Conservative: 0  
Best Local Similarity: 99.78% Mismatches: 1  
Query Match: 99.79% Indels: 0  
DB: 8 Gaps: 0  
  
US-10-070-794A-30 (1-464) x AAD49456 (1-2781)  
  
QY 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrrProSerProAlaValThrSerSer 20  
Db 96 ATGAGCTTCCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC 155  
QY 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrrThrArgGlnLysSer 40  
Db 156 TCAGAAAGAATCCGTGGGAAACCGAGGGCCAAAGCCTTGAGATGGACAAAGGCAGAGTCG 215  
QY 41 ValGluGluGlyGluProProGlyGlnGlyGlyProArgSerArgProThrAlaGlu 60  
Db 216 GTGGAGGAGAGGGAGCCACCAGGTGAGGGGAGAGTCCCGGTCCAGCCAGCTGCTGAG 275  
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
Db 276 TCCACCGGGCTGGAGGCCACATTCGCCAAGACACACACCTTGGCTCAAGCTGATCTGCC 335  
QY 81 GlyValGlyThrProThrGlyThrAspCysLeuProSerAspCysThrAlaSerAla 100

Db 336 GGGGTGGGCACTCCACCAACAGAGGTGGACTGCTCCCTCTGACTGTACAGCCTCAGCT 395  
QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrrp 120  
Db 396 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGAGTTCGCCAGCCACAGAGGCTCGG 455  
QY 121 GluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAla 140  
Db 456 GAGTGTGAGCTAGAAGCCCTGCTGGAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 515  
QY 141 ProPheProLysLeuGlyTrrAspAspGluLeuArgLysProGlyAlaGlnIleTrrMet 160  
Db 516 CCATTTCCTCAAGCTGGGCTGGGATGACAACTCGGGAACCCCGCGCCAGATCTCATG 575  
QY 161 ArgPheMetGlnGluHisThrCysTrrAspAlaMetAlaThrSerSerLysLeuValle 180  
Db 576 CGCTTTCATGAGGAGCACACTGCTACGATGCCATGGAACCTAGCTCCAAGCTAGTCATC 635  
QY 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
Db 636 TTCGACACCATGCTGGAGATCAAGAGGCTTCTTGTCTCTGGTGGCCAAACGGTGTGGG 695  
QY 201 AlaAlaProLeuTrrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
Db 696 GCAGCCCTCTATGGGACAGCAGACAGAGCTTTGTGGGATGCTGACCATCACTGAC 755  
QY 221 PheIleLeuValLeuHisArgTrrArgSerProLeuValGlnIleTrrGluIleGlu 240  
Db 756 TTCATCTGCTGCTCATCGTACTACAGGTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 815  
QY 241 GlnHisLysIleGluThrTrrArgGluIleTrrLeuGlnGlyCysPheLysProLeuVal 260  
Db 816 CAACATAGATGTAGACTGCTGGAGGAGATCTTACCTGCAAGGCTCTTCAAGCCCTCTGTC 875  
QY 261 SerIleSerProAsnAspSerLeuPheGluAlaValTrrThrLeuIleLysAsnArgIle 280  
Db 876 TCCATCTCTCTATGATGCTGCTTTGAAGCTGTCTACACCTCATCAAGACCGGATC 935  
QY 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisLysLeuThrHisLys 300  
Db 936 CATCGCTGCTGCTGCTTGTGACCGGTGTCAGGCAACGTACTCCACATCTCTCACACAAA 995  
QY 301 ArgLeuLeuLysPheLeuHisLysIlePheCysSerLeuLeuProArgProSerPheLeuTyr 320  
Db 996 CGCTGCTCAAGTTCCTGACATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1055  
QY 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340  
Db 1056 CGCATATCCAAGATTTGGGCATCGGCACATTCGAGACTTTGGTGTGCTGCTGGAGACA 1115  
QY 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal 360  
Db 1116 GCACCCATCTCTGACTGACATCTTTGTGACCGCGGTGTGCTGCTGCTGCTGCTGCTG 1175  
QY 361 ValAsnGluCysGlyGlnValValGlyLeuTrrSerArgPheAspValIleHisLeuAla 380  
Db 1176 GTCAACGAATGTGGTTCAGTGTGGGCTCTATTTCCTGCTTGTGCTGCTGCTGCTGCTG 1235  
QY 381 AlaGlnGlnThrTrrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
Db 1236 GCCCAGCAAACTACACACCATCGACATGATGTGGGAGAGGCCCTCGAGGCAGAGGACA 1295  
QY 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGluValleAsp 420  
Db 1296 CTATGTCTGGAGGGAGTCTCTTTCTCTGCCAGGCCACAGAGAGCTTGGGGGAAGTGTG 1355  
QY 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
Db 1356 AGGATGTCTGGGAGCAGGTACACAGGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1415  
QY 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyLeAsp 460

Db 1416 GCGTGGTCTCCCTCCGACATCTTCAGGCACTGGTGTCTAGCCCTGCTGGCATCGAT 1475

Qy 461 AlaleuGlyAla 464  
|||||

Db 1476 GCCCTCGGGGC 1487

RESULT 7

AAD03296

ID AAD03296 standard; DNA; 2109 BP.

XX AC AAD03296;

XX DT 13-JUN-2001 (first entry)

XX DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.

XX KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;

XX KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;

XX KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;

XX KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.

XX OS Homo sapiens.

XX FH Key

XX FT 5'UTR

XX FT Location/Qualifiers

XX FT 1..471

XX FT /\*tag= a

XX FT CDS

XX FT 472..1389

XX FT /\*tag= b

XX FT /\*product= "Human Prkag3 protein"

XX FT 3'UTR

XX FT 1390..2109

XX FT /\*tag= c

XX W0200120003-A2.

XX PD 22-MAR-2001.

XX PF 11-SEP-2000; 2000WO-EP009896.

XX PR 10-SEP-1999; 99EP-00402236.

XX PR 18-MAY-2000; 2000EP-00401388.

XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.

XX PA (ANDE)/ ANDERSSON L.

XX PA (LOOF)/ LOOFT C.

XX PA (KALM)/ KALM E.

XX PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX DR WPI; 2001-244810/25.

XX DR P-PSDB; AAE00221.

XX PT New variants of the gamma subunit of vertebrate adenosine monophosphate-

XX PT activated kinase for diagnosis or treatment of disorders associated with

XX PT energy metabolism such as diabetes, obesity, and myopathy.

XX PS Claim 12; Fig 2; 71pp; English.

XX CC The present sequence is a cDNA encoding human adenosine monophosphate

XX CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,

XX CC PRKAG3. Mutation in Prkag3 results in an altered regulation of

XX CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is

XX CC useful as therapeutic for treating carbohydrate metabolism disorders such

XX CC as diabetes, obesity, and disorders associated with muscle metabolism

XX CC such as myopathy and cardiovascular diseases, to modulate AMPK activity,

XX CC and for restoring a normal AMPK function. PRKAG3 sequence and its

XX CC functionally altered mutants are useful for the diagnostic evaluation,

XX CC genetic testing and prognosis of a metabolic disorder, preferably a

XX CC carbohydrate metabolism disorder. Primers that can detect a genetic

XX CC polymorphic marker linked to a sequence encoding PRKAG3 are useful for

XX CC detecting a dysfunction of carbohydrate metabolism resulting from the

XX CC expression of a functionally altered allele of PRKAG3. Transgenic animal

XX CC and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting

CC of PRKAG3 or its mutant, are useful for screening compounds able to

CC modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for

CC detecting mutations in a Prkag3 gene, or in a sequence encoding the first

CC cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene

CC therapy

XX

SO Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.02e-173 Length: 2109

Score: 2394.00 Matches: 462

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatch: 0

Query Match: 99.63% Indels: 0

DB: 4 Gaps: 0

US-10-070-794A-30 (1-464) x AAD03296 (1-2109)

Qy 3 PheLeuGluGlnGluAenSerSerSerTTPProSerProAlaValThrSerSerSerGlu 22

Db 1 TTCTAGAGCAAGAAACAGCAGCTCATGGCCATCACAGCTGTGACCCAGCTCAGAA 60

Qy 23 ArgIleArgGlyLysArgArgAlaLysAlaLeuArgTTPThrArgGlnLysSerValGlu 42

Db 61 AGAATCCGTGGAAACAGGAGGCGCAAGCCCTTGAGATGGCAAGCGAAGTCCGTGGAG 120

Qy 43 GluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGluSerThr 62

Db 121 GAAGGGAGGCCACAGGTGAGGGGAGGTCCCGGTCCAGGCCACTGTGATGCCACC 180

Qy 63 GlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAlaGlyVal 82

Db 181 GGGCTGGAGGCCACATTCGCCAAGACCACACCCCTTGCTCAAGCTGATCTCTGCCGGGTG 240

Qy 83 GlyThrProThrGlyTTPAspCysLeuProSerSerSerCysThrAlaSerAlaGly 102

Db 241 GGCACTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTATACAGCTCAGCTGCAGGC 300

Qy 103 SerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTTPGluCys 122

Db 301 TCCAGCACAGTATGTGGAGCTGGCCAGGAGTTCCAGCCACAGAGGCTCTGGAGTGT 360

Qy 123 GluLeuGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAlaProPhe 142

Db 361 GAGCTAGAGGCTGCTGGAGAGAGGCTCTCTGCTGCTGCTGCCCGAGGCCCATTT 420

Qy 143 ProLysLeuGlyTTPAspAspGluLeuArgLysProGlyAlaGlnIleTyrMetArgPhe 162

Db 421 CCCAAGCTGGGCTGGGATGACGAACCTGCGAAGCCCGCGCCAGATCTACATCGCTTC 480

Qy 163 MetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePheAsp 182

Db 481 ATCAGGAGGACACCTGTCTACGATGCCATGGCAACTAGCTCCAAAGCTAGTCACTTCGAC 540

Qy 183 ThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAlaAla 202

Db 541 ACCATGCTGGAGATCAAGAGGCTCTCTTGTCTGTGGTGGCCCAACGGTGTGGGGAGCC 600

Qy 203 ProLeuTTPAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIle 222

Db 601 CCTCTATGGGACAGCAAGAGAGAGAGGCTTTGTGGGATGCTGACCATCCTGACTTCATC 660

Qy 223 LeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGlnHis 242

Db 661 CTGGTCTGCTATCGCTACTACAGTCCCTCCCTGGTCCAGATCTATGATGTAACACAT 720

Qy 243 LysIleGluThrTTPArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIle 262

Db 721 AAGATTGAGACCTGGAGGAGAGTCTACCTGCAAGGCTGCTTCAAGCTCTGGTCTCCATC 780

Qy 263 SerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArg 282

Db 781 TCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCCCTCATCAAGAACCGGATCCATCGC 840

QY 283 LeuProValLeuAspProValSerGlyAsnValLeuHisLeuThrHisLysArgLeu 302  
 DB 841 CTGCCTGTTCTTACCGGGTGTACAGCAAGTACTCCACATCTCTCACACAAACGGCTG 900  
 QY 303 LeuLysPheLeuHisLlePheGlySerLeuLeuProArgProSerPheLeuTyrArgThr 322  
 DB 901 CTCAGGTTCCTGACATCTTTGGTTCCTGCTGCCCGGGCCCTCTTCTCTACCGCACT 960  
 QY 323 IleGlnAspLeuGlyLleGlyThrPheArgAspLeuAlaValValLeuGluThrAlaPro 342  
 DB 961 ATCCAGATTGGGATCGGCACATTCGAGACTTGGCTGTGGTGTGGAGACGACACC 1020  
 QY 343 IleLeuThrAlaLeuAspLlePheValAspArgValSerAlaLeuProValValAsn 362  
 DB 1021 ATCTGACTGCACTGGACATCTTTGTGACCGGGCTGTGTCTGCACCTGCCTGTGGTCAAC 1080  
 QY 363 GluCysGlyGlnValValGlyLeuTyrSerArgPheAspValLleHisLeuAlaAlaGln 382  
 DB 1081 GAATGTGTGTCAGGTGCTGGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCAG 1140  
 QY 383 GlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeuCys 402  
 DB 1141 CAAACCTACACACCTGGACATGATGTGTGGAGAGCCCTGAGCGACGACACTATGT 1200  
 QY 403 LeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValLleAspArgLle 422  
 DB 1201 CTGGAGGGAGTCTCTTCTGTCAGCCCAAGAGCTTGGGGGAAGTATCGACAGGATT 1260  
 QY 423 AlaArgGluGlnValHisArgValLeuValValAspGluThrGlnHisLeuLeuGlyVal 442  
 DB 1261 GCTCGGGAGCAGGTACACAGGCTGGTGTGTGTGACGAGACCCAGCACTCTTCTGGGGTG 1320  
 QY 443 ValSerLeuSerAspLleLeuGlnAlaLeuValLeuSerProAlaGlyLleAspAlaLeu 462  
 DB 1321 GTCTCCCTCTCGACATCTTTCAGGCACTGTGTGCTCAGCCCTGTGGCATGATGATCCCTC 1380  
 QY 463 GlyAla 464  
 DB 1381 GGGGCC 1386  
 RESULT 8  
 ID ABQ61173 standard; cDNA; 2314 BP.  
 XX  
 AC ABQ61173;  
 XX  
 DT 26-FEB-2003 (first entry)  
 DE AMP kinase gamma 3 subunit encoding sequence.  
 XX  
 KW Neuroprotective; immunomodulator; cancer; chromosome 2; cytostatic;  
 KW anti-inflammatory; gene therapy; nutritional supplement; wound; burn;  
 KW ulcer; Alzheimer's disease; Huntington's disease; inflammation;  
 KW amyotrophic lateral sclerosis; autoimmune disorder;  
 KW vulnerable; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200231111-A2.  
 XX  
 PD 18-APR-2002.  
 XX  
 PF 11-OCT-2001; 2001WO-US027760.  
 XX  
 PR 12-OCT-2000; 2000US-00687527.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
 XX WPI; 2002-426278/45.  
 DB

DR N-PSDB; ABP43929.  
 XX New polypeptides and their encoded proteins, useful as nutritional  
 PT sources or supplements, or in gene therapy, particularly for treating  
 PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or  
 PT inflammation.  
 XX Claim 1; SEQ ID # 386; 357pp + Sequence Listing; English.  
 PS  
 XX The invention relates to 446 newly isolated polynucleotide sequences. The  
 CC activity of polynucleotides of the invention may be described as,  
 CC vulnerable, neuroprotective, immunomodulator, cytostatic and anti-  
 CC inflammatory. Compositions comprising nucleic acids of the invention are  
 CC useful for treating a mammalian subject, or as nutritional sources or  
 CC supplements. These are useful in gene therapy, particularly for treating  
 CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,  
 CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or  
 CC inflammation. The nucleic acids and polypeptides are also useful in  
 CC diagnostic and research methods. The sequences given in records ABQ60788-  
 CC ABQ61233 represent polynucleotides of the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 2314 BP; 513 A; 677 C; 618 G; 506 T; 0 U; 0 Other;  
 Alignment Scores: 5.76e-173 Length: 2314  
 Pred. No.: 2391.00 Matches: 461  
 Score: 2391.00  
 Percent Similarity: 99.78% Conservative: 2  
 Best Local Similarity: 99.35% Mismatches: 1  
 Query Match: 99.50% Indels: 0  
 DB: 6 Gaps: 0  
 US-10-070-794A-30 (1-464) x ABQ61173 (1-2314)  
 QY 1 MetSerPheLeuGluGlnGluAsnSerSerTyrProSerProAlaValThrSerSer 20  
 DB 97 ATGAGCTTCTTAGAGCAAGAAACAGAGCTCATGGCCATCACCAGCTGTGACGAGC 156  
 QY 21 SerGluArgLleArgGlyLysArgArgAlaLysAlaLeuArgTyrThrArgGlnLysSer 40  
 DB 157 TCAGAAAGATCCCTGGGAAACGGAGGGCCAAAGCTTGAGATGGACAAAGCAAGTCG 216  
 QY 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
 DB 217 GTGGAGGAAGGGGAGCCACCAAGGTTCAGGGGAAGGTCCCGGTCCAGGCCAGCTGTGAG 276  
 QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
 DB 277 TCCACCGGGCTGGAGGCCACATTCGCCAGACACACACCTTGGCTCAAGCTGATCCTGCC 336  
 QY 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100  
 DB 337 GGGGTGGGCACTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCTTCAGCT 396  
 QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120  
 DB 397 GCAGGCTCCAGCACAGATGATGTGGAGTGGCCAGGAGTTCGCCAGCCACAGAGGCTTGG 456  
 QY 121 GluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAla 140  
 DB 457 GAGTGTGAGCTAGAGGGCTGCTGGAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 516  
 QY 141 PropheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnLleTyrMet 160  
 DB 517 CCATTTCCAAAGCTGGGCTGGGATGACGAACCTCGCGAAACCCCGGGCCAGATCTACATG 576  
 QY 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValLle 180  
 DB 577 CGCTTCATCGAGGAGGACACACCTGCTACCATGCGCACTAGCTTCCAGCTAGCTCATC 636  
 QY 181 PheAspThrMetLeuGluLleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200

Db	637	TTCCACACCATGCTGGAGATCAAGAGCCCTTCTTGTCTGGTGGCCAAACGGGTGTGGG	696
Qy	201	AlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp	220
Db	697	GCAGCCCTCTATGGACAGCAGAGCAGAGCTTTGTGGGATGCTGACCATCACTGAC	756
Qy	221	PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu	240
Db	757	TTTCATCTCTGGTGGTGCATCGTACTACAGGTCCGCCCTGTGTCAGATCTATGAGATTGAA	816
Qy	241	GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal	260
Db	817	CAACATAGATTGAGCTTGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTCTGGTC	876
Qy	261	SerIleSerProAnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle	280
Db	877	TCCATCTCTCTAATGATAGCTGTGTGAAGCTGTCTACACCTTCATCAAGACCGGATC	936
Qy	281	HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys	300
Db	937	CATCGCTGCTGCTTCTTGAACCCGGTGTGAGGCAACGTACTCCACATCTCCACACAAA	996
Qy	301	ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr	320
Db	997	CGCTGCTCAAGTTCCTGACATCTTTGTGTTCCTGTGCCCCGGCCCTCTCTCTAC	1056
Qy	321	ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr	340
Db	1057	CGCACTATCAAGATTGGGCATCGGCACATTCGAGACATTGGCTGTGTGTGGAGACA	1116
Qy	341	AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal	360
Db	1117	GCACCCATCTCTGACTGACATCTTTGTGACCGCGGTGTGTCTGCACTGCCCTGTG	1176
Qy	361	ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla	380
Db	1177	GTCACCAAGTGTGTGAGTGTGGGCTCTATTCCCGCTTTGATGATTCACCTGGCT	1236
Qy	381	AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr	400
Db	1237	GCCCAGCAACCTACACACCTGACATGATGATGTGGAGAGCCCTGAGCAGAGACA	1296
Qy	401	LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp	420
Db	1297	CTATGTCTGGAGGAGTCTTTCTCTGCGAGCCCGCAGAGAGCTTGGGGAGATGATCGAC	1356
Qy	421	ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu	440
Db	1357	AGGATTGCTCGGAGAGGTACACAGGTGTGTGTGTGACAGAGACCCAGCATCTCTTG	1416
Qy	441	GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp	460
Db	1417	GGCTGTGTCTCCCTCTCGACATCTTCAGGCATGTGTGTGTGTGTGTGTGTGTGTGTGT	1476
Qy	461	AlaLeuGlyAla 464	
Db	1477	GCCCTCGGGGCC 1488	

RESULT 9

ADP87618  
ID ADP87618 standard; DNA; 2290 BP.

XX	AC	ADP87618;	
XX	AC		
DT	23-SEP-2004	(first entry)	
XX			
DE	Human NOVX polypeptide encoding DNA, NOV10b.		
XX			
KW	anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;		
KW	insulin resistance; hybridization probe; chromosome mapping;		
KW	tissue typing; preventive medicine; pharmacogenomics; NOVX; human; gene;		
KW	db.		

XX	OS	Homo sapiens.
XX	FN	W02004056961-A2.
XX	PD	08-JUL-2004.
XX	PF	27-OCT-2003; 2003WO-US034114.
XX	PR	25-OCT-2002; 2002US-0421239P.
PR	28-OCT-2002; 2002US-0421700P.	
PR	31-OCT-2002; 2002US-0422776P.	
PR	13-NOV-2002; 2002US-0426197P.	
PR	20-DEC-2002; 2002US-0435498P.	
PR	20-DEC-2002; 2002US-0435510P.	
PR	20-DEC-2002; 2002US-0435568P.	
PR	21-MAR-2003; 2003US-0456812P.	
XX	PA	(CURA-) CURAGEN CORP.
XX	XX	Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;
XX	PI	P-PSDB; ADP87619.
XX	DR	WPI: 2004-500293/47.
XX	XX	
PT	PT	New NOVX nucleic acid molecules and polypeptides useful for preventing or
PT	PT	treating NOVX-associated disorders, e.g. diabetes, insulin resistance or
XX	XX	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
PS	PS	Claim 1; SEQ ID NO 75; 570pp; English.
XX	CC	The invention relates to a novel isolated nucleic acid molecule
CC	CC	comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base
CC	CC	pairs) fully defined in the specification; or encodes any of the amino
CC	CC	acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the
CC	CC	specification. The invention further comprises: an isolated polypeptide
CC	CC	comprising any of the amino acid sequences cited above; a method for
CC	CC	identifying compounds that modulate target polypeptide activity; an
CC	CC	antibody that immunospecifically binds to the target polypeptide; where
CC	CC	the target polypeptide comprises any of the above-mentioned amino acid
CC	CC	sequences, an amino acid sequence that is at least 95% identical to the
CC	CC	above amino acid sequences, an amino acid sequence of at least one domain
CC	CC	of the above-mentioned amino acid sequences, or an amino acid sequence
CC	CC	that is at least 95% identical to the domain of the above amino acid
CC	CC	sequences; a method for identifying a potential therapeutic agent for use
CC	CC	in treatment of a pathology, where the pathology is related to aberrant
CC	CC	expression or aberrant physiological interactions of a target polypeptide
CC	CC	; and a method of screening for a modulator of activity of or of latency
CC	CC	or predisposition to a pathology associated with a target polypeptide.
CC	CC	The modulating compounds have anorectic and antidiabetic activities. The
CC	CC	nucleic acid sequences of the invention may be used in gene therapy to
CC	CC	treat disorders. The proteins of the invention may be used in creating a
CC	CC	vaccine. The composition and methods are useful for identifying compounds
CC	CC	that modulate protein activity or for diagnosing, preventing or treating
CC	CC	diverse pathological conditions, such as obesity, diabetes or insulin
CC	CC	resistance. The nucleic acids are also used as hybridization probes, in
CC	CC	chromosome mapping, tissue typing, preventive medicine, and
CC	CC	pharmacogenomics. This polynucleotide sequence represents the DNA
CC	CC	encoding a NOVX polypeptide of the invention.
XX	SQ	Sequence 2290 BP; 501 A; 674 C; 617 G; 498 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	1,61e-171	Length:	2290
Score:	2372.00	Matches:	457
Percent Similarity:	99.35%	Conservative:	3
Best Local Similarity:	98.70%	Mismatches:	3
Query Match:	98.71%	Indels:	0
DB:	12	Gaps:	0

US-10-070-794A-30 (1-464) x ADP87618 (1-2290)

Qy 1 MetSerPheLeuGluGlnGluAenSerSerSerTrpProSerProAlaValThrSerSer 20

Db 97 ATGAGCTCTCCAGAGCAAGAAAACGACGCTCATCGGCATCACAGCTGTGACCAAGCAGC 156  
 Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgThrArgGlnLysSer 40  
 Db 157 TCAGAAAGATCCGTGGNAACGAGGCGCCAAAGCCTTGAGATGGACAGGAGAGTCG 216  
 Qy 41 ValGluGluGlyGluProProGlyGlnGlyGlyGlyProArgSerArgProThrAlaGlu 60  
 Db 217 GTGGAGGAAGGGAGCCACCAAGGTGAGGGGAAAGTCCCGGTCCAGCGCCAGCTGCTGAG 276  
 Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
 Db 277 TCCACCGGGCTGGAGGCCACATTCCTCCAGACCAACACCTTGGCTCAAGCTGATCTCTGCC 336  
 Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100  
 Db 337 GGGGTGGGCACTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTGTACAGCCTCAGCT 396  
 Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120  
 Db 397 GCAGGCTCCACACAGATGATGTGAGCTGGCCACGGAGTTCCAGGCCACAGAGGCTGG 456  
 Qy 121 GluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAla 140  
 Db 457 GAGTGTGAGCTAGAAAGGCTGCTGGAGAGGAGCTGCCCTGTGCTGCTGCCCGCAGGCC 516  
 Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160  
 Db 517 CCATTTCCAAAGCTGGGCTGGGATGACGAACCTGGGAAACCCGGCGCCAGATCTACATG 576  
 Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180  
 Db 577 CGCTTTCAGGAGCACACCTGCTACATGCCATGGCAATAGCTTCAAGCTAGTCAATC 636  
 Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
 Db 637 TTGACACCATGCTGGAGATCAAGAGGCTTCTTGTCTGTGGCCACGGTGTGGCG 696  
 Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
 Db 697 GCAGCCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGATGCTGACCATCACTGAC 756  
 Qy 221 PheIleLeuValLeuHisArgTyrTrpArgSerProLeuValGlnIleTyrGluIleGlu 240  
 Db 757 TTCACTCTGGTGTGCTGCTACTACAGGTCCCGCCCTGGTCCAGATCTATGAGATTGAA 816  
 Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260  
 Db 817 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGTC 876  
 Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280  
 Db 877 TCCATCTCTCCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 936  
 Qy 281 HisArgLeuProValIleAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
 Db 937 CATCCCTGCTGCTTCTTGGCCCGGTGTCAGGCAACGATCTCCATCTTACACACAAA 996  
 Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
 Db 997 CGCCTGCTCAAGTCTCTGCACATCTTGGTTCCTGCTGCCCGCCCTCTCTCTCTAC 1056  
 Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340  
 Db 1057 CGCACTATCAAGATTGGGATCGGCATCGGCACATTCGAGAGCTTGGCTGTGGTGTGGAGCA 1116  
 Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal 360  
 Db 1117 GCACCATCTCTGACTGCACTGACATCTTTGGGACCGGCGGTGTGTGCTGCTGCTGTG 1176  
 Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380

Db 1177 GTCAACGAATGTGTGTCAGGTGCTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1236  
 Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
 Db 1237 GCCCAGCAAACTTACAAACCACTTGGACATGAGTGTGGAGAGCCCTTGAGGAAGAGGACA 1296  
 Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420  
 Db 1297 CTATGTCTGGAGGAGTCTCTTCTGCCAGCCCCACGAGAGCTTGGGGGAAGTATCGAC 1356  
 Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
 Db 1357 AGCATTTGCTCGGAGCAGGTACACAGGCTGGTGTCTAGTCAGCAGAGCCAGCATCTCTTG 1416  
 Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460  
 Db 1417 GGGTGTGTCTCCCTCTCCGACATCTTTCAGGCATGCTGTCTCAGCCCTGCTGGCATCGAT 1476  
 Qy 461 AlaLeuGly 463  
 Db 1477 CCCTCGGG 1485  
 RESULT 10  
 AEB69127  
 ID AEB69127 standard; DNA; 2290 BP.  
 XX AC AEB69127;  
 XX 20-OCT-2005 (first entry)  
 DT Human modulator of IGFR pathway polynucleotide #4.  
 DE Screening; insulin growth factor receptor; IGFR; diagnosis; cancer;  
 KW neoplasm; cytostatic; gene; ds.  
 KW Homo sapiens.  
 OS WO2005073723-A1.  
 PN 11-AUG-2005.  
 PD 27-JAN-2005; 2005WO-US002638.  
 XX 28-JAN-2004; 2004US-0539837P.  
 PR 12-MAR-2004; 2004US-0552634P.  
 PR 21-JUN-2004; 2004US-0581696P.  
 XX (EXEL-) EXELIXIS INC.  
 PA (NICO/) NICOLL M.  
 XX Nicoll M, Friedman L, Francis-Lang H, Parks A, Shaw KJ, Zhang H;  
 PI Bjerke LM, Adamkiewicz J, Hitz BC, Lickteig K, Jin Y;  
 XX WPI; 2005-582573/59.  
 DR P-PSDB; AEB69187.  
 XX Identifying a candidate insulin growth factor receptor (IGFR) pathway  
 PT modulating agents useful for diagnosing or treating, for e.g. cancer,  
 PT comprises screening for agents that modulate the activity of a modifier  
 PT of IGFR (MIGFR).  
 XX Example; SEQ ID NO 4; 334pp; English.  
 PS The invention relates to a method of identifying a candidate insulin  
 CC growth factor receptor (IGFR) pathway modulating agent comprising  
 CC screening for agents that modulate the activity of a modifier of IGFR  
 CC (MIGFR). The method comprises providing an assay system comprising an  
 CC MIGFR polypeptide or polynucleotide, contacting the assay system with a  
 CC test agent under conditions where, but for the presence of the test  
 CC agent, the system provides a reference activity and detecting the test  
 CC agent-biased activity of the assay system, where a difference between the  
 CC test agent-biased activity and the reference activity identifies the test  
 CC agent as a candidate IGFR pathway modulating agent. The invention also

CC relates to methods for modulating an IGR pathway of a cell or in a  
 CC mammalian cell and a method for diagnosing a disease in a patient. The  
 CC methods are useful for diagnosing or treating cancer or for identifying  
 CC modulators of an IGR pathway, which may be utilized as therapeutic  
 CC targets for disorders associated with defective IGR function, such as  
 CC cancer. This sequence represents a human modulator of IGR pathway  
 CC polynucleotide of the invention.

XX SQ Sequence 2290 BP; 501 A; 674 C; 617 G; 498 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,61e-171 Length: 2290  
 Score: 2372.00 Matches: 457  
 Percent Similarity: 99.35% Conservatism: 3  
 Best Local Similarity: 98.70% Mismatches: 3  
 Query Match: 98.71% Indels: 0  
 DB: 14 Gaps: 0

US-10-070-794A-30 (1-464) x ABB69127 (1-2290)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20  
 Db 97 ATGAGCTCTCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCCAGCAGC 156  
 Qy 21 SerGluArgIleArgGlyArgAlaLysAlaLysAlaLysArgTrpThrArgGlnLysSer 40  
 Db 157 TCAGAAAGATCCGTGGGAAACGGAGGCCAAAGCCTTGATGGACAAAGCAAGATGCG 216  
 Qy 41 ValGluGluGlyGluProGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGly 60  
 Db 217 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 276  
 Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80  
 Db 277 TCCACCGGGCTGGAGGCCACATCCCAAGACACACACCTTGGCTCAAGCTGATCTCTGCC 336  
 Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100  
 Db 337 GGGGTGGGCACTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCCCTCAGCT 396  
 Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrPheProLysThrThrProAlaThrGluAlaTrp 120  
 Db 397 GCAGGCTCCAGCAGATGATGTGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 456  
 Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140  
 Db 457 GAGTGTGAGCTAGAGGCTCTGGAAGAGAGGCTGCCCTGTGCTGCTCCCGCAGGCC 516  
 Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160  
 Db 517 CCATTTCAGAGCTGGGCTGGGATGAGCAACTGGGAAACCCGGCGCCAGATCTACATG 576  
 Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180  
 Db 577 CGCTTTCAGAGGAGCACCCTGTAGATGCCATGCCACTAGCTCCAAAGCTAGTGCATC 636  
 Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200  
 Db 637 TTCGACACCATGCTGGAGATCAGAGGCTCTCTTGTCTGTGGGCAACCGGTGCGG 696  
 Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220  
 Db 697 GCAGCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCAGTAC 756  
 Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240  
 Db 757 TTCATCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 816  
 Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260  
 Db 817 CAACATAGATTGAGCTGGAGGAGATCTACTCTGCAAGGCTGCTTCAAGCCCTCTGGTC 876  
 Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280

Db 877 TCCATCTCTCTATATAGCTCTTTGAAGCTGTCTACACCTCATCAAGACCGGATC 936  
 Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300  
 Db 937 CATCCCTGCTGCTGTCTGACCCCGGTGTGAGCAACGTACTTCCACATCTCTCACACAAA 996  
 Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320  
 Db 997 CGCCTGCTCAAGTTCTCTGCACATCTTTGGTTTCCCTGCTGCCCGGCCCTCTCTCTAC 1056  
 Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340  
 Db 1057 CGCACTATCAAGATTGGGCGCATCGGCACATTCGAGACTTGGCTGTGGTGTGGAGACA 1116  
 Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360  
 Db 1117 GCACCCATCTGACTGCACCTGGACATCTTTGTGAGCGGCTGTGTGCACTGCCTGTG 1176  
 Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380  
 Db 1177 GTCAACGAATGTGTCAGGTCGTGGGCTCTATTTCCTGCTTTGATGTGATTCCACTGGCT 1236  
 Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400  
 Db 1237 GCCCAGCAAACTACACACCTGAGCATGATGATGGGAGAGCCCTGAGGAGAGGACA 1296  
 Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420  
 Db 1297 CTATGCTGGAGGAGTCTCTTCTGTCAGCCCGCCAGAGCTTGGGGGAAAGTATCGAC 1356  
 Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440  
 Db 1357 AGGATTCTCGGAGCAGGTACACAGCTGTGTCTAGTGGAGCAGACCCAGCATCTCTTG 1416  
 Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460  
 Db 1417 GGGTGTGCTCTCCCTCTCCGACATCTTTCAGGCACTGGTGTGCTCAGCCCTGCTGGCATCGAT 1476  
 Qy 461 AlaLeuGly 463  
 Db 1477 CCCTCGGG 1485

RESULT 11  
 AAD36457  
 ID AAD36457 standard; DNA; 1873 BP.  
 XX  
 AC AAD36457;  
 XX  
 DT 09-AUG-2002 (first entry)  
 XX  
 DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).  
 XX  
 KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;  
 KW screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;  
 KW variant; ds.  
 XX  
 OS Sus scrofa.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..1395  
 FT /\*tag= a  
 FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"  
 FT replace(89, C)  
 FT /\*tag= b  
 FT variation  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 XX  
 PN WO200220850-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-US028283.  
 XX



PR 08-SEP-2000; 2000US-0231045P.  
 PR 08-JAN-2001; 2001US-0260239P.  
 PR 18-JUN-2001; 2001US-0299111P.  
 XX (IOWA ) UNIV IOWA STATE RES FOUND INC.  
 PA  
 XX  
 XX  
 PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;  
 DR WPI; 2002-393850/42.  
 DR P-PSDB; AAE22985.  
 XX  
 PT Screening animals to determine those likely to produce larger litters and  
 PT improved meat quality traits involves assaying for the presence of  
 PT polymorphisms in the AMP activated protein kinase regulatory gamma  
 PT subunit gene.  
 XX  
 XX Disclosure; Page 89-91; 109pp; English.  
 XX  
 CC The invention relates to a method for screening animals to determine  
 CC those more likely to produce large litters and improved meat quality  
 CC traits. The method involves assaying for the presence of a genotype in  
 CC the sample of genetic material obtained from animal. The genotype is  
 CC characterised by polymorphism(s) in the AMP activated protein kinase  
 CC regulatory gamma subunit (PRKAG3) gene. The method is used for screening  
 CC animals e.g., pigs to determine those most likely to exhibit improved  
 CC meat quality traits and to produce larger litters. The present sequence  
 CC is pig PRKAG3 polymorphic variant DNA (PRKAG3-30)  
 XX  
 SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 3.51e-144 Length: 1873  
 Score: 2013.00 Matches: 400  
 Percent Similarity: 90.11% Conservative: 19  
 Best Local Similarity: 86.02% Mismatches: 44  
 Query Match: 83.77% Indels: 2  
 DB: 6 Gaps: 2

US-10-070-794A-30 (1-464) x AAD36457 (1-1873)

QY 1 MetSerPheLeuGluGlnGluAsnSerSerTrrProSerProAlaValThrSerSer 20  
 DB 1 ATGAGCTTCTAGACAGAGGAGAGCGTTCATGGCCATCCGAGCTGTAAACACCCAGC 60  
 QY 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrrThrArgGlnLysSer 40  
 DB 61 TCAGAAAGAGGCATGGGACCCAGGGACCAAGGCTCTAGATGGACAAGGCAGGAGGAT 120  
 QY 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60  
 DB 121 GTAGAGGAAGGGGGCCCTCCGGGCCCGAGGGAAGGTCCCCAGTCCAGGCCAGTTGCTGAG 180  
 QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79  
 DB 181 TCCACCGGGCAGAGGCCACATTCCTCCAGGCCACACCTTGGCCCAAGCCGCTCCCTTG 240  
 QY 80 AlaGlyValGlyThrProProThrGlyTrrPheCysLeuProSerAspCysThrAlaSer 99  
 DB 241 GCCGAGGTGGACAACCCCAACAGAGCGGACATCTCTCCCTCTGACTGTGCAGCCTCA 300  
 QY 100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119  
 DB 301 GCCTCCGACTCCAAACAGACACATCTGGATCTGGGCATAGAGTTCTACGCTCCGGCGCG 360  
 QY 120 TrrPheCysLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139  
 DB 361 TCGGGGGATGAGCTT---GGGCTGGTGGAGAGAGCCAGCCCGCTGCCCATCCCCAGAG 417  
 QY 140 AlaProPheProLysLeuGlyTrrPheAspGluLeuArgLysProGlyAlaGlnIleTyr 159  
 DB 418 GTGCTGTTACCCAGGCTGGCTGGGATGATGAGCTGCAGAACCCGGGGGCCAGGCTCTAC 477  
 QY 160 MetArgPheMetGlnGluThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179

DB 478 ATGCACTTCATGAGGAGCACACTGCTACATGCTCATGGCCATGGCCAGCTCCAACTGGTC 537  
 QY 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199  
 DB 538 ATCTTCGACACCATGCTGGAGATCAAGAGGCTCTCTTGGCTGGTGGCCACGCGGTC 597  
 QY 200 ArgAlaAlaProLeuTrrPheSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219  
 DB 598 CGAGCGGCACCTTGTGGGACAGCAAGACAGAGCTTCGTGGGATGCTGACCATCACA 657  
 QY 220 AspPheIleLeuValLeuHisArgTrrTyrArgSerProLeuValGlnIleTrrGluIle 239  
 DB 658 GACTTCATCTTGGTGTGTCACCGCTATTACAGGTCCCTCCCTGGTCCAGATCTACGAGAT 717  
 QY 240 GluGlnHisLysLysLeuGluThrTrrPheArgGluIleTrrLeuGlnGlyCysPheLysProLeu 259  
 DB 718 GAAGAACATAAGATTGAGACTTGAGAGCTTGAGGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777  
 QY 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTrrThrLeuIleLysAsnArg 279  
 DB 778 GTCTCCATCTCTCCCAATGACAGCCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837  
 QY 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299  
 DB 838 ATCCACCGCTTCGCGGTCTCGGAGCTGTCTCCGGGGCTGTGCTCCACATCTCTCACAT 897  
 QY 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319  
 DB 898 AAGCGGCTTCTCAAGTTCCTGACATCTTTGGCACCTTGTGGCACCTGTGCTGCGCTGCTCTC 957  
 QY 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339  
 DB 958 TACCGCACCATCCAAAGATTGGGCGCATCGGCACATTCGAGACTTGGCCGTGGTCTGGAA 1017  
 QY 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359  
 DB 1018 ACGGCGCCATCTCTGACCGCAGCTGACATCTTCTGGAGCGCGGTGTGCTGCGCTGCT 1077  
 QY 360 ValValAsnGluCysGlyGlnValValGlyLeuTrrSerArgPheAspValIleHisLeu 379  
 DB 1078 GTGGTCAACGAAACTGGACAGGTAGTGGGCTCTTACTCTCGCTTTGATGTATACCTG 1137  
 QY 380 AlaAlaGlnGlnThrTrrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399  
 DB 1138 GCTGCCCAACAAACATACACCATCGACATGAATGTGGAGAGAGCCCTGAGGAGCGG 1197  
 QY 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 419  
 DB 1198 ACATGTGTCTGGGAAGGCTCTTTCTCTGCCAGCCACAGACCTTGGGGAGTGCATT 1257  
 QY 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439  
 DB 1258 GACCGGATTGTCGGGAACAGGTGCACCGCTGTGCTGCTGATGAGACCCAGCACCTT 1317  
 QY 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459  
 DB 1318 CTGGCGGTGGTGTCCCTCTCTGACATCTTCTGAGCTCTGGTGTCTGAGCCCTGCTGAAAT 1377  
 QY 460 AspAlaLeuGlyAla 464  
 DB 1378 GATGCCCTCGGGGCC 1392  
 RESULT 12  
 AAD03319  
 ID AAD03319 standard; cDNA; 1873 BP.  
 XX  
 AC AAD03319;  
 XX  
 DT 13-JUN-2001 (first entry)  
 XX  
 DE Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.  
 XX



Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;  
 PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;  
 genetic testing; carbohydrate metabolism disorder; skeletal muscle;  
 cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;  
 chromosome 15; 88.

Sus scrofa.

Key Location/Qualifiers  
 CDS 1..1395  
 /tag= a  
 /product= "Sus scrofa complete Prkag3 protein"

WO200120003-A2.

22-MAR-2001.

11-SEP-2000; 2000WO-EP009896.

10-SEP-1999; 99EP-00402236.

18-MAY-2000; 2000EP-00401388.

(INRG ) INRA INST NAT RECH AGRONOMIQUE.

(ANDE/) ANDERSSON L.

(LOOF/) LOOFT C.

(KALM/) KALM E.

Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

Iannuccelli N, Gellin J, Le Roy P, Chardon P;

WPI; 2001-244810/25.

P-PSDB; RAE00222.

New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and myopathy.

Claim 12; Page 62-64; 71pp; English.

The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. PRKAG3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy

SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 U; 0 Other;

Alignment Scores:

Pred No.:	4.99e-144	Length:	1873
Score:	2011.00	Matches:	400
Percent Similarity:	90.11%	Conservative:	19
Best Local Similarity:	86.02%	Mismatches:	44
Query Match:	83.69%	Indels:	2
DB:	4	Gaps:	2

US-10-070-794A-30 (1-464) x AAD03319 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20

1	ATGAGCTTCCTAGAGCAAGGAGAGAGCGCTTCATGGCCATCCCGAGCTGTAAACCAACGAGC	60
21	SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer	40
61	TCAGAAAGAAGCCATGGGGACCGGGGAACAGGCCCTCTAGATGGACAGGAGGAGAT	120
41	ValGluGluGluProProGlyGlnGlyProArgSerArgProThrAlaGlu	60
121	GTAGAGGAAGGGGGCTCCGGGCCGAGGAGGAGTCCCGAGTCCAGGCCAGTTGTCGAG	180
61	SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro---	79
181	TCACACGGGAGGAGGCCACATTCCTCCCAAGGCCACACCTTGGCCCAAGCCGCTCCCTTG	240
80	AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer	99
241	GCCGAGGTGACAAACCCCAACAGACGGGACATCTCTCCCTCTGACTGTGGAGCCCTCA	300
100	AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla	119
301	GCCTCCGACTCCAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCTCGCGCGC	360
120	TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln	139
361	TCGGGGGATGAGCTT---GGGCTGGTGAAGAGAGCCGCGTGCCTATCCCAAGAG	417
140	AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyValAlaGlnIleTr	159
418	GTGCTGTATCCAGGCTGGGCTGGGATGATGAGCTGCAGAGCCGGGGCCAGGCTGTAC	477
160	MetArgPheMetGlnGluHisThrCysTyAspAlaMetAlaThrSerSerLysLeuVal	179
478	ATGCACCTTCATGCAGGAGCACACCTGTACGATGCCATGGCGACAGCTCCAAACTGTC	537
180	IlePheAspThrMetLeuGluLysLeuAlaPheAlaLeuValAlaAsnGlyVal	199
538	ATCTTCGACACCATGCTGGAGATCAAGAGGCCCTTCTTGCCTGGTGGCCAAAGCGGTC	597
200	ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	219
598	CGAGCGGACCTTGTGGGACAGCAAGAGCAGAGCTTCGTGGGGATGTGACCATACA	657
220	AspPheIleLeuValLeuHisArgTyTrpArgSerProLeuValGlnIleTyGluIle	239
658	GACTTCATCTTGGTGTGCTGACCGCTATTACAGGTCCCGCTGCTCCAGATCTACGAGAT	717
240	GluGlnHisLysIleGluThrTrpArgGluLysLeuGlnGlyCysPheLysProLeu	259
718	GAAGAACATAGATTGAGACCTGGAGGGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG	777
260	ValSerIleSerProLeuAspSerLeuPheGluAlaValTyThrLeuIleLysAsnArg	279
778	GTCTCCCATCTCTCCCAAGACAGCTGTTCGAGCTGTCTACGCCCTCATCAAGAACCGG	837
280	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	299
838	ATCCACCGCTGCGGGTCTGGACCTGTCTCCGGGCTGTGCTCCACATCTCCACACAT	897
300	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	319
898	AAGCGGCTTCTCAAGTTCTTCGCACATCTTTTGGCACCTGTGCTGGCCCGCCCTCTCTC	957
320	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu	339
958	TACCGACCATCAAGATTGGGGCATTCGGCACATTCGAGAGCTTGGCCGTGGTCTCGAA	1017
340	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	359
1018	ACGGGCGCCATCTGACCGGACATCTTCTGGTGGACCGGCGTGTCTGCGCTGCT	1077
360	ValValAsnGluCysGlyGlnValValGlyLeuTySerArgPheAspValIleHisLeu	379

Db 1078 GTGTCACAGAACTGGACAGGTAGTGGCCCTCTACTCTCGCTTTGTATGATCCACCTG 1137

Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399

Db 1138 GCTGCCCAACAACATACACACCTGACATGAATGTGGGAGAAGCCCTGAGCAGCGG 1197

Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 419

Db 1198 ACATGTGTCTGGGAAGCGTCTCTTCCTGCAGCCCCACGAGACCTTGGGGGAAGTCATT 1257

Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439

Db 1258 GACCGGATTGTCGGGAACAGGTGCACCGCTGTGCTGTGGATGAGACCCAGCACTT 1317

Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuValLeuSerProAlaGlyIle 459

Db 1318 CTGGGCGTGTCTCTGACATCTCTCAGGCTCTGTGCTCAGCCCTGTCTGGAATT 1377

Qy 460 AspAlaLeuGlyAla 464

Db 1378 GATGCCCTCGGGCC 1392

RESULT 13

ID AAD36456 standard; DNA; 1873 BP.

XX AC AAD36456;

XX AC

DT 09-AUG-2002 (first entry)

XX AC

DE Pig wild-type PRKAG3 gene.

KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;

KW screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;

KW de.

XX OS Sus scrofa.

XX FH

FT Key

FT CDS

FT Location/Qualifiers

FT 1..1395

FT /tag= a

FT /product= "Pig PRKAG3 wild-type protein"

FT replace(89,C)

FT /tag= b

FT /standard\_name= "Single nucleotide polymorphism (SNP)"

FT replace(154,A)

FT /tag= c

FT /standard\_name= "Single nucleotide polymorphism (SNP)"

FT replace(595,A)

FT /tag= d

FT /standard\_name= "Single nucleotide polymorphism (SNP)"

FT replace(599,A)

FT /tag= e

FT /standard\_name= "Single nucleotide polymorphism (SNP)"

XX WO200220850-A2.

XX 14-MAR-2002.

XX 10-SEP-2001; 2001WO-US028283.

XX 08-SEP-2000; 2000US-0231045P.

PR 08-JAN-2001; 2001US-0260239P.

PR 18-JUN-2001; 2001US-0299111P.

XX (IOWA ) UNIV IOWA STATE RES FOUND INC.

XX PI Rothschild MF, Ciobanu DC, Malek M, Piastow G;

XX WPI; 2002-393850/42.

DR P-PSDB; AAE22984.

XX Screening animals to determine those likely to produce larger litters and

PT improved meat quality traits involves assaying for the presence of

PT polymorphisms in the AMP activated protein kinase regulatory gamma

PT subunit gene.

XX Claim 17; Fig 1; 109pp; English.

XX

CC The invention relates to a method for screening animals to determine

CC those more likely to produce large litters and improved meat quality

CC traits. The method involves assaying for the presence of a genotype in

CC the sample of genetic material obtained from animal. The genotype is

CC characterised by polymorphism(s) in the AMP activated protein kinase

CC regulatory gamma subunit (PRKAG3) gene. The method is used for screening

CC animals e.g., pigs to determine those most likely to exhibit improved

CC meat quality traits and to produce larger litters. The present sequence

CC is pig wild-type PRKAG3 gene

XX

SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,99e-144 Length: 1873

Score: 2011.00 Matches: 400

Percent Similarity: 90.11% Conservative: 19

Best Local Similarity: 86.02% Mismatches: 44

Query Match: 83.69% Indels: 2

DB: Gaps: 2

US-10-070-794A-30 (1-464) x AAD36456 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20

Db 1 ATGAGCTTCTTAGAGCAAGGAGAGAGCGCTTCATGGCCATCCCGAGCTGTAAACCCAGC 60

Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40

Db 61 TCAGAAAGAGCCATGGGACCCAGGGAAACAGGCGCTCTAGTAGACACAGCAGAGAT 120

Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60

Db 121 GTAGAGGAGGGGGCCCTCCGGGCCGAGGGAAGTCCCCAGTCCAGSCCAGTTGCTGAG 180

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79

Db 181 TCCACCGGGCAGGAGGCGCACATTCGCCAAGGCCACACCTTGGGCCCAAGCGCTCCCTTG 240

Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99

Db 241 GCCAGGTGGACAAACCCCCCAACAGAGCGGACATCTCCCTCTGACTGTGACGCTCA 300

Qy 100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119

Db 301 GCCTCCGACTCCACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCTCGGCGCG 360

Qy 120 TrpGluCysGluLeuGluGlyLeuGluGluGluAlaLeuCysLeuSerProGln 139

Db 361 TCGGGGATGAGCTT---GGGCTGTGTGAAGAAGCCAGCCCGCTGCCCATCCCCAGAG 417

Qy 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyValGlnIleTyr 159

Db 418 GTGCTGTTACCCAGCGCTGGGATGATGAGCTGCAGAGAGCCCGGGGCCAGGCTCTAC 477

Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179

Db 478 ATGCACTTCATGCAGGAGACACACCTGTCTACGATGCCATGGGACCCAGCTCCAACTGGTC 537

Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199

Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGGCTGTGGTGGCCACCGCTC 597

Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219

Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGAGCAGCTTCGTGGGATGCTGACCATCACA 657

Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239

Db 658 GACATTCATCTTGGTGTGCTGACCGCTATTACAGGTCCCGCTGGTCCAGATCTACGAGATT 717  
 Qy GluGlnHisLysIleGluThrTTPArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259  
 Db 718 GAAGACATAGATTGAGACTGGAGGAGATCTACCTTCAAGGTGCTTCAAGCCCTCTG 777  
 Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279  
 Db 778 GTCTCCATCTCTCCATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGACCGG 837  
 Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299  
 Db 838 ATCCACCGCCCTGCCGCTCTGGACCTGTCTCCGGGCTGTGCTCCACATCTCCACAT 897  
 Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319  
 Db 898 AAGCGGCTTCTCAAGTCTCTGACATCTTTGGACCTCTGCTGCCCGCCCTCTCTCTC 957  
 Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339  
 Db 958 TACCGCACCATCAAGATTTCGGCATCGGCACATTCGAGACTTGGCGTGTGCTGGAA 1017  
 Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359  
 Db 1018 ACGCGCCCATCTCTGACCGCATCTGACATCTTCGTGGACCGCGTGTCTGCGCTGCT 1077  
 Qy 360 ValValLeuGluCysGlyGlnValValGlyValGlyTyrSerArgPheAspValIleHisLeu 379  
 Db 1078 GTGTGTCAAGAACTGGACAGTGTGTGGCTCTTACTCTGCTTTGTATGTATCCACTG 1137  
 Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399  
 Db 1138 GCTGCCCAACAACATACACACCTGACATGATGTGGAGAGCCCTGAGCGCGG 1197  
 Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValle 419  
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 Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439  
 Db 1258 GACCGGATGTTCGGGAACAGTGCACCGCTGTGTGCTGTGTGATGAGACCCACCTT 1317  
 Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyle 459  
 Db 1318 CTGGCGGTGTGTCTCTGACATCTTCTGAGCTCTGTGCTCTGAGCCCTGCTGGAATT 1377  
 Qy 460 AspAlaLeuGlyAla 464  
 Db 1378 GATGCCCTCGGGGCC 1392

## RESULT 14

AAD03321

ID AAD03321 standard; DNA; 2022 BP.

XX AC AAD03321;

XX XX AAD03321;

DT 13-JUN-2001 (first entry)

XX XX

DE Sus scrofa PRKAG3 splice variant DNA.

XX XX

KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;  
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;  
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;  
 KW cystathione beta synthase; CBS; cardiatic; gene therapy; ds.

XX OS Sus scrofa.

XX XX

XX FH Location/Qualifiers

XX FT 1..1545

XX FT /\*tag= a

XX FT /product= "Sus scrofa Prkag3 splice variant"

XX FT

XX XX

PN

XX

XX

PD

XX

XX

PF

XX

XX

PR

XX

PR

XX

XX

PA

XX

PA

XX

PA

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PI

XX

PI

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XX

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PT

XX

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CC

SQ

XX

XX

Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 5.5e-144 Length: 2022  
 Score: 2011.00 Matches: 400  
 Percent Similarity: 90.11% Conservative: 19  
 Best Local Similarity: 86.02% Mismatches: 44  
 Query Match: 83.69% Indels: 2  
 DB: 4 Gaps: 2

US-10-070-794A-30 (1-464) x AAD03321 (1-2022)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20

Db 151 ATGAGCTTCTTAGAGCAAGGAGAGAGCGGTTTCATGGCCATCCCGAGCTGTAACCCAGC 210

Qy 21 SerGluArgIleArgGlyLysArgArgAlaIleValLeuArgTrpThrArgGlnLysSer 40

Db 211 TCAGAAAGAGCCATCGGGGACCGGGGAAACAGGCGCTCTAGATGGACAGCGAGGAT 270

Qy 41 ValGluGluGlyGluProArgSerProGlyGlnGlyGluArgSerArgProThrAlaGlu 60

Db 271 GTAGAGGAAGGGGGCGCTCCGGGCCCGAGGAGAGTCCCGAGTCCAGGCCAGGCTGCTGAG 330

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79

Db 331 TCCACGGGAGGAGCCACATTTCCCAAGGCCACACCTTGGCCCAAGCGCTCCCTTG 390  
 Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99  
 Db 391 GCCGAGGTGGACAACCCCAACAGAGCGGACATCTCTCCCTCTGAGTGTGACGCTCA 450  
 Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119  
 Db 451 GCCTCCGACTCAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCCTCGCGCGCG 510  
 Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGln 139  
 Db 511 TCGGGGATGAGCTT---GGCTGTGTGAAGAGAGCCAGCCCGCTGCCATCCACAG 567  
 Qy 140 AlaProPheProLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159  
 Db 568 GTGCTGTTACCCAGGCTGGGCTGGATGATGAGCTGCAGAGCGCGGGGGCCAGGTCTAC 627  
 Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerIleLeuVal 179  
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 Db 688 ATCTTCGACACCATGCTGAGATCAAGAGGCTCTTTGGCTGGTGGCCACAGCGGCTC 747  
 Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219  
 Db 748 CGAGCGGCACCTTTGCGGACAGCAAGAGCAGAGCTTCGTGGGATGCTGACCATCACA 807  
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 Db 808 GACTTCATCTTGGTGTGTCACCGCTATTACAGGTCCTCCCTGGTCCAGATCTACAGATT 867  
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 Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279  
 Db 928 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 987  
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 Db 988 ATCCACCGCTCGCGCTGACCTGTCTCCGGGCTGTGCTCCACATCTCTACACAT 1047  
 Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319  
 Db 1048 AAGCGGCTTCTCAAGTCTGCACATCTTGGACCTGCTGCCCGCGCTCTCTCTC 1107  
 Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339  
 Db 1108 TACCGCACCATCAAGATTGGGCATCGGCATCTCCGAGACTTGGCGGTGGTGTGGAA 1167  
 Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359  
 Db 1168 ACGGCGCCCATCTGACCGCATGGACATCTTCTGGAGCCGGCTGTGTCTCGCTGCT 1227  
 Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379  
 Db 1228 GTGGTCAAGAACTGGACAGGTAGTGGCTCTACTCTGCTTTGATGTGATCCACCTG 1287  
 Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399  
 Db 1288 GCTGCCCAACAACATACCAACCTGGACATGAATGTGGGAGAAGCCCTGAGGAGCGG 1347  
 Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerIleGlyValIle 419  
 Db 1348 ACACGTGTGTGGAAGGCTCTTCTCTCCAGCCCGCCAGACCTTGGGGGAAGTCATT 1407  
 Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439

Db 1408 GACCGATTTCGGGGAAACAGGTGACCGCTGCTGCTGATGATGAGACCCAGCACCTT 1467  
 Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459  
 Db 1468 CTGGCGCTGTGTGCTCTCTGACATCTTCAGGCTCTGGTGTCTCAGCCCTGCTGGAATT 1527  
 Qy 460 AspAlaLeuGlyAla 464  
 Db 1528 GATGCCCTCGGGGCC 1542  
 RESULT 15  
 ID AAD36459 standard; DNA; 1873 BP.  
 XX AAD36459;  
 .XX  
 DT 09-AUG-2002 (first entry)  
 XX  
 DB Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).  
 XX  
 KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;  
 screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;  
 variant; ds.  
 KW  
 XX  
 OS Sus scrofa.  
 XX  
 FH  
 FT Key Location/Qualifiers  
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 FT /\*tag= a /product= "Pig PRKAG3 polymorphic variant (PRKAG3-199)"  
 FT /replace(595, A)  
 FT variation /tag= b /standard\_name= "Single nucleotide polymorphism (SNP)"  
 FT  
 XX WO200220850-A2.  
 PD 14-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-US028283.  
 XX  
 PR 08-SEP-2000; 2000US-0231045P.  
 PR 08-JAN-2001; 2001US-0260239P.  
 PR 18-JUN-2001; 2001US-0299111P.  
 XX  
 PA (IOWA ) UNIV IOWA STATE RES FOUND INC.  
 XX  
 PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;  
 XX  
 DR WPI; 2002-393850/42.  
 P-PSDB; AAE22987.  
 XX  
 PT Screening animals to determine those likely to produce larger litters and  
 improved meat quality traits involves assaying for the presence of  
 polymorphisms in the AMP activated protein kinase regulatory gamma  
 subunit gene.  
 XX  
 PS Disclosure; Page 98-100; 109pp; English.  
 CC  
 CC The invention relates to a method for screening animals to determine  
 those more likely to produce large litters and improved meat quality  
 traits. The method involves assaying for the presence of a genotype in  
 the sample of genetic material obtained from animal. The genotype is  
 characterised by polymorphism(s) in the AMP activated protein kinase  
 regulatory gamma subunit (PRKAG3) gene. The method is used for screening  
 animals e.g., pigs to determine those most likely to exhibit improved  
 meat quality traits and to produce larger litters. The present sequence  
 is pig PRKAG3 polymorphic variant DNA (PRKAG3-199)  
 CC  
 SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 5.95e-144 Length: 1873  
 Score: 2010.00 Matches: 399

Percent Similarity: 90.11%    Conservatives: 20  
Best Local Similarity: 85.81%    Mismatches: 44  
Query Match: 83.65%    Indels: 2  
DB: 6    Gaps: 2

US-10-070-794A-30 (1-464) x AAD36459 (1-1873)

```
Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCCTAGAGCAAGAGAGAGCGCTTTCATGGCCATCCCGAGCTGTAACACCAGC 60
Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 61 TCAGAAAGAGCCATGGGAGCCAGGGGAAACAGGCGCTCTAGATGGACAGGAGGAT 120
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGAGAGGGGGCGCTCCGGGCGGAGGAGGTCCCCAGTCCAGGCCAGTTGCTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACCGGGCAGGAGGCGCACATTCGCCAAGGCCACAGCCTTGGGCCCAAGCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCGAGGTGGAAACCCCCCAACAGCGGAGACATCTCCCTCTGACTGTGACAGCCTCA 300
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCCACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCTCGCGCGGCG 360
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGGATGAGCTT---GGGCTGGTGAAGAGAGCCAGCGCCGCTGCCATCCACAG 417
Qy 140 AlaProPheProLysLeuGlyTrpAspAspGlnLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGTGTTTACCGAGCTGGGCTGGGATGATGAGCTGAGAGCGCGGGGGCGGCGGCTAC 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCACCTTCATGACAGGAGCACACCTGTACGATGCCATGGGACACAGCTCCAAACTGGTC 537
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAGCCCTTTTGGCCCTGGTGGCCAAACGGCATC 597
Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGGATGCTGACCATCACA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCATCTTGGTGTGACCGCTATACAGGTCCCGGCTGGTCCAGATCTACGAGATT 717
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAGAAACATAAGATTGAGACCTGGAGGAGAGATCTACCTTCAAGGCTGCTTCAAGCCCTCTG 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCCAATGACAGCGCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCTTCGCGGCTGGACCTGTCTCCGGGCTGTGCTCCACATCCTCACACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTTCTCAAGTTCTCTGACATCTTTGGCACCTGTGTCGCCCGGCGCTCTCTCTC 957
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
```

```
Db 958 TACGCGACCATCCAAAGATTGGGGCATTCGGCACATTCGAGACCTTGGCGGTGCTGGAA 1017
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
Db 1018 ACGGGGCCCATCTGACCGGCATCGGACATCTTCGTGGACCGGCGTGTCTGCGCTGCT 1077
Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 1078 GTGGTCAACCGAAACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGTGATCCACCTG 1137
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCCAACAAACATCAACACCTGGACATGATGTGGAGAACCCCTGAGGAGCGG 1197
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 419
Db 1198 ACATGTGTCTGGAAGGCGTCTTTCTGCGCAGCCCCACGAGACCTTGGGGGNAAGTCATT 1257
Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATTGTCCGGGAAACAGGTGCACCGCTCGTGTCTCGTGGATGAGACCCAGCACCTT 1317
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGGCGTGGTGTCCCTCTCTGACATCCTTTGAGGCTCTGGTGTCTCAGCCCTGCTGGAATT 1377
Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392
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Search completed: January 25, 2006, 22:26:39  
Job time : 746.8 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2006, 21:54:27 ; Search time 83.6866 Seconds  
(without alignments)  
1601.338 Million cell updates/sec

Title: US-10-070-794A-4  
Perfect score: 1551  
Sequence: 1 MRFMQHTCYDMATSSKLV.....LSDIQLALVLSPIGIDALGA 305

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1551	100.0	305	4 AAE00221	Aae00221 Human AMP
2	1551	100.0	464	4 AAE00223	Aae00223 Human AMP
3	1551	100.0	464	8 ADP43223	Adp43223 Human AMP
4	1551	100.0	489	4 AAB47679	Aab47679 PRKAG3_1
5	1551	100.0	489	6 AAE32034	Aae32034 Human kin
6	1551	100.0	489	7 ADF50310	Adf50310 Human AMP
7	1551	100.0	489	8 ADP87617	Adp87617 Human NOV
8	1550	99.9	305	4 AAE00329	Aae00329 Human Prk
9	1547	99.7	305	4 AAE00328	Aae00328 Human Prk
10	1544	99.5	489	5 ABA43929	Abp43929 AMP activ
11	1529	98.6	489	7 AAE38410	Aae38410 Human Prk
12	1529	98.6	489	7 ADF50314	Adf50314 Human AMP
13	1525	98.3	492	9 AEB69187	Adp87619 Human NOV
14	1525	98.3	492	9 AEB69187	Aeb69187 Human mod
15	1507	97.2	305	4 AAE00220	Aae00220 Pig AMPK
16	1507	97.2	464	4 AAE00222	Aae00222 Pig AMPK
17	1507	97.2	464	5 AAE22984	Aae22984 Pig wild-
18	1507	97.2	464	5 AAE22985	Aae22985 Pig PRKAG
19	1507	97.2	464	5 AAE22986	Aae22986 Pig PRKAG
20	1507	97.2	514	4 AAE00224	Aae00224 Sus scrof
21	1506	97.1	305	4 AAE00226	Aae00226 Sus scrof
22	1506	97.1	464	5 AAE22987	Aae22987 Pig PRKAG
23	1503	96.9	305	4 AAE00225	Aae00225 Sus scrof
24	1503	96.9	464	5 AAE22988	Aae22988 Pig PRKAG

25	1490	96.1	489	8 ADP87682	Adp87682 AMPK rat
26	1489	96.0	489	8 ADP43210	Adp43210 Mouse AMP
27	1479	95.4	489	7 ADF50312	Adf50312 Murine AM
28	1064	68.6	328	2 AAW8438	Aaw8438 Disease a
29	1064	68.6	328	4 AAB93432	Aab93432 Human pro
30	1064	68.6	328	5 AAO18496	Aao18496 Human ins
31	1064	68.6	328	8 ADP87611	Adp87611 Human NOV
32	1064	68.6	328	8 ADP87613	Adp87613 Human NOV
33	1064	68.6	352	5 AAO18495	Aao18495 Human ins
34	1064	68.6	352	8 ADP43208	Adp43208 Human AMP
35	1064	68.6	414	9 ADZ80782	Adz80782 Amino aci
36	1064	68.6	569	8 ADP43207	Adp43207 Human AMP
37	1064	68.6	569	8 ADP43217	Adp43217 Human AMP
38	1064	68.6	569	9 AEB69186	Aeb69186 Human mod
39	1060	68.3	328	8 ADP87694	Adp87694 Human AMP
40	1059	68.3	328	8 ADP87615	Adp87615 Human NOV
41	1009	65.1	331	2 AAW29817	Aaw29817 Mammalian
42	1009	65.1	331	5 AAO18497	Aao18497 Human ins
43	1009	65.1	331	6 ABU04258	Abu04258 Human exp
44	1009	65.1	331	6 ABU04261	Abu04261 Human exp
45	1009	65.1	331	6 ABU04262	Abu04262 Human exp

## ALIGNMENTS

RESULT 1  
AAE00221  
ID AAE00221 standard; protein; 305 AA.

XX AAE00221;

DT 13-JUN-2001 (first entry)

DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3.

XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;  
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;  
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;  
KW cystathione beta synthase; CBS; cardiant; gene therapy.

OS Homo sapiens.

PN WO200120003-A2.

XX 22-MAR-2001.

PF 11-SEP-2000; 2000WO-EP009896.

XX 10-SEP-1999; 99EP-00402236.

PR 18-MAY-2000; 2000EP-00401388.

XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.

PA (ANDE/) ANDERSSON L.

PA (LOOF/) LOOFT C.

XX (KALM/) KALM E.

PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

PI Tannuccelli N, Gallin J, Le Roy P, Chardon P;

DR WPI; 2001-244810/25.

XX N-PSDB; AAD03296.

PT New variants of the gamma subunit of vertebrate adenosine monophosphate-

PT activated kinase for diagnosis or treatment of disorders associated with  
energy metabolism such as diabetes, obesity, and myopathy.  
PS Claim 4; Page 55-57; 71pp; English.  
XX The present sequence is human adenosine monophosphate (AMP)-activated  
kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in  
CC Prkag3 results in an altered regulation of carbohydrate metabolism,  
CC particularly in skeletal muscle. PRKAG3 is useful as therapeutic for

CC treating carbohydrate metabolism disorders such as diabetes, obesity, and  
 CC disorders associated with muscle metabolism such as myopathy and  
 CC cardiovascular diseases, to modulate AMPK activity, and for restoring a  
 CC normal AMPK function. PRKAG3 sequence and its functionally altered  
 CC mutants are useful for the diagnostic evaluation, genetic testing and  
 CC prognosis of a metabolic disorder, preferably a carbohydrate metabolism  
 CC disorder. Primers that can detect a genetic polymorphic marker linked to  
 CC a sequence encoding PRKAG3, are useful for detecting a dysfunction of  
 CC carbohydrate metabolism resulting from the expression of a functionally  
 CC altered allele of PRKAG3. Transgenic animal and host cell transformed  
 CC with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant,  
 CC are useful for screening compounds able to modulate AMPK activity.  
 CC Nucleic acid encoding PRKAG3 is useful for detecting mutations in a  
 CC Prkag3 gene, or in a sequence encoding the first cystathione beta  
 CC synthase (CBS) domain of PRKAG3 and is useful in gene therapy  
 XX  
 SQ Sequence 305 AA;

Query Match 100.0%; Score 1551; DB 4; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-165;  
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
 DB 1 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
 QY 61 DFILVLRHRYRSPVQIYEIQHKTWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNR 120  
 DB 61 DFILVLRHRYRSPVQIYEIQHKTWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNR 120  
 QY 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
 DB 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
 QY 181 TAPILTALDIFVDRRSALPVNCGQVVGYSRFDVTHLAAQTYNHLDSVGEALRQR 240  
 DB 181 TAPILTALDIFVDRRSALPVNCGQVVGYSRFDVTHLAAQTYNHLDSVGEALRQR 240  
 QY 241 TLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDIQLVLSPAGI 300  
 DB 241 TLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDIQLVLSPAGI 300  
 QY 301 DALGA 305  
 DB 301 DALGA 305

RESULT 2  
 ID AAE00223 standard; protein; 464 AA.  
 XX  
 AC AAE00223;  
 XX  
 DT 13-JUN-2001 (first entry)  
 XX

XX Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3.

DE Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;  
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;  
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;  
 KW cystathione beta synthase; CBS; cardiant; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers  
 PH 172..225  
 FT Domain /label= CBS  
 FT /note= "Cystathione beta synthase domain"  
 FT Misc-difference 200  
 FT /note= "RN- mutation site"  
 FT Domain 253..307  
 FT /label= CBS  
 FT /note= "Cystathione beta synthase domain"

FT Domain 329..382  
 FT /label= CBS  
 FT /note= "Cystathione beta synthase domain"  
 FT Domain 400..453  
 FT /label= CBS  
 FT /note= "Cystathione beta synthase domain"  
 XX  
 PN WO200120003-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PD 11-SEP-2000; 2000WO-EP009896.  
 PF  
 XX 10-SEP-1999; 99EP-00402236.  
 PR 18-MAY-2000; 2000EP-00401388.  
 XX  
 XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 PA (ANDE/) ANDERSSON L.  
 PA (LOOF/) LOOFT C.  
 PA (KALM/) KALM E.  
 XX  
 PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;  
 XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;  
 DR WPI: 2001-244810/25.  
 DR N-PSDB; AAD03320.

New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and myopathy.

Claim 5; Fig 3; 71pp; English.

The present sequence is human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3 are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy

SQ Sequence 464 AA;

Query Match 100.0%; Score 1551; DB 4; Length 464;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-165;  
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
 DB 160 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 219  
 QY 61 DFILVLRHRYRSPVQIYEIQHKTWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNR 120  
 DB 220 DFILVLRHRYRSPVQIYEIQHKTWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNR 279  
 QY 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
 DB 280 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 339  
 QY 181 TAPILTALDIFVDRRSALPVNCGQVVGYSRFDVTHLAAQTYNHLDSVGEALRQR 240



Db 340 TAPILTALDIFVDRRSALPVNCGVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQ 399  
Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSAGI 300  
Db 400 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSAGI 459  
Qy 301 DALGA 305  
Db 460 DALGA 464  
RESULT 3  
ADP43223  
ID ADP43223 standard; protein; 464 AA.  
XX AC ADP43223;  
XX DT 09-SEP-2004 (first entry)  
XX DE Human AMPK gamma-3 subunit.  
XX KW Cardiovascular; neuroprotective; dermatological; cytostatic;  
KW AMPK modulator; AMPK agonist; gene therapy;  
KW adenosine monophosphate-activated protein kinase; AMPK;  
KW cardiovascular disorder; neurological disorder; metabolic disorder;  
KW dermatological disorder; neoplastic disorder; age-associated disorder;  
KW geriatric disorder.  
XX OS Homo sapiens.  
XX PN WO2004050898-A2.  
XX PD 17-JUN-2004.  
XX PF 04-DEC-2003; 2003WO-US038628.  
XX PR 04-DEC-2002; 2002US-0430804P.  
XX PR 18-JUL-2003; 2003US-0488261P.  
XX PA (BLIX-) ELIXIR PHARM INC.  
XX PI Apfeld J, O'Connor G;  
XX DR WPI; 2004-450740/42.  
XX PT Evaluating a compound, useful for treating e.g., age-related disorder,  
PT comprises contacting a polypeptide at least 85% identical to e.g., alpha  
PT adenosine monophosphate-activated protein kinase (AMPK) subunit with a  
PT test compound.  
XX PS Disclosure; SEQ ID NO 26; 160pp; English.  
XX CC The invention relates to a method of evaluating a compound by contacting  
CC a polypeptide comprising a sequence at least 85% identical to alpha, beta  
CC or gamma adenosine monophosphate-activated protein kinase (AMPK) subunit  
CC or a functional domain in vitro with a test compound, evaluating  
CC interaction between compound and polypeptide, contacting a cell or  
CC organism that produces the polypeptide with test compound, and evaluating  
CC a rate of aging of the cell or organism. A method comprising providing a  
CC modulator of the AMPK pathway to the subject is useful for treating or  
CC preventing a disease or disorder in a subject, preferably a  
CC cardiovascular disorder, a neurological disorder, a metabolic disorder, a  
CC dermatological disorder, a neoplastic disorder, an age-associated  
CC disorder, or a geriatric disorder. A compound that alters the expression  
CC or activity of an AMPK pathway component is useful for altering lifespan  
CC regulation in a cell or organism. This sequence represents a protein  
CC sequence of an AMPK pathway member or its homologue used in the method of  
CC the invention.  
XX SQ Sequence 464 AA;

Query Match 100.0%; Score 1551; DB 8; Length 464;

Best Local Similarity 100.0%; Pred. No. 3.8e-165;  
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRFMQHTCYDANATSKLVIFDTMLEIKKAFKAFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
Db 160 MRFMQHTCYDANATSKLVIFDTMLEIKKAFKAFALVANGVRAAPLWDSKKQSFVGMLTIT 219  
Qy 61 DFILVLRHYRSPVLQIYEIEQHKIETWREIYLQGCFKPLVSI SPNDSLFEAVVTLIKNR 120  
Db 220 DFILVLRHYRSPVLQIYEIEQHKIETWREIYLQGCFKPLVSI SPNDSLFEAVVTLIKNR 279  
Qy 121 IHRPLVLPDVGNNVILHILTHKRLKFLHIFGSLPRPSFLYRTIQDIGITFRDLAVVLE 180  
Db 280 IHRPLVLPDVGNNVILHILTHKRLKFLHIFGSLPRPSFLYRTIQDIGITFRDLAVVLE 339  
Qy 181 TAPILTALDIFVDRRSALPVNCGVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQ 240  
Db 340 TAPILTALDIFVDRRSALPVNCGVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQ 399  
Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSAGI 300  
Db 400 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSAGI 459  
Qy 301 DALGA 305  
Db 460 DALGA 464  
RESULT 4  
AAB47679  
ID AAB47679 standard; protein; 489 AA.  
XX AC AAB47679;  
XX DT 21-JAN-2002 (first entry)  
XX DE PRKAG3.  
XX KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;  
KW metabolic disease; diabetes; obesity; substitution; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 71 /note= "Possible variation point P71A"  
XX FT Misc-difference 340 /note= "Possible variation point R340W"  
XX WO200177305-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-SB000765.  
XX PR 07-APR-2000; 2000US-0195665P.  
XX PA (AREX-) AREXIS AB.  
XX XX Andersson L, Luthman H, Marklund S;  
XX WPI; 2001-657170/75.  
XX N-PSDB; AAH43685.  
XX New variants of human AMP-activated protein kinase gamma3 subunit  
XX associated with a metabolic disease e.g. diabetes or obesity and method  
XX for determining a risk estimate of diseases in subject by detecting the  
XX variant.  
XX PS Disclosure; Fig 5; 25pp; English.  
XX CC This sequence is encoded by the full length cDNA encoding the human AMP-  
XX activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence

CC of the PRXAG3 DNA, or a variant, is useful in determining a risk estimate  
CC of a metabolic disease, such as diabetes or obesity, in a subject. The  
CC variation may occur in exons 3, 4 or 10. In exon 3 variation may be a  
CC substitution of a G for a C at nucleotide 320, resulting in the amino  
CC acid substitution P71A; in exon 4 variation may be a substitution of a T  
CC for a C at nucleotide 550; and in exon 10 variation may be a substitution  
CC of a T for a C at nucleotide 1037, resulting in the amino acid  
CC substitution R340W. There may also be nucleotide variation in intron 6.  
CC The numbering of these variations is based on the full length cDNA,  
CC rather than on position 1 of the open reading frame  
XX  
SQ Sequence 489 AA;

Query Match 100.0%; Score 1551; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 4.1e-165;  
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFQEHCTCYDAMATSSKLVIFDTMLETKKAFPAALVANGVRAAPLWDSKKQSFVGMLTIT 60  
DB 185 MRFQEHCTCYDAMATSSKLVIFDTMLETKKAFPAALVANGVRAAPLWDSKKQSFVGMLTIT 244  
QY 61 DFILVLHRYRSPVQIYEIEHQKIEWREIYLGQCFKPLVSIISPNDSLFEAVYTLIKNR 120  
DB 245 DFILVLHRYRSPVQIYEIEHQKIEWREIYLGQCFKPLVSIISPNDSLFEAVYTLIKNR 304  
QY 121 IHRPLVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTTODLIGTFRDLAVLLE 180  
DB 305 IHRPLVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTTODLIGTFRDLAVLLE 364  
QY 181 TAPILTALDIFDVRVSPALPVNCGVVGYSRFDVTHLAAQOTYNNHLMDSVGEALRQR 240  
DB 365 TAPILTALDIFDVRVSPALPVNCGVVGYSRFDVTHLAAQOTYNNHLMDSVGEALRQR 424  
QY 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETQHLLGWVSLSDILQALVLSPAGI 300  
DB 425 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETQHLLGWVSLSDILQALVLSPAGI 484  
QY 301 DALGA 305  
DB 485 DALGA 489

RESULT 5  
ID AAE32034 standard; protein; 489 AA.  
XX  
AC AAE32034;  
XX  
DT 24-MAR-2003 (first entry)  
XX  
DE Human kinase and phosphatase (KPP)-15.

XX Human; kinase and phosphatase; KPP; cardiovascular; hypertension;  
KW myocardial infarction; angina pectoris; Alzheimer's disease; epilepsy;  
KW acquired immune deficiency syndrome; AIDS; Grave's disease; diabetes;  
KW neurological; Parkinson's disease; cirrhosis; psoriasis; gene therapy;  
KW hypercholesterolaemia; anticonvulsant; hepatotropic; lipid myopathy;  
KW cell proliferative disorder; cancer; cardiatic; neuroprotective; enzyme;  
KW nootropic; ophthalmological; anorectic; cytostatic; cataract; obesity.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH 197..251  
FT Domain /note="CBS domain"  
FT Domain 204..226  
FT Domain /note="Transmembrane domain"  
FT Domain 278..332  
FT Domain /note="CBS domain"  
FT Domain 353..406  
FT Domain /note="CBS domain"  
FT Domain 425..478  
FT Domain /note="CBS domain"

XX WO200283709-A2.  
PN 24-OCT-2002.  
XX  
XX 05-APR-2002; 2002WO-US010818.  
XX  
XX 06-APR-2001; 2001US-0282119P.  
PR 13-APR-2001; 2001US-0283588P.  
PR 13-APR-2001; 2001US-0283759P.  
PR 20-APR-2001; 2001US-0285589P.  
PR 27-APR-2001; 2001US-0287036P.  
PR 27-APR-2001; 2001US-0287037P.  
PR 04-MAY-2001; 2001US-028608P.  
PR 04-MAY-2001; 2001US-0288712P.  
PR 09-MAY-2001; 2001US-0289909P.  
PR 17-MAY-2001; 2001US-0292246P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.

XX Recipon SA, Burrill JD, Marcus GA, Zingler KA, Tang YT;  
XX Thornton M, Borowsky ML, Baughn MR, Burford N, Lee SY, Bandman O;  
XX Hafalia AJA, Yao MG, Rankumar J, Wallia NK, Lu DAM, Arvizu CS;  
XX Ison CH, Ding L, Lu Y, Gururajan R, Walsh RT, Gandhi AR;  
XX Swarnakar A, Forsythe IJ, Yue H, Au-Young JK, Elliott VS, Lee S;  
XX  
XX WPI; 2003-092995/08.  
XX N-PSDB; AAD49456.

XX New human kinases and phosphatases (KPP), useful for diagnosing, treating  
XX and preventing diseases or conditions associated with the aberrant KPP  
XX expression, e.g. hypertension, cancer, AIDS, diabetes, cataract,  
XX psoriasis, obesity.

XX Claim 1; Page 176-178; 195pp; English.

XX The invention relates to human kinases and phosphatases (KPP), and their  
XX corresponding nucleic acids. The polypeptides and polynucleotides of the  
XX invention are useful in diagnosing, treating and preventing diseases or  
XX conditions associated with the decreased expression or overexpression of  
XX KPP, such as cardiovascular (e.g. hypertension, myocardial infarction,  
XX angina pectoris), immune (e.g. acquired immune deficiency syndrome  
XX (AIDS), Grave's disease, diabetes), neurological (e.g. Parkinson's  
XX disease, Alzheimer's disease, epilepsy), disorders affecting growth and  
XX development (e.g. cirrhosis, psoriasis, cataract), lipid (e.g.  
XX hypercholesterolaemia, obesity, lipid myopathies), cell proliferative  
XX disorders, or cancer. They are also useful in assessing the effects of  
XX exogenous compounds on the expression of nucleic acid and amino acid  
XX sequences of KPP. The KPP or its fragments are useful in screening  
XX compounds for effectiveness as agonist or antagonist of the polypeptides,  
XX or in altering the expression of the target polynucleotide and compounds  
XX that specifically bind to or modulate the activity of the polypeptide.  
XX The microarray is useful in monitoring or measuring protein-protein  
XX interactions, drug-target interactions, and gene expression profiles. KPP  
XX DNA is used in gene therapy. The present sequence is human KPP protein

XX Sequence 489 AA;

Query Match 100.0%; Score 1551; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 4.1e-165;  
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFQEHCTCYDAMATSSKLVIFDTMLETKKAFPAALVANGVRAAPLWDSKKQSFVGMLTIT 60  
DB 185 MRFQEHCTCYDAMATSSKLVIFDTMLETKKAFPAALVANGVRAAPLWDSKKQSFVGMLTIT 244  
QY 61 DFILVLHRYRSPVQIYEIEHQKIEWREIYLGQCFKPLVSIISPNDSLFEAVYTLIKNR 120  
DB 245 DFILVLHRYRSPVQIYEIEHQKIEWREIYLGQCFKPLVSIISPNDSLFEAVYTLIKNR 304  
QY 121 IHRPLVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTTODLIGTFRDLAVLLE 180  
DB 305 IHRPLVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTTODLIGTFRDLAVLLE 364

QY 181 TAPILTALDIFVDRRVSALPVNCGQVGLYSRFDVHLLAAQTYNHLDMVSVEALRQR 240  
 DB 365 TAPILTALDIFVDRRVSALPVNCGQVGLYSRFDVHLLAAQTYNHLDMVSVEALRQR 424  
 QY 241 TLEGLVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLGLVVSLSDSLQALVLSAGI 300  
 DB 425 TLEGLVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLGLVVSLSDSLQALVLSAGI 484  
 QY 301 DALGA 305  
 DB 485 DALGA 489

RESULT 6  
 ID ADF50310 standard; protein; 489 AA.  
 XX ADF50310;  
 AC  
 XX 12-FEB-2004 (first entry)  
 DT  
 XX Human AMP-activated protein kinase (AMPK)-gamma 3 protein subunit.  
 DE  
 XX human; transgenic; AMP-activated protein kinase gamma 3 subunit; Prkg3;  
 KW AMPK; energy metabolism; obesity; dyslipidaemia;  
 KW insulin resistance syndrome; type 2 diabetes; antidiabetic; anorectic;  
 KW antilipaeic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003063586-A1.  
 XX  
 XX 07-AUG-2003.  
 XX  
 XX 31-JAN-2003; 2003WO-IB000912.  
 XX  
 PF  
 XX 01-FEB-2002; 2002US-0353430P.  
 PR  
 XX (AREX-) AREXIS AB.  
 PA  
 XX Andersson L, Marklund S;  
 PI  
 XX WPI; 2003-663404/62.  
 DR  
 XX N-PSDB; ADP50309.  
 DR  
 XX New transgenic non-human animals expressing an AMP-activated protein  
 PT kinase gamma 3 subunit, useful as models for improving treatment,  
 PT prevention or diagnosis of diseases related to energy metabolism, e.g.  
 PT obesity or type 2 diabetes.  
 XX  
 PS Claim 3; SEQ ID NO 2; 46pp; English.  
 XX  
 CC This invention relates to novel transgenic non-human animals expressing  
 CC an AMP-activated protein kinase (AMPK)-gamma 3 subunit. Specifically, it  
 CC relates to the transgene Prkg3 gene that encodes the AMPK gamma3 subunit  
 CC or a variant thereof, where the nucleic acid is operably linked to a  
 CC regulatory element. AMPK is involved in the regulation of energy  
 CC metabolism in eukaryotic cells, and is recognised as a major regulator of  
 CC lipid biosynthetic pathways due to its role in the phosphorylation and  
 CC inactivation of key enzymes such as acetyl-CoA carboxylase. The present  
 CC invention describes transgenic animals expressing AMPK-gamma 3 to be used  
 CC as models for energy metabolism diseases and also methods for the  
 CC development of drugs for the treatment or prevention of obesity,  
 CC dyslipidaemia, insulin resistance syndrome or type 2 diabetes.  
 CC Accordingly, the compositions of this invention have various activities  
 CC including antidiabetic, anorectic and antilipaeic. This polypeptide  
 CC sequence is the human AMPK-gamma3 protein subunit of the invention.  
 XX  
 SQ Sequence 489 AA;

Query Match 100.0%; Score 1551; DB 7; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-165;

Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRFQHEHTCYDAMATSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
 DB 185 MRFQHEHTCYDAMATSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 244  
 QY 61 DFILVHRYRSPVQIYEIEQHKIETWRIYIQQCFKPLVSPNDLSLFEAVVTLIKNR 120  
 DB 245 DFILVHRYRSPVQIYEIEQHKIETWRIYIQQCFKPLVSPNDLSLFEAVVTLIKNR 304  
 QY 121 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPRSPFLYRTIQDGLGTFRDLAVVLE 180  
 DB 305 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPRSPFLYRTIQDGLGTFRDLAVVLE 364  
 QY 181 TAPILTALDIFVDRRVSALPVNCGQVGLYSRFDVHLLAAQTYNHLDMVSVEALRQR 240  
 DB 365 TAPILTALDIFVDRRVSALPVNCGQVGLYSRFDVHLLAAQTYNHLDMVSVEALRQR 424  
 QY 241 TLEGLVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLGLVVSLSDSLQALVLSAGI 300  
 DB 425 TLEGLVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLGLVVSLSDSLQALVLSAGI 484  
 QY 301 DALGA 305  
 DB 485 DALGA 489

RESULT 7  
 ID ADP87617 standard; protein; 489 AA.  
 XX ADP87617;  
 AC  
 XX 23-SEP-2004 (first entry)  
 DT  
 XX Human NOVX polypeptide, NOV10a.  
 DE  
 XX anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;  
 KW insulin resistance; hybridization probe; chromosome mapping;  
 KW tissue typing; preventive medicine; pharmacogenomics; NOVX; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004056961-A2.  
 XX  
 XX 08-JUL-2004.  
 PD  
 XX 27-OCT-2003; 2003WO-US034114.  
 PF  
 XX 25-OCT-2002; 2002US-0421239P.  
 PR 28-OCT-2002; 2002US-0421700P.  
 PR 31-OCT-2002; 2002US-0422776P.  
 PR 13-NOV-2002; 2002US-0426197P.  
 PR 20-DEC-2002; 2002US-0435498P.  
 PR 20-DEC-2002; 2002US-0435510P.  
 PR 21-MAR-2003; 2003US-0456812P.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;  
 PI WPI; 2004-500293/47.  
 XX N-PSDB; ADP87616.  
 DR  
 XX New NOVX nucleic acid molecules and polypeptides useful for preventing or  
 PT treating NOVX-associated disorders, e.g. diabetes, insulin resistance or  
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.  
 XX  
 PS Claim 3; SEQ ID NO 74; 570pp; English.  
 XX  
 CC The invention relates to a novel isolated nucleic acid molecule  
 CC comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base

CC pairs) fully defined in the specification; or encodes any of the amino  
CC acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the  
CC specification. The invention further comprises: an isolated polypeptide  
CC comprising any of the amino acid sequences cited above; a method for  
CC identifying compounds that modulate target polypeptide activity; an  
CC antibody that immunospecifically binds to the target polypeptide, where  
CC the target polypeptide comprises any of the above-mentioned amino acid  
CC sequences, an amino acid sequence that is at least 95% identical to the  
CC of the above-mentioned amino acid sequences, or an amino acid sequence  
CC that is at least 95% identical to the domain of the above amino acid  
CC sequences; a method for identifying a potential therapeutic agent for use  
CC in treatment of a pathology, where the pathology is related to aberrant  
CC expression or aberrant physiological interactions of a target polypeptide  
CC; and a method of screening for a modulator of activity of or of latency  
CC or predisposition to a pathology associated with a target polypeptide.  
CC The modulating compounds have anorectic and antidiabetic activities. The  
CC nucleic acid sequences of the invention may be used in gene therapy to  
CC treat disorders. The proteins of the invention may be used in creating a  
CC vaccine. The composition and methods are useful for identifying compounds  
CC that modulate protein activity or for diagnosing, preventing or treating  
CC diverse pathological conditions, such as obesity, diabetes or insulin  
CC resistance. The nucleic acids are also used as hybridization probes, in  
CC chromosome mapping, tissue typing, preventive medicine, and  
CC pharmacogenomics. This sequence represents a NOVX polypeptide of the  
CC invention.

XX SQ Sequence 489 AA;

Query Match 100.0%; Score 1551; DB 8; Length 489;  
Best Local Similarity 100.0%; Pred. No. 4.1e-165;  
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
DB 185 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 244  
QY 61 DFILVLHRYRSPVQIYEIQHKTETWREIYLOGCFKPLVSIISPNDLSLFAVYTLIKNR 120  
DB 245 DFILVLHRYRSPVQIYEIQHKTETWREIYLOGCFKPLVSIISPNDLSLFAVYTLIKNR 304  
QY 121 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGFRDLAVVLE 180  
DB 305 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGFRDLAVVLE 364  
QY 181 TAPILTALDIFDVRVSALPVNVEGQVVGYSRFDVHLAAQQTYNHLDMSVGEALRQR 240  
DB 365 TAPILTALDIFDVRVSALPVNVEGQVVGYSRFDVHLAAQQTYNHLDMSVGEALRQR 424  
QY 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVETQHLGVLVSLSDILQALVLSGAGI 300  
DB 425 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVETQHLGVLVSLSDILQALVLSGAGI 484  
QY 301 DALGA 305  
DB 485 DALGA 489

RESULT 8  
AAE00329  
ID AAE00329 standard; protein; 305 AA.

XX AAE00329;  
AC  
XX  
DT 13-JUN-2001 (first entry)  
XX  
DE Human Prkag3 V401 mutant.  
XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;  
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;  
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;  
KW cystathione beta synthase; CBS; cardiac; gene therapy; mutant; mutein;  
KW variant.

XX Homo sapiens.  
XX OS  
XX FH Key Location/Qualifiers  
XX Misc-difference 40  
FT FT /note= "Wild-type Val substituted with Ile"  
XX

XX W0200120003-A2.

XX 22-MAR-2001.

XX 11-SEP-2000; 2000MO-EP009896.

XX 10-SEP-1999; 99EP-00402236.

XX 18-MAY-2000; 2000EP-00401388.

XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.

XX (ANDE/) ANDERSSON L.

XX (LOOF/) LOOFT C.

XX (KALM/) KALM E.

XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX WPI; 2001-244810/25.

XX New variants of the gamma subunit of vertebrate adenosine monophosphate-  
XX activated kinase for diagnosis or treatment of disorders associated with  
XX energy metabolism such as diabetes, obesity, and myopathy.

XX Disclosure; Page; 71pp; English.

XX The present sequence is a V401 mutant of human muscle-specific isoform of  
XX gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK)  
XX Prkag3. This mutant sequence results in decreased glycogen content in  
XX human skeletal muscle. Mutation in Prkag3 results in an altered  
XX regulation of carbohydrate metabolism, particularly in skeletal muscle.  
XX PRKAG3 is useful as therapeutic for treating carbohydrate metabolism  
XX disorders such as diabetes, obesity, and disorders associated with muscle  
XX metabolism such as myopathy and cardiovascular diseases, to modulate AMPK  
XX activity, and for restoring a normal AMPK function. PRKAG3 sequence and  
XX its functionally altered mutants are useful for the diagnostic  
XX evaluation, genetic testing and prognosis of a metabolic disorder,  
XX preferably a carbohydrate metabolism disorder. Primers that can detect a  
XX genetic polymorphic marker linked to a sequence encoding PRKAG3, are  
XX useful for detecting a dysfunction of carbohydrate metabolism resulting  
XX from the expression of a functionally altered allele of PRKAG3.

XX Transgenic animal and host cell transformed with PRKAG3 or a  
XX heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for  
XX screening compounds able to modulate AMPK activity. Nucleic acid encoding  
XX PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a  
XX sequence encoding the first cystathione beta synthase (CBS) domain of  
XX PRKAG3 and is useful in gene therapy. Note: The present sequence is not  
XX shown in the specification, but is derived from the human Prkag3 sequence  
XX SEQ.ID.NO.4 shown in page 57-58 of sequence listing (AAE00221)

XX Sequence 305 AA;

Query Match 99.9%; Score 1550; DB 4; Length 305;  
Best Local Similarity 99.7%; Pred. No. 2.7e-165;  
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60

DB 1 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60

QY 61 DFILVLHRYRSPVQIYEIQHKTETWREIYLOGCFKPLVSIISPNDLSLFAVYTLIKNR 120

DB 61 DFILVLHRYRSPVQIYEIQHKTETWREIYLOGCFKPLVSIISPNDLSLFAVYTLIKNR 120

QY 121 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGFRDLAVVLE 180

DB 121 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGFRDLAVVLE 180

QY 181 TAPILTALDIFVDRVSALPVNNECGVGVGLYSRFDVHLLAAQTYNHLDMVSGEALRQR 240  
 DB 181 TAPILTALDIFVDRVSALPVNNECGVGVGLYSRFDVHLLAAQTYNHLDMVSGEALRQR 240  
 QY 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPAGI 300  
 DB 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPAGI 300  
 QY 301 DALGA 305  
 DB 301 DALGA 305

RESULT 9  
 AA000328  
 ID AAE00328 standard; protein; 305 AA.

AC AAE00328;  
 XX 13-JUN-2001 (first entry)  
 DT Human Prkag3 R41Q mutant.  
 DE Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;  
 KW Prkag3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;  
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;  
 KW cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;  
 KW variant.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Misc-difference 41 /note= "Wild-type Arg substituted with Gln"  
 FT WO200120003-A2.  
 XX 22-MAR-2001.

XX 11-SEP-2000; 2000WO-EP009896.  
 XX 10-SEP-1999; 99EP-00402236.  
 XX 18-MAY-2000; 2000EP-00401388.  
 XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 XX (ANDE/) ANDERSSON L.  
 XX (LOOF/) LOOFT C.  
 XX (KALM/) KALM E.  
 XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;  
 XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;  
 XX WPI; 2001-244810/25.  
 XX New variants of the gamma subunit of vertebrate adenosine monophosphate-  
 XX activated kinase for diagnosis or treatment of disorders associated with  
 XX energy metabolism such as diabetes, obesity, and myopathy.

XX Disclosure; Page; 71pp; English.  
 XX The present sequence is a R41Q mutant of human muscle-specific isoform of  
 XX gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK)  
 XX Prkag3. This mutant sequence results in increased glycogen content in  
 XX human skeletal muscle. Mutation in Prkag3 results in an altered  
 XX regulation of carbohydrate metabolism, particularly in skeletal muscle.  
 XX PRKAG3 is useful as therapeutic for treating carbohydrate metabolism  
 XX disorders such as diabetes, obesity, and disorders associated with muscle  
 XX metabolism such as myopathy and cardiovascular diseases, to modulate AMPK  
 XX activity, and for restoring a normal AMPK function. PRKAG3 sequence and  
 XX its functionally altered mutants are useful for the diagnostic  
 XX evaluation, genetic testing and prognosis of a metabolic disorder,  
 XX preferably a carbohydrate metabolism disorder. Primers that can detect a

CC genetic polymorphic marker linked to a sequence encoding PRKAG3, are  
 CC useful for detecting a dysfunction of carbohydrate metabolism resulting  
 CC from the expression of a functionally altered allele of PRKAG3.  
 CC Transgenic animal and host cell transformed with PRKAG3 or a  
 CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for  
 CC screening compounds able to modulate AMPK activity. Nucleic acid encoding  
 CC PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a  
 CC sequence encoding the first cystathione beta synthase (CBS) domain of  
 CC PRKAG3 and is useful in gene therapy. Note: The present sequence is not  
 CC shown in the specification, but is derived from the human Prkag3 sequence  
 CC SEQ.ID.NO.4 shown in page 57-58 of sequence listing (AAE00221)  
 XX  
 SQ Sequence 305 AA;

Query Match 99.7%; Score 1547; DB 4; Length 305;  
 Best Local Similarity 99.7%; Pred. No. 5.9e-165;  
 Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60  
 DB 1 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60  
 QY 61 DFILVLRHYRSPVQIYEIEQHKIETWREIYLGQCFKPLVSPNDSLFEAVVTLIKR 120  
 DB 61 DFILVLRHYRSPVQIYEIEQHKIETWREIYLGQCFKPLVSPNDSLFEAVVTLIKR 120  
 QY 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLLPSPFLYRTIQDILGIGTFRDLAVVLE 180  
 DB 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLLPSPFLYRTIQDILGIGTFRDLAVVLE 180  
 QY 181 TABILTALDIFVDRVSALPVNNECGVGVGLYSRFDVHLLAAQTYNHLDMVSGEALRQR 240  
 DB 181 TABILTALDIFVDRVSALPVNNECGVGVGLYSRFDVHLLAAQTYNHLDMVSGEALRQR 240  
 QY 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPAGI 300  
 DB 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPAGI 300  
 QY 301 DALGA 305  
 DB 301 DALGA 305

RESULT 10  
 ABP43929  
 ID ABP43929 standard; protein; 489 AA.

AC ABP43929;  
 XX 26-FEB-2003 (first entry)  
 DT AMP activated protein kinase gamma 3 subunit.  
 DE Neuroprotective; immunomodulator; cancer; chromosome 2; cytostatic;  
 KW anti-inflammatory; gene therapy; nutritional supplement; wound; burn;  
 KW ulcer; Alzheimer's disease; Huntington's disease;  
 KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;  
 KW vulnery.  
 XX Homo sapiens.  
 XX WO200231111-A2.  
 XX 18-APR-2002.  
 XX 11-OCT-2001; 2001WO-US027760.  
 XX 12-OCT-2000; 2000US-00687527.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
 XX Xue AJ, Yang Y, Wehrman T, Drmanac RT;

XX WPI; 2002-426278/45.  
DR N-PSDB; ABQ61173.  
XX  
XX  
PT New polypeptides and their encoded proteins, useful as nutritional  
PT sources or supplements, or in gene therapy, particularly for treating  
PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or  
PT inflammation.  
XX  
XX Claim 20; SEQ ID # 832; 357pp + Sequence Listing; English.  
XX  
XX The invention relates to 446 newly isolated polynucleotide sequences. The  
CC activity of polynucleotides of the invention may be described as,  
CC vulnary, neuroprotective, immunomodulator, cytostatic and anti-  
CC inflammatory. Compositions comprising nucleic acids of the invention are  
CC useful for treating a mammalian subject, or as nutritional sources or  
CC supplements. These are useful in gene therapy, particularly for treating  
CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,  
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or  
CC inflammation. The nucleic acids and polypeptides are also useful in  
CC diagnostic and research methods. The sequences given in records ABP43544-  
CC ABP43989 represent polypeptides encoded by polynucleotides of the  
CC invention. NOTE: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 489 AA;

Query Match 99.5%; Score 1544; DB 5; Length 489;  
Best Local Similarity 99.3%; Pred. No. 2.5e-164; Indels 0; Gaps 0;  
Matches 303; Conservative 2; Mismatches 0;  
Qy 1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
Db 185 MRFIEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 244  
Qy 61 DFILVLRHYRSPVQIYEIEQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 120  
Db 245 DFILVLRHYRSPVQIYEIEQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 304  
Qy 121 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
Db 305 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364  
Qy 181 TAPILTALDIFVDRVSALPVVNECGQVVGYSRFDVIHLAAQQTYNHLDMSVGEALRQR 240  
Db 365 TAPILTALDIFVDRVSALPVVNECGQVVGYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424  
Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAGI 300  
Db 425 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAGI 484  
Qy 301 DALGA 305  
Db 485 DALGA 489

RESULT 11  
AAE38410  
ID AAE38410 standard; protein; 489 AA.  
XX  
XX AAE38410;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Human Prkag3 protein.  
XX  
XX Human; Prkag3; transcription; therapy; prevention; energy metabolism;  
KW obesity; dyslipidaemia; insulin resistance syndrome; type II diabetes;  
KW anorectic; antilipaemic; antidiabetic.  
XX  
XX Homo sapiens.  
XX

PN WO2003064465-A2.  
XX  
XX 07-AUG-2003.  
XX  
XX 31-JAN-2003; 2003WO-IB000762.  
XX  
XX 01-FEB-2002; 2002US-0353429P.  
XX  
XX (AREX-) AREXIS AB.  
XX  
XX Svensson T;  
XX  
XX WPI; 2003-636796/60.  
DR N-PSDB; AAD58250.  
XX  
XX Novel isolated nucleic acid encoding human Prkag3 promoter capable of  
PT directing transcription of a heterologous coding sequence, useful for  
PT screening compounds which modulate human Prkag3 promoter activity.  
XX  
XX Disclosure; Page 52-53; 53pp; English.  
XX  
XX The present invention relates to novel human Prkag3 promoter capable of  
CC directing transcription of a heterologous coding sequence, useful for  
CC screening compounds which modulate human Prkag3 promoter activity. The  
CC invention is useful for treating or preventing diseases related to energy  
CC metabolism e.g. Obesity, dyslipidaemia, insulin resistance syndrome or  
CC type II diabetes. The present sequence is human Prkag3 protein  
XX  
XX SQ Sequence 489 AA;

Query Match 98.6%; Score 1529; DB 7; Length 489;  
Best Local Similarity 98.7%; Pred. No. 1.2e-162; Indels 0; Gaps 0;  
Matches 301; Conservative 1; Mismatches 3;  
Qy 1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
Db 185 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 244  
Qy 61 DFILVLRHYRSPVQIYEIEQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 120  
Db 245 DFILVLRHYRSPVQIYEIEQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 304  
Qy 121 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
Db 305 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364  
Qy 181 TAPILTALDIFVDRVSALPVVNECGQVVGYSRFDVIHLAAQQTYNHLDMSVGEALRQR 240  
Db 365 TAPILTALDIFVDRVSALPVVNECGQVVGYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424  
Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAGI 300  
Db 425 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAGI 484  
Qy 301 DALGA 305  
Db 485 DALGA 489

RESULT 12  
ADF50314  
ID ADF50314 standard; protein; 489 AA.  
XX  
XX ADF50314;  
XX  
XX 12-FEB-2004 (first entry)  
XX  
XX Human AMPK-gamma 3 protein subunit (SeqID 6).  
XX  
XX human; transgenic; AMP-activated protein kinase gamma 3 subunit; Prkag3;  
KW AMPK; energy metabolism; obesity; dyslipidaemia;  
KW insulin resistance syndrome; type 2 diabetes; antidiabetic; anorectic;  
KW antilipaemic.

XX OS Homo sapiens.  
 XX PN WO2003063586-A1.  
 XX AC ADP87619.  
 XX PD 07-AUG-2003.  
 XX PF 31-JAN-2003; 2003WO-IB000912.  
 XX PR 01-FEB-2002; 2002US-0353430P.  
 XX PA (AREX-) AREXIS AB.  
 XX PI Andersson L, Marklund S;  
 XX DR WPI; 2003-663404/62.  
 XX DR N-PSDB; ADP87619.  
 XX PT New transgenic non-human animals expressing an AMP-activated protein  
 PT kinase gamma 3 subunit, useful as models for improving treatment,  
 PT prevention or diagnosis of diseases related to energy metabolism, e.g.  
 PT obesity or type 2 diabetes.  
 XX PS Example 1; SEQ ID NO 6; 46pp; English.  
 XX CC This invention relates to novel transgenic non-human animals expressing  
 CC an AMP-activated protein kinase (AMPK)-gamma 3 subunit. Specifically, it  
 CC relates to the transgene Prkag3 gene that encodes the AMPK gamma3 subunit  
 CC or a variant thereof, where the nucleic acid is operably linked to a  
 CC regulatory element. AMPK is involved in the regulation of energy  
 CC metabolism in eukaryotic cells, and is recognised as a major regulator of  
 CC lipid biosynthetic pathways due to its role in the phosphorylation and  
 CC inactivation of key enzymes such as acetyl-CoA carboxylase. The present  
 CC invention describes transgenic animals expressing AMPK-gamma 3 to be used  
 CC as models for energy metabolism diseases and also methods for the  
 CC development of drugs for the treatment or prevention of obesity,  
 CC dyslipidaemia, insulin resistance syndrome or type 2 diabetes.  
 CC According to the compositions of this invention have various activities  
 CC including antidiabetic, anorectic and antilipemic. This polypeptide  
 CC sequence is the human AMPK-gamma3 protein subunit of the invention.  
 XX SQ Sequence 489 AA;

Query Match 98.6%; Score 1529; DB 7; Length 489;  
 Best Local Similarity 98.7%; Pred. No. 1.2e-162;  
 Matches 301; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MRFMQHTCYDAMATSSKLVIFDTMLIKKAPFALVANGVRAAPLWDSKKQSFVGM	60
Db	185	MRFMQHTCYDAMATSSKLVIFDTMLIKKAPFALVANGVRAAPLWDSKKQSFVGM	244
Qy	61	DFILVHLRYRSPVQIYEIQHKEIETWREIYLGCCFKPLVSPNDLPEAVVTLIKNR	120
Db	245	DFILVHLRYRSPVQIYEIQHKEIETWREIYLGCCFKPLVSPNDLPEAVVTLIKNR	304
Qy	121	IHLPLVLDPVSGNVHLTHLTKRLKFLHIFGSLLPSPFLYRTQDGLIGTFRLAVLLE	180
Db	305	IHLPLVLDPVSGNVHLTHLTKRLKFLHIFGSLLPSPFLYRTQDGLIGTFRLAVLLE	364
Qy	181	TAPILTALDIFDVRVSALPVNCEGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR	240
Db	365	TAPILTALDIFDVRVSALPVNCEGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR	424
Qy	241	TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGVVSLSDIILQALVLSPAGI	300
Db	425	TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGVVSLSDIILQALVLSPAGI	484
Qy	301	DALGA 305	
Db	485	DALGA 489	

RESULT 13

ADP87619  
 ID ADP87619 standard; protein; 492 AA.  
 XX AC ADP87619;  
 XX DT 23-SEP-2004 (first entry)  
 XX DE Human NOVX polypeptide, NOV10b.  
 XX KW anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;  
 KW insulin resistance; hybridization probe; chromosome mapping;  
 KW tissue typing; preventive medicine; pharmacogenomics; NOVX; human.  
 XX OS Homo sapiens.  
 XX PN WO2004056961-A2.  
 XX PD 08-JUL-2004.  
 XX PF 27-OCT-2003; 2003WO-US034114.  
 XX PR 25-OCT-2002; 2002US-0421239P.  
 PR 28-OCT-2002; 2002US-0421700P.  
 PR 31-OCT-2002; 2002US-0422776P.  
 PR 13-NOV-2002; 2002US-0426197P.  
 PR 20-DEC-2002; 2002US-0435498P.  
 PR 20-DEC-2002; 2002US-0435510P.  
 PR 20-DEC-2002; 2002US-0435568P.  
 PR 21-MAR-2003; 2003US-0456812P.  
 XX PA (CURA-) CURAGEN CORP.  
 XX PI Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;  
 XX DR WPI; 2004-500293/47.  
 DR N-PSDB; ADP87618.  
 XX PT New NOVX nucleic acid molecules and polypeptides useful for preventing or  
 PT treating NOVX-associated disorders, e.g. diabetes, insulin resistance or  
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.  
 XX PS Claim 3; SEQ ID NO 76; 570pp; English.  
 XX CC The invention relates to a novel isolated nucleic acid molecule  
 CC comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base  
 CC pairs) fully defined in the specification; or encodes any of the amino  
 CC acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the  
 CC specification. The invention further comprises: an isolated polypeptide  
 CC comprising any of the amino acid sequences cited above; a method for  
 CC identifying compounds that modulate target polypeptide activity; an  
 CC antibody that immunospecifically binds to the target polypeptide, where  
 CC the target polypeptide comprises any of the above-mentioned amino acid  
 CC sequences, an amino acid sequence that is at least 95% identical to the  
 CC above amino acid sequences, an amino acid sequence of at least one domain  
 CC of the above-mentioned amino acid sequences, or an amino acid sequence  
 CC that is at least 95% identical to the domain of the above amino acid  
 CC sequences; a method for identifying a potential therapeutic agent for use  
 CC in treatment of a pathology, where the pathology is related to aberrant  
 CC expression or aberrant physiological interactions of a target polypeptide  
 CC; and a method of screening for a modulator of activity of or of latency  
 CC or predisposition to a pathology associated with a target polypeptide.  
 CC The modulating compounds have anorectic and antidiabetic activities. The  
 CC nucleic acid sequences of the invention may be used in gene therapy to  
 CC treat disorders. The proteins of the invention may be used in creating a  
 CC vaccine. The composition and methods are useful for identifying compounds  
 CC that modulate protein activity or for diagnosing, preventing or treating  
 CC diverse pathological conditions, such as obesity, diabetes or insulin  
 CC resistance. The nucleic acids are also used as hybridization probes, in  
 CC chromosome mapping, tissue typing, preventive medicine, and  
 CC pharmacogenomics. This sequence represents a NOVX polypeptide of the  
 XX SQ Sequence 492 AA;

CC	screening for agents that modulate the activity of a modifier of IGFR
CC	(MIGFR). The method comprises providing an assay system comprising an
CC	MIGFR polypeptide or polynucleotide, contacting the assay system with a
CC	test agent under conditions where, but for the presence of the test
CC	agent, the system provides a reference activity and detecting a test
CC	agent-biased activity of the assay system, where a difference between the
CC	test agent-biased activity and the reference activity identifies the test
CC	agent as a candidate IGFR pathway modulating agent. The invention also
CC	relates to methods for modulating an IGFR pathway of a cell or in a
CC	mammalian cell and a method for diagnosing a disease in a patient. The
CC	methods are useful for diagnosing or treating cancer or for identifying
CC	modulators of an IGFR pathway, which may be utilized as therapeutic
CC	targets for disorders associated with defective IGFR function, such as
CC	cancer. This sequence represents a human modulator of IGFR pathway
CC	polypeptide of the invention.
XX	
SQ	Sequence 492 AA;
	Query Match 98.3%; Score 1525; DB 9; Length 492;
	Best Local Similarity 98.4%; Pred. No. 3.5e-162;
	Matches 299; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy	1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGM
Db	185 MRFIEHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGM
Qy	61 DFILVLRHYRSPVLQIYEIEQHKIETWREIYLGCGFKPLVSI SPNDSLFEAVYTLIKNR
Db	245 DFILVLRHYRSPVLQIYEIEQHKIETWREIYLGCGFKPLVSI SPNDSLFEAVYTLIKNR
Qy	121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE
Db	305 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE
Qy	181 TAPILTALDIFVDRRVSALPVNCGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR
Db	365 TAPILTALDIFVDRRVSALPVNCGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR
Qy	241 TLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHQLLGVVLSLSDILQALVLS
Db	425 TLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHQLLGVVLSLSDILQALVLS
Qy	301 DALG 304
Db	485 DPSG 488
	RESULT 15
	AAE00220
ID	AAE00220 standard; protein; 305 AA.
XX	
AC	AAE00220;
XX	
DT	13-JUN-2001 (first entry)
XX	
DE	Pig AMPK gamma subunit muscle-specific isoform, PRKAG3.
XX	
KW	Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW	PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW	genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW	cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
KW	chromosome 15.
XX	
OS	Sus scrofa.
XX	
FH	Key
FT	Domain
FT	13..66
FT	/label= CBS
FT	/note= "Cystathione beta synthase domain"
FT	94..148
FT	/label= CBS
FT	/note= "Cystathione beta synthase domain"
FT	170..223



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FT /label= CBS
FT /note= "Cystathione beta synthase domain"
FT 241..294
FT /label= CBS
FT /note= "Cystathione beta synthase domain"
XX WO200120003-A2.
XX
XX 22-MAR-2001.
XX
XX 11-SEP-2000; 2000WO-EP009896.
XX
XX 10-SEP-1999; 99EP-00402236.
XX 18-MAY-2000; 2000EP-00401388.
XX
XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX (ANDE/) ANDERSSON L.
XX (LOOF/) LOOFT C.
XX (KALM/) KALM E.
XX
XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
XX WPI: 2001-244810/25.
XX N-PSDB; AAD03295.
XX
XX New variants of the gamma subunit of vertebrate adenosine monophosphate-
XX activated kinase for diagnosis or treatment of disorders associated with
XX energy metabolism such as diabetes, obesity, and myopathy.
XX
XX Claim 4; Fig 2; 71pp; English.
XX
XX The present amino acid sequence is pig adenosine monophosphate (AMP)-
XX activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3.
XX Prkag3 gene is located in the RN locus of chromosome 15. Mutation in
XX Prkag3 results in an altered regulation of carbohydrate metabolism,
XX particularly in skeletal muscle. PRKAG3 is useful as therapeutic for
XX treating carbohydrate metabolism disorders such as diabetes, obesity, and
XX disorders associated with muscle metabolism such as myopathy and
XX cardiovascular diseases, to modulate AMPK activity, and for restoring a
XX normal AMPK function. PRKAG3 sequence and its functionally altered
XX mutants are useful for the diagnostic evaluation, genetic testing and
XX prognosis of a metabolic disorder, preferably a carbohydrate metabolism
XX disorder. Primers that can detect a genetic polymorphic marker linked to
XX a sequence encoding PRKAG3, are useful for detecting a dysfunction of
XX carbohydrate metabolism resulting from the expression of a functionally
XX altered allele of PRKAG3. Transgenic animal and host cell transformed
XX with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant,
XX are useful for screening compounds able to modulate AMPK activity.
XX Nucleic acid encoding PRKAG3 is useful for detecting mutations in a
XX Prkag3 gene, or in a sequence encoding the first cystathione beta
XX synthase (CBS) domain of PRKAG3 and is useful in gene therapy
XX
XX Sequence 305 AA;
```

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Job time : 84.6866 secs

Db	181	TAPILTALDIFVDRRVSVLALPVVNETGVVGLYSRFDVIHLAAOQTYNHLDMNVGEALRQR	240
Qy	241	TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSPAGI	300
Db	241	TLCLEGVLSQPHETLGEVIDRIVREQVHRLVLDVDETHLLGVVSLSDIILQALVLSPAGI	300
Qy	301	DALGA 305	
Db	301	DALGA 305	

Query Match

Best Local Similarity 97.2%; Score 1507; DB 4; Length 305;

Mismatches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy	1	MRFMQEHCTYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT	60
Db	1	MHFMQEHCTYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT	60
Qy	61	DFILVHLHYRSPVLQVYEIEQHKIETWRIYLGQCFKPLVSI SPNDSLFEAVYTLIKNR	120
Db	61	DFILVHLHYRSPVLQVYEIEEHKIETWRIYLGQCFKPLVSI SPNDSLFEAVYTLIKNR	120
Qy	121	IHLPLVLDPVSGNVHLTHLTKRLKFLHIFGSLLPSPFLYRTIQDLGIGTFRDLAVLLE	180
Db	121	IHLPLVLDPVSGAVHLTHLTKRLKFLHIFGTLPPSPFLYRTIQDLGIGTFRDLAVLLE	180
Qy	181	TAPILTALDIFVDRRVSVLALPVVNETGVVGLYSRFDVIHLAAOQTYNHLDMNVGEALRQR	240

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:02:17 ; Search time 19.4343 Seconds  
(without alignments)  
1510.014 Million cell updates/sec

US-10-070-794A-4

Title: 1551

Sequence: 1 MRFQHEHTCYDMATSSKLV.....LSDLQLVLSPAGIDALGA 305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1007	64.9	330	2 T10759	AMP-activated prot
2	485	31.3	478	2 T25899	hypothetical prote
3	457	29.5	322	1 RGBYC3	regulatory protein
4	372.5	24.0	274	2 S67444	probable 5'-AMP-ac
5	243.5	15.7	391	2 B86222	hypothetical prote
6	217	14.0	443	2 T25854	Pv42 protein - kid
7	214	13.8	379	2 T10971	hypothetical prote
8	207.5	13.4	460	2 T24248	hypothetical prote
9	189.5	12.2	352	2 F86287	hypothetical prote
10	188.5	12.2	629	2 T18227	hypothetical prote
11	188	12.1	424	2 T46197	hypothetical prote
12	176	11.3	399	2 D96832	hypothetical prote
13	163	10.5	447	2 B96720	hypothetical prote
14	161.5	10.4	392	2 G75056	dehydrogenase PAB0
15	155.5	10.0	392	2 D71175	hypothetical prote
16	148.5	9.6	250	2 C90449	conserved hypotet
17	148	9.5	92	2 T50087	probable 5'-AMP-ac
18	147.5	9.5	280	1 H64452	conserved hypotet
19	146	9.4	313	1 B69030	conserved hypotet
20	141.5	9.1	157	1 F69185	yhcv homolog MTH64
21	140	9.0	527	2 S46088	hypothetical prote
22	139	9.0	152	2 AF2282	conserved hypotet
23	139	9.0	300	1 S08244	conserved hypotet
24	138.5	8.9	421	2 C64475	hypothetical prote
25	138	8.9	485	1 JC4998	IMP dehydrogenase
26	137	8.8	284	1 H69355	conserved hypotet
27	136.5	8.8	527	2 S64060	probable membrane
28	134	8.6	1286	2 A12195	two-component hybr
29	130.5	8.4	792	2 A84308	chloride channel [

30	129.5	8.3	1344	2 AD2103	two-component hybr
31	126.5	8.2	168	1 A64478	hypothetical prote
32	126	8.1	486	1 E71456	IMP dehydrogenase
33	125.5	8.1	157	2 AF3344	IMP dehydrogenase
34	123.5	8.0	287	2 F72780	hypothetical prote
35	122	7.9	292	2 C75148	hypothetical prote
36	120.5	7.8	223	2 T36952	conserved hypotet
37	120.5	7.8	278	2 A72781	probable acetoin u
38	120.5	7.8	284	1 H69232	M1225-related MTH18
39	119	7.7	122	2 B69119	yhcv homolog MTH18
40	119	7.7	485	2 E75015	IMP dehydrogenase
41	116.5	7.5	382	2 AD2762	conserved hypotet
42	116.5	7.5	382	2 C97543	hypothetical prote
43	115.5	7.4	285	1 C71188	conserved hypotet
44	115	7.4	482	2 C72264	IMP dehydrogenase
45	114.5	7.4	215	2 H72290	conserved hypotet

## ALIGNMENTS

## RESULT 1

T10759

AMP-activated protein kinase (EC 2.7.1.1-) gamma chain - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C;Accession: T10759

R;Woods, A.; Cheung P, C.F.; Smith, F.C.; Davison, M.D.; Scott, J.; Beri, R.K.; Carling,

J. Biol. Chem. 271, 10282-10290, 1996

A;Title: Characterization of AMP-activated protein kinase beta and gamma subunits: Assem

A;Reference number: 206738; MUID:96215327; PMID:8626596

A;Accession: T10759

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-330 &lt;WOO&gt;

A;Cross-references: UNIPROT:P80385; UNIPARC:UPI00001250B4; EMBL:X95578; NID:g1185270; PI

A;Experimental source: strain wistar

C;Complex: heterotrimer; alpha, beta and gamma chains

C;Function:

A;Description: is responsible for the regulation of fatty acid synthesis by phosphorylat

C;Superfamily: CAT3 protein

C;Keywords: fatty acid biosynthesis; phosphotransferase

Query Match 64.9%; Score 1007; DB 2; Length 330;

Best Local Similarity 65.3%; Pred. No. 8.6e-79;

Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;

QY 3 FMOEHTCYDMATSSKLVIPDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDF 62

DB 31 FMKSHRCYDLIPTSSKLVVFDTSQVKKAFALVANGVRAAPLWDSKKQSFVGMLTITDF 90

QY 63 ILVLRHYRSPVQIYEIEQHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNRIH 122

DB 91 INILHRYYSKALVQIYELEHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNRIH 150

QY 123 RLPVLPDVGSNVLHIILTHKRLKFLHIFGSLLRPSFLYRTIQDLGIGTFDRDLAVLETA 182

DB 151 RLPVIDPESGNTLYILTHKRLKFLHIFGSLLRPSFLYRTIQDLGIGTFDRDLAVLETA 210

QY 183 PILTALDIFDVRVSLPVPVNECGVGLYSRFDVHLAAQQTINHLDMVSGEALRORTL 242

DB 211 PVVVALGIFVQHRVSLPVPVNECGVGLYSRFDVHLAAQQTINHLDMVSGEALRORTL 270

QY 243 CLEGVSLSCQPSGLGVIRAREQVHRLVLDVETQHLGLQWLSLDTLQALVLVS 296

DB 271 YFEGVLKCYLHETLEAIINRLVVEAEVHRLVLDVETQHLGLQWLSLDTLQALVLVS 324

## RESULT 2

T25899

hypothetical protein T20F7.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000



Db 18 FISRSTYDVLPTSFRLIVFDVTLVFKTSLSLTLNNIVSAPLWDSSEANKEFAGLLTWADF 77  
 Qy 63 ILVLHRYRSPV--QIYEIOHQKIETWREIYLQ--GCFKP--LVSISPNDSLFEAVYTLIK 118  
 Db 78 VNIKYQSSPEAEIDKFKLLGLREVERKIGALPETIYVHPMSLMDACLAMSK 137  
 Qy 119 NRHLRPLVDPVSGN-----VLHILTHKRLKFLHIFGSLPRPSFLYRT-IDOLGIGTF 172  
 Db 138 SRARRIPLID-VDETGETSEMIVSLVTLQYRIKFT-----SNCKETAMLRVPLNQMTIGTW 192  
 Qy 173 RDLAVLETAIPILTALDIFVDRRVSALPVNVEGQVGLYSRFDVHLAAQQTYNHLDMS 232  
 Db 193 SNLATASMETKYVDVVKMLAEKNISAVPIVNSEGLTLNYESVDVHMLIQDGYSDNLDLS 252  
 Qy 233 VGEALRQRTLCLEGLVSCQ 251  
 Db 253 VGEALLKRPANFDGVHTCR 271  
 RESULT 5  
 B6222  
 hypothetical protein [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C:Accession: B6222  
 R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 anen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: B6222  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-391 <STO>  
 A:Cross-references: UNIPROT:O04028; UNIPARC:UPI00000AB393; GB:AE005172; NID:g2342682; PI  
 C:Genetics:  
 A:Map position: 1  
 Query Match 15.7%; Score 243.5; DB 2; Length 391;  
 Best Local Similarity 29.5%; Pred. No. 3.6e-13;  
 Matches 79; Conservative 53; Mismatches 89; Indels 47; Gaps 12;  
 Qy 39 GVRAPLWDSKQSFVGLMPTITPILVHRY--YRSPVQIYIEQHKIETWRE--IYLQ 94  
 Db 121 GIPLAPLWDFGKQFVGLPGLDFILRLGTHGNSLTE-ESELTHTIAAWKEGKAHIS 179  
 Qy 95 GCF-----KPLVSPNSDSLFEAVYTLKRIHRLPVL-----DPVSGNVHLHILTHK 141  
 Db 180 RQYDGGRRPYRPLVQVGPYDNLKVALKTLQNKVAAPVIVSYSLQDGSYPQLLHLASLS 239  
 Qy 142 RLK-----FLHIFGSLPRPSFLYRTIDOLGIGTF-----RDLAVLETAIPILTA 187  
 Db 240 GILKICRYFRHSSSL-----PILOQPCISIPIGTWVPRIGSSSKPLATLRPHSLGSA 295  
 Qy 188 LDIFVDRRVSALPVNVEGQVGLYSRFDVHLAAQQTYN--HL-DMSVGEALR--QRTL 242  
 Db 296 LALLVQAEVSIPIVDNDNSLDIYSRSDITAKAKAYAIHLDDMTVHQALQLQDAS 355  
 Qy 243 CLEGLV-----CQPHESLGEVIDRIA 264  
 Db 356 PPIGIFNGQRCHMCLRSDSLKVIMERLA 383  
 RESULT 6  
 T25854  
 hypothetical protein T01B6.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T25854  
 R:Johnson, D.  
 submitted to the EMBL Data Library, August 1996  
 A:Description: The sequence of C. elegans cosmid T01B6.  
 A:Reference number: Z20100  
 A:Accession: T25854  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-443 <JOH>  
 A:Cross-references: UNIPARC:UPI000017B339; EMBL:U67950; PIDN:AAB07568.1; GSPDB:GN00028;  
 A:Experimental source: strain Bristol N2; clone T01B6  
 C:Genetics:  
 A:Gene: CESP:T01B6.3  
 A:Map position: X  
 A:Introns: 5/3; 45/2; 72/1; 105/3; 153/3; 179/2; 200/3; 225/3; 255/3; 349/3; 397/2  
 Query Match 14.0%; Score 217; DB 2; Length 443;  
 Best Local Similarity 26.2%; Pred. No. 8e-11;  
 Matches 83; Conservative 59; Mismatches 117; Indels 58; Gaps 12;  
 Qy 3 FMOEHTCYDAMATSSKLVIPFDITMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILT---- 58  
 Db 81 FMSITCYDLPQPHSSLVVDFGDKTKVAAVHALSQHGHIAAVVNTDTKYQAEQVNNMGHC 140  
 Qy 59 ITDFILVL--HRYRSPVQIYIEQHKIETWREIYLQCGFKPLVSPNSDSLFEAVYTL 116  
 Db 141 LTAILLVAGNRVASKTL-----VEFLKEIGSGN----IICSGVQNSVWEAANII 187  
 Qy 117 IKNRHRLPVL--PVSGNVHLHILTHKRLK-----FLHIFGSLPRPSFL 160  
 Db 188 SHNKISFVPIFDITIPKGPGLYFLTPRMILQETVLKLSDFGDAILLHV-----R 237  
 Qy 161 YRTIQLGTFED--LAVLETAIPILTALDIFVDRRVSALPVNVEGQVGLYSRFDVI 218  
 Db 238 QATLDQKKGITWMDVILKIGLNTT-IEEAIKLSERKMSFTIPVVPDFKQIVNMLARKDII 296  
 Qy 219 -HLAAQQTYNHLDMSVGEALRQRTLCLEGLVLS-----CQPHESLGEVIDRIAEOHRLVL 273  
 Db 297 LEIMSHQGNFHDH-----LKEPVKILQSLRSLVYGRSSYTFETVAKMWTSDKSLPI 351  
 Qy 274 VDETQHLLGVVSLSDIL 290  
 Db 352 IDEGKRILAVVSCDIL 368  
 RESULT 7  
 T10971  
 P42 protein - kidney bean  
 C:Species: Phaseolus vulgaris (kidney bean)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
 C:Accession: T10971  
 R:Abu, H.  
 submitted to the EMBL Data Library, November 1995  
 A:Reference number: Z17236  
 A:Accession: T10971  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-379 <ABE>  
 A:Cross-references: UNIPROT:Q41108; UNIPARC:UPI00000ACD11; EMBL:U40713; NID:g1113940; PI  
 Query Match 13.8%; Score 214; DB 2; Length 379;  
 Best Local Similarity 23.5%; Pred. No. 1.2e-10;  
 Matches 85; Conservative 73; Mismatches 122; Indels 82; Gaps 17;  
 Qy 4 MOEHTCYDAMATSSKLVIPFDITMLEIKKAPFALVANGVRAAPL-----W-----DS 48  
 Db 17 LKEKKVKDMMVGKRLVEVPYATSLAQIMNTLVANKIVAVPVAAAPQGMWAGGSMVES 76  
 Qy 49 KQQS-----FVGMILTITFILVL-----HRYRSPVQIYIEQHKIETWREIY---LQ 95  
 Db 77 DKQTGAVRKHYIGMTVMTDLIAHAGDDHLSCGDNITQ--DLDRMSDSVSSIIHGSFEG 134



Qy	13	MATSSKLVIPDTWLEIKKAFVALVANGVRAAPLWDSKK--QSFVGLMTI-----TDFIL	64
Db	149	LTESNKLISHTSHSHSVQSAFETLLKYNLTSPVSVISKSDPHDLTNCLTFDYSDLNTVLLL	208
Qy	65	VLHRRYRSPJ-----VOIYEIOH-----KIETWREIYLOGCFK-----PLVUSIS	104
Db	209	IMNKINYSELNWDGIDGNPISPOEHBHEFTQTISKAKRGEEVPVEFTIKLHPKNPFIKFN	368
Qy	105	PNDLSFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLKFLHIFOSLLPRPSP--LYRT	163
Db	269	ETDITLFSVMEIT--GNGVHRIAITNEEGNKITGILSQORLLIKYMWENARRPSPDLFTLTST	327
Qy	164	IQDLGIGTFRDLAVLETAPILTALDI FVDRRSVALPVNNECGVGLYSRFDVIHLAAQ	223
Db	328	LQDLKLGSSNPI--TYIEDQMLEALHKMFNERVSSLAVIDRSRTLIGNISVIDVKNVTS	386
Qy	224	QTYNHLDMSV---GEALRQRTLCLEG-----VLSCQPHESLGEVIDRIAREQVHRLVLV	274
Db	387	KNSHLLFKSVLNFISVNLQKGI--EEGQDQPIPHVNNQTSLGRVIKLVATQSHRLWIV	445
Qy	275	DETQHLLGVVSLS	287
Db	446	DSSROASSMSAS	458

RESULT 11

T46197

hypothetical protein T8P19.40 - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C;Accession: T46197

R;Choiane, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa  
submitted to the Protein Sequence Database, December 1999

A;Reference number: Z23008

A;Accession: T46197

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-424 <CHO>

A;Cross-references: UNIPROT:Q9S7M6; UNIPARC:UPI00000AB74A; EMBL:AL133315

A;Experimental source: cultivar Columbia; BAC clone T8P19

C;Genetics:

A;Map position: 3

A;Introns: 69/1; 126/3; 178/3; 270/3; 325/2

A;Note: T8P19.40

Query Match	12.1%;	Score 188;	DB 2;	Length 424;
Best Local Similarity	21.9%;	Pred. No. 2.3e-08;		
Matches	79;	Conservative	78;	Mismatched 133; Indels 70; Gaps 14;
QY	7	HTCYDAMATSKLVIFDTM--LEIK-----KAPFALVANGVRAPLWD-----SKQS	52	
Db	50	NACFESIPVAFPLSSDSQDIETRSDTSLAEAVQTLSKFVKLSAPVDVDPEDASWDR	109	
QY	53	FVGMLTITTDIL-VLHRY--RSPVVQIYEIQH-----KIE	87	
Db	110	YIGIVEPPIGVLLHQLEPPSPRPSPAASNGFSHDFTDVLNCGDSAVTSGNFEVLT	169	
QY	88	WREIY-----LQCCKF--PLVISPNDSLFEAVYTLIKNIHRPLVPDPVSGNVLIHL	138	
Db	170	SSELYKNTKVRDISGTRWPAFLAKENGSFLTMLLLLKYKKMSIPWDLGVAKIENII	229	
QY	139	THKRLLKFLHI FGSLLPRPSFLVRTIODLGIGTFP--DLAVVLETAPIILLDIFVDRPV	196	
Db	230	TQSGVIHMLAEAGLLWFEDWGIXITLSEVGLPFIMSKOHIKIYDEVEVLQAFLMRRKRI	289	
QY	197	SALFPVNNECQG--VVGLYSRFDV--IHLLAAQOTYN-----HLDMSVGEALRQRTLC-	243	
Db	290	GGIPVIERNSEKPGNISLRDVQFLTLTAPEIYHDYRSITTTKNFLVSVREHEK---CGDT	346	
QY	244	----LEGVLSQPCHSELGEVIDRIARQVIRLVLVDETQHLLGVVLSUJLOALVLPSPAG	299	
Db	347	SAPIMSGVIACKTNHTLKELIIMDLADKIHRIYVDDFGNLGELITURDIIARLVHPSPG	406	

RESULT 12  
D96832

hypothetical protein F18B13.17 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: D96832  
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: D96832  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-399 <STO>  
A/Cross-references: UNIPROT:Q9SD0; UNIPARC:UPI000009F89F; GB:AE005173; NID  
C/Genetics:  
A/Gene: F18B13.17  
A/Map position: 1

Query Match	11.3%	Score 176;	DB 2;	Length 399;
Best Local Similarity	25.2%;	Pred. No. 2.3e-07;		
Matches	90;	Conservative 58;	Mismatches 109;	Indels 100; Gaps 19;
Qy	8	TCYDAMATSKLVIPTMLEIKFAFALVANGVRAAPL	-----W-----	46
Db	65	TLGDALNTM-----TILGIKP-----VANRVRAVPVAAKPGQWLGAGGSMIVELDKQS	112	
Qy	47	DSKKQSFVGMLLTITDFIL-----VLHRRYRSPLVQIYEIEQHKIETWREIYLQGCF	97	
Db	113	GSARKQYIGVMTWLDVVAHTAGDGGSLDGKMAAPVSSIIHCPCGLSLW-----	163	
Qy	98	KPLVSTSPNDSLEFAVYVTLIKRIHRLPVLDPVSGNVHLIHTHRLKLKFUHFGLS--LP	155	
Db	164	-----SLNPNTSIMDCMEMLSKG-IHR--VLVPLDSTNTENI--TGPELVESASAVAMLSQMD	215	
Qy	156	RPSFLYRTIQDL-GI--GTFRDIAVLVLETAPILT-----ALDIFVDRVSVALPVVNEC	205	
Db	216	LISFFPDQSSQLHGILSHVTWTLDSAHTNVLATSOARVKDAIQCMSIAMLNRAVPIVEAS	275	
Qy	206	GQ-----VWGLSRFDV--IHLAAQQTYNHLDMSVGBALRO--RTLCEG--	246	
Db	276	GGEGDHQKLVDGKRRVVGTFSSDLKGCHLALRSW--LPINALRFEVEKIPRTLFTAA	333	
Qy	247	-----VLSQPHESLGEVIDRIAREQVHRLVLVDTEQHLGLGVSLSDILOALVLS	296	
Db	334	TSTPGRELVTCTVSTLAQVIMHTVTKRVHVRVWVDPONGLOGLSLTDII-AVRS	389	

RESULT 13  
B96720

hypothetical protein T17F3.17 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2004 #text\_change 09-Jul-2004  
C:Accession: G96720  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.  
ansen, N.F.; Hughes, B.; Huizlar, L.  
Nature 408, 816-820, 2000  
C.A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, F.  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A>Title: Sequence and analysis of chromosome 12 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96720  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-447 <STO>  
A:Cross-references: UNIK  
C:Genetics:  
A:Gene: T17F3.17  
A:Map position: 1

Query Match	10.5%	Score 163;	DB 2;	Length 447;
Best Local Similarity	25.5%;	Pred. No. 3.5e-06;		
Matches	63;	Conservative 39;	Mismatches 107;	Indels 38; Gaps 10;
Qy	78	YEI-----EQHKIETWRBIYILQGC	FKPLVSISPNDSLFEAVVTLIKRIHRLPVLDPVSGN	133
Db	194	YEVLQEEPFKSTTVRTILKSRWAPFLPV	STESSMLSVMLLSKYRLRNVPVIKTGPD	253
Qy	134	VLHLTHKRLK-----FLHIFGSLIPRSP	FLYRTIQDLGIGTFRDLAVV-LETA	182
Db	254	IKNVYTSQAVVHGLEGCKGRDWFHII--	SALP-----ISDGLGLPFMSPNEVISIESE	303
Qy	183	P-IILTALDIFVDRRVSAIPVYNECG-Q	VGVLYSRPDIHLLAAQ-----TYNHLD	231
Db	304	ELILEAFKMRDNNIGGLPVVEGLNKKY	IGNISMRIYRLLQLPEVSNFQRLVTKSFAT	363
Qy	232	SVGALQRTLCLEGVLSQPHESI	GEVIDRIAREQVHRL-VLVDETHLLGVVSLSDIL	290
Db	364	KIATAGEYGLAIPAI-TCRPDSTLGS	VINSLASRSHRVVVAAGDENELGVITLRDVI	422
Qy	291	QALVLSP	297	
Db	423	SCFVSEP	429	

RESULT 14

G75056 dehydrogenase PAB0961 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C:Accession: G75056

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure

A:Reference number: A75001

A:Accession: G75056

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-392 <KAW>

A:Cross-references: UNIPROT:Q9UYR4; UNIPARC:UPI000003454F; GB:AJ248287; GB:AL096836; NID

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB0961

	Query Match	10.4%; Score 161.5; DB 2; Length 392;
	Best Local Similarity	23.4%; Pred. No. 3.9e-06;
	Matches	63; Conservative 54; Mismatches 103; Indels 49; Gaps 12;
Qy	43 APLWDSKKQSFGMLTITDFTILVL---HRYKRSPLVQIYEIEQHKIETW-----REIY 92    :::    :	
Db	21 APLSEA----IGIIKEKDPDLILVFDDNVYKGVLTQDLIRSHL--KWDFTKAKVRDVY 73    :::    :	
Qy	93 LQCCKPLVLSIPNDSLPEAVVTLIKRIHLPVLDPSGNNVLHILTHRLLLKFHLIFGS 152    :::    :	
Db	74 -----KPAPVVVKPTDLSHAARKLLETDLRSLPVGEN--KABILGVISDMALLE----- 120    :::    :	
Qy	153 LLPRSPFLYRTIODLGICTGRDLAVLLETALTDIFVDRRYSALPVNNECGOVGLY 212    :::    :	
Db	121 RVABEFGCKRVKEEF---WTKDVTILGPDDTVAKALATMRDHGISRIPIVDUEEGKLEGLV 177    :::    :	
Qy	213 SRFDVI-----HLAAOQTNYHLMVSVE-----ALRQRTICLEGVLSQCPHESLGEVID 261    :::    :	
Db	178 TLHDULIRFIKPRFKAQ--YGEL---AGEKIPPFSMKLRIMAKIGVTIIMEPATIRSAVS 232    :::    :	

Qy 262 RIAREQVHRLVLVDETQHLLGWVSLSDIL 290  
: ||: ||| :|::: |:|  
pb 233 TMKDNIDGLVVVDENNKKVGILTVKDL 261

## RESULT 15

D71175  
hypothetical protein PH0600 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998  
C:Accession: D71175  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, M.; Ofuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of A:Reference number: A71000; MUID:98344137; PMID:967  
A:Accession: D71175  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-392 <KAW>  
A:Cross-references: UNIPROT:O58317; UNIPARC:UPI00000  
A:Experimental source: strain OT3  
A>Note: this accession replaces an interim accession  
C:Genetics:  
A:Gene: PH0600  
F:217-265/Domain: CBS homology <CBS>

Query Match	10.0%;	Score	155.5;	DB	2;	Length	392;
Best Local Similarity	22.3%;	Pred. No.	1.3e-05;				
Matches	59;	Conservative	58;	Mismatches	109;	Indels	39;
						Gaps	10;
QY	42	AAPLWDSEKQSGVCMGLTITDFILVL---	HRYSPLQVIEIEOHKIETW-----	REI	91		
DB	20	SAPLSEA-----IGIIEKEDPDLILVFPDDNVYKGLVQDILLIRSHL--	KMDPTKAKVQVDI	72			
QY	92	YLOGCFKPLVSIISNDLSLFEAVYTLIKNRIHRLPVLDPVSGNVLIHLITKRLKLLKFLHIFG	151				
DB	73	Y-----KPAPVKVETDLSHAKULLFTDLRSLPVGEN-KAEIGIVSIDALLE-----	120				
QY	152	SLLPRPSGLYRTIOQLGIGTGFRLDAVLVETAPILTALDIFVDRRVSAALPVNNECGQVVGL	211				
DB	121	-RVVAEFGKKVVEEF---MTKOVITLTPDDTVAKALAVMRDHGISRIPIVNEESGKLEGL	176				
QY	212	YSRFDVIHLAAQTYN-HLDMVSVE-----ALRORTLCLEVLSCQPHESLGEVIDRIAR	265				
DB	177	VTLHDLILRFIKPRFKAQTGELGVEKIPPEFSMKLREAMIRGVITILPTATVREAVATMKD	236				
QY	266	EQVHRLVLVDETQHLGLVWSLSDIL	290				
DB	237	NDIDGLVVVDENGNKVGLITVKDLIL	261				

Search completed: January 24, 2006, 22:15:10  
Job time : 21.4343 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2006, 22:14:24 ; Search time 67.4252 Seconds  
(without alignments)  
1890.063 Million cell updates/sec

Title: US-10-070-794A-4  
Perfect score: 1551  
Sequence: 1 MRFQEHCTCYDAMATSSKLV.....LSDLQLVLSPAGIDALGA 305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1551	100.0	489	3	US-09-826-581-6
2	1551	100.0	489	4	US-10-473-670-15
3	1551	100.0	489	4	US-10-705-137-6
4	1551	100.0	489	5	US-10-503-175-2
5	1529	98.6	489	5	US-10-503-039-2
6	1529	98.6	489	5	US-10-503-175-6
7	1525	98.3	492	5	US-10-756-149-5028
8	1507	97.2	464	3	US-09-950-022-2
9	1507	97.2	464	3	US-09-950-022-4
10	1507	97.2	464	3	US-09-950-022-6
11	1507	97.2	464	6	US-11-075-134-2
12	1507	97.2	464	6	US-11-075-134-4
13	1507	97.2	464	6	US-11-075-134-6
14	1506	97.1	464	3	US-09-950-022-8
15	1506	97.1	464	6	US-11-075-134-8
16	1503	96.9	464	3	US-09-950-022-10
17	1503	96.9	464	6	US-11-075-134-10
18	1479	95.4	489	5	US-10-503-175-4
19	1064	68.6	328	3	US-09-769-970-7
20	1064	68.6	328	5	US-10-466-162-14
21	1064	68.6	352	5	US-10-466-162-12
22	1009	65.1	331	3	US-09-769-970-21
23	1009	65.1	331	5	US-10-473-127-923
24	1009	65.1	331	5	US-10-473-127-924
25	1009	65.1	331	5	US-10-473-127-927
26	1009	65.1	331	5	US-10-473-127-928
27	1009	65.1	331	5	US-10-466-162-16

28 1009 65.1 344 3 US-09-925-297-461 Sequence 461, App  
29 1009 65.1 344 5 US-10-473-127-925 Sequence 925, App  
30 862.5 55.6 488 5 US-10-450-763-50437 Sequence 50437, A  
31 851.5 54.9 634 6 US-11-097-143-25527 Sequence 25527, A  
32 851.5 54.9 1207 4 US-10-108-605-71 Sequence 71, Appl  
33 827 53.3 383 5 US-10-450-763-50439 Sequence 50439, A  
34 758 48.9 181 4 US-10-276-774-1611 Sequence 1611, Ap  
35 494 31.9 180 4 US-10-106-698-6572 Sequence 6572, Ap  
36 396 25.5 149 4 US-10-264-237-1653 Sequence 1653, Ap  
37 357 23.0 448 4 US-10-425-115-187601 Sequence 187601, A  
38 357 23.0 477 4 US-10-425-114-50202 Sequence 50202, A  
39 352.5 22.7 368 4 US-10-425-114-54796 Sequence 54796, A  
40 352.5 22.7 493 4 US-10-424-599-187700 Sequence 187700, A  
41 350.5 22.6 365 4 US-10-425-114-69679 Sequence 69679, A  
42 348 22.4 461 4 US-10-424-599-222531 Sequence 222531, A  
43 347.5 22.4 497 4 US-10-425-115-274759 Sequence 274759, A  
44 347.5 22.4 514 4 US-10-425-114-38422 Sequence 38422, A  
45 347 22.4 451 4 US-10-437-963-168583 Sequence 168583, A

## ALIGNMENTS

## RESULT 1

US-09-826-581-6  
; Sequence 6, Application US/09826581  
; Patent No. US20020142310A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersson, Leif  
; APPLICANT: Luthman, L. Holger  
; APPLICANT: Marklund, Stefan  
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT  
; FILE REFERENCE: 11145-007001  
; CURRENT APPLICATION NUMBER: US/09/826,581  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: US 60/195,665  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 489  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-826-581-6

Query Match 100.0%; Score 1551; DB 3; Length 489;  
Best Local Similarity 100.0%; Pred No. 3.4e-148;  
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRFQEHCTCYDAMATSSKLVIPDTMLEIKKAFKAFKALVANGVRAAPLWDSKKQSFVGMLTIT 60  
Db 185 MRFQEHCTCYDAMATSSKLVIPDTMLEIKKAFKAFKALVANGVRAAPLWDSKKQSFVGMLTIT 244  
Qy 61 DFTLVHRYRSLPQIYEIEQHKIETWRIYLGCCFKPLVSPNDLSLFEAVYTLTKNR 120  
Db 245 DFTLVHRYRSLPQIYEIEQHKIETWRIYLGCCFKPLVSPNDLSLFEAVYTLTKNR 304  
Qy 121 IHRPLVLPDVPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDGLGIGTFRDLAVVLE 180  
Db 305 IHRPLVLPDVPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDGLGIGTFRDLAVVLE 364  
Qy 181 TAPILTALDIFVDRRVSALPVVNECCGVGLYGRFVHLLAAQOTYNHLDMSVGEALRQR 240  
Db 365 TAPILTALDIFVDRRVSALPVVNECCGVGLYGRFVHLLAAQOTYNHLDMSVGEALRQR 424  
Qy 241 TLCLEGVLSQCPHESIGEVIDRIARQVHRLVLVDETHLLGVVLSLSDIILQALVLSPAGI 300  
Db 425 TLCLEGVLSQCPHESIGEVIDRIARQVHRLVLVDETHLLGVVLSLSDIILQALVLSPAGI 484  
Qy 301 DALGA 305  
Db 485 DALGA 489

## RESULT 2

US-10-473-670-15  
 ; Sequence 15, Application US/10473670  
 ; Publication No. US20040110180A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RECIPON, Shirley A.; BURRILL, John D.;  
 ; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;  
 ; APPLICANT: TANG, Y. Tom; THORNTON, Michael;  
 ; APPLICANT: BOROWSKY, Mark L.; BAUGHN, Mariah R.;  
 ; APPLICANT: BURFORD, Neil; LEE, Soo Yeun;  
 ; APPLICANT: BANDMAN, Olga; HAFALIA, April J.A.;  
 ; APPLICANT: YAO, Monique G.; RAMKUMAR, Jayalaxmi;  
 ; APPLICANT: CHAWLA, Narinder K.; LU, Dyrung Aina M.;  
 ; APPLICANT: ARVIZU, Chandra S.; ISON, Craig H.;  
 ; APPLICANT: DING, Li; LU, Yan;  
 ; APPLICANT: GURURAJAN, Rajagopal; WALSH, Roderick T.;  
 ; APPLICANT: GANDHI, Ameera R.; SWARNAKAR, Anita;  
 ; APPLICANT: FORSYTHE, Ian J.; YUE, Henry;  
 ; APPLICANT: AU-YOUNG, Janice K.; ELLIOTT, Vicki S.;  
 ; APPLICANT: LEE, Sally  
 ; TITLE OF INVENTION: KINASES AND PHOSPHATASES  
 ; FILE REFERENCE: PI-0398 USN  
 ; CURRENT APPLICATION NUMBER: US/10/473,670  
 ; CURRENT FILING DATE: 2003-10-01  
 ; PRIOR APPLICATION NUMBER: PCT/US02/10818  
 ; PRIOR FILING DATE: 2002-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/282,119  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: US 60/283,588  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: US 60/283,759  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: US 60/285,589  
 ; PRIOR FILING DATE: 2001-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/287,037  
 ; PRIOR FILING DATE: 2001-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/287,036  
 ; PRIOR FILING DATE: 2001-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/288,608  
 ; PRIOR FILING DATE: 2001-05-04  
 ; PRIOR APPLICATION NUMBER: US 60/288,712  
 ; PRIOR FILING DATE: 2001-05-04  
 ; PRIOR APPLICATION NUMBER: US 60/289,909  
 ; PRIOR FILING DATE: 2001-05-09  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 15  
 ; LENGTH: 489  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No: 7474666CD1

Query Match 100.0%; Score 1551; DB 4; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-148;  
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRFQHTCYDAMATSSKLVIFDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGM	160
Db	185	MRFQHTCYDAMATSSKLVIFDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGM	244
Qy	61	DFILVHRYRSPVQIYEIOHKIETWREIYLGCCFKPLVSPNDSLFPAVYTLIKNR	120
Db	245	DFILVHRYRSPVQIYEIOHKIETWREIYLGCCFKPLVSPNDSLFPAVYTLIKNR	304
Qy	121	IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE	180
Db	305	IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE	364

Qy	181	TAPILTALDIFVDRRVVSALPVVNECGVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR	240
Db	365	TAPILTALDIFVDRRVVSALPVVNECGVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR	424
Qy	241	TLCLGVLSCQPHESLGEVIDRIAREQVHRLVLDVETQHLGVVSLSDIILQALVLS	300
Db	425	TLCLGVLSCQPHESLGEVIDRIAREQVHRLVLDVETQHLGVVSLSDIILQALVLS	484
Qy	301	DALGA 305	
Db	485	DALGA 489	

## RESULT 3

US-10-705-137-6  
 ; Sequence 6, Application US/10705137  
 ; Publication No. US20040121385A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andersson, Leif  
 ; APPLICANT: Luthman, L. Holger  
 ; APPLICANT: Marklund, Stefan  
 ; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT  
 ; FILE REFERENCE: 11145-007002  
 ; CURRENT APPLICATION NUMBER: US/10/705,137  
 ; CURRENT FILING DATE: 2003-11-10  
 ; PRIOR APPLICATION NUMBER: US 09/826,581  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/195,665  
 ; PRIOR FILING DATE: 2000-04-07  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0  
 ; SEQ ID NO 6  
 ; LENGTH: 489  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-705-137-6

Query Match 100.0%; Score 1551; DB 4; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-148;  
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRFQHTCYDAMATSSKLVIFDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGM	160
Db	185	MRFQHTCYDAMATSSKLVIFDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGM	244
Qy	61	DFILVHRYRSPVQIYEIOHKIETWREIYLGCCFKPLVSPNDSLFPAVYTLIKNR	120
Db	245	DFILVHRYRSPVQIYEIOHKIETWREIYLGCCFKPLVSPNDSLFPAVYTLIKNR	304
Qy	121	IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE	180
Db	305	IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE	364
Qy	181	TAPILTALDIFVDRRVVSALPVVNECGVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR	240
Db	365	TAPILTALDIFVDRRVVSALPVVNECGVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR	424
Qy	241	TLCLGVLSCQPHESLGEVIDRIAREQVHRLVLDVETQHLGVVSLSDIILQALVLS	300
Db	425	TLCLGVLSCQPHESLGEVIDRIAREQVHRLVLDVETQHLGVVSLSDIILQALVLS	484
Qy	301	DALGA 305	
Db	485	DALGA 489	

## RESULT 4

US-10-503-175-2  
 ; Sequence 2, Application US/10503175  
 ; Publication No. US20050172348A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andersson, Leif  
 ; APPLICANT: Marklund, Stefan

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; TITLE OF INVENTION: Transgenic animals expressing prkag3
; FILE REFERENCE: 11145-020US1
; CURRENT APPLICATION NUMBER: US/10/503,175
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00912
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,430
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-503-175-2

Query Match 100.0%; Score 1551; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.4e-148;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
Db 185 MRPMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 244
Qy 61 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 120
Db 245 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 304
Qy 121 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 305 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
Qy 181 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLSDMSVGEALRQR 240
Db 365 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLSDMSVGEALRQR 424
Qy 241 TLCLEGLVSCQPHEISLGEVIDRIAREQVHRLVLDVETQHLGLGVVSLSDILOALVLS PAGI 300
Db 425 TLCLEGLVSCQPHEISLGEVIDRIAREQVHRLVLDVETQHLGLGVVSLSDILOALVLS PAGI 484
Qy 301 DALGA 305
Db 485 DALGA 489

RESULT 5
US-10-503-039-2
; Sequence 2, Application US/10503039
; Publication No. US20050155091A1
; GENERAL INFORMATION:
; APPLICANT: Svensson, Thomas
; TITLE OF INVENTION: prkag3 gene promoter and uses thereof
; FILE REFERENCE: 11145-022US1
; CURRENT APPLICATION NUMBER: US/10/503,039
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00762
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,429
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-503-039-2

Query Match 98.6%; Score 1529; DB 5; Length 489;
Best Local Similarity 98.7%; Pred. No. 5.7e-146;
Matches 301; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MRPMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
Db 185 MRPMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 244
Qy 61 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 120
Db 245 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 304
Qy 121 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 305 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
Qy 181 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLSDMSVGEALRQR 240
Db 365 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLSDMSVGEALRQR 424
Qy 241 TLCLEGLVSCQPHEISLGEVIDRIAREQVHRLVLDVETQHLGLGVVSLSDILOALVLS PAGI 300
Db 425 TLCLEGLVSCQPHEISLGEVIDRIAREQVHRLVLDVETQHLGLGVVSLSDILOALVLS PAGI 484
Qy 301 DALGA 305
Db 485 DALGA 489

RESULT 6
US-10-503-175-6
; Sequence 6, Application US/10503175
; Publication No. US20050172348A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Leif
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: Transgenic animals expressing prkag3
; FILE REFERENCE: 11145-020US1
; CURRENT APPLICATION NUMBER: US/10/503,175
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00912
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,430
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-503-175-6

Query Match 98.6%; Score 1529; DB 5; Length 489;
Best Local Similarity 98.7%; Pred. No. 5.7e-146;
Matches 301; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MRPMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
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Qy 61 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 120
Db 245 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 304
Qy 121 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 305 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
Qy 181 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLSDMSVGEALRQR 240
Db 365 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLSDMSVGEALRQR 424
Qy 241 TLCLEGLVSCQPHEISLGEVIDRIAREQVHRLVLDVETQHLGLGVVSLSDILOALVLS PAGI 300
Db 425 TLCLEGLVSCQPHEISLGEVIDRIAREQVHRLVLDVETQHLGLGVVSLSDILOALVLS PAGI 484
Qy 301 DALGA 305
Db 485 DALGA 489

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Db 220 DFILVLRHRYRSPVQIYEIEBEHKIETWREIYLGCCFKPLVISPNDLSLFEAVVALIKNR 279  
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Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE 339  
Qy 181 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOQYTNHLDMSVGEALRQR 240  
Db 340 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOQYTNHLDMSVGEALRQR 399  
Qy 241 TLCLEGLVSCQPHEIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALVLSGAGI 300  
Db 400 TLCLEGLVSCQPHEIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALVLSGAGI 459  
Qy 301 DALGA 305  
Db 460 DALGA 464  
RESULT 10  
US-09-950-022-6  
; Sequence 6, Application US/09950022  
; Publication No. US20030017470A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for  
; TITLE OF INVENTION: Reproductive and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950,022  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-09-950-022-6  
Query Match 97.2%; Score 1507; DB 3; Length 464;  
Best Local Similarity 97.0%; Pred. No. 9e-144;  
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMILTIT 60  
Db 160 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMILTIT 219  
Qy 61 DFILVLRHRYRSPVQIYEIEBEHKIETWREIYLGCCFKPLVISPNDLSLFEAVVALIKNR 120  
Db 220 DFILVLRHRYRSPVQIYEIEBEHKIETWREIYLGCCFKPLVISPNDLSLFEAVVALIKNR 279  
Qy 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE 339  
Qy 181 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOQYTNHLDMSVGEALRQR 240  
Db 340 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOQYTNHLDMSVGEALRQR 399  
Qy 241 TLCLEGLVSCQPHEIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALVLSGAGI 300  
Db 400 TLCLEGLVSCQPHEIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALVLSGAGI 459  
Qy 301 DALGA 305  
Db 460 DALGA 464

Db 460 DALGA 464  
RESULT 11  
US-11-075-134-2  
; Sequence 2, Application US/11075134  
; Publication No. US20050208551A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for  
; TITLE OF INVENTION: Reproductive and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/11/075,134  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: US/09/950,022  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-11-075-134-2  
Query Match 97.2%; Score 1507; DB 6; Length 464;  
Best Local Similarity 97.0%; Pred. No. 9e-144;  
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMILTIT 60  
Db 160 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMILTIT 219  
Qy 61 DFILVLRHRYRSPVQIYEIEBEHKIETWREIYLGCCFKPLVISPNDLSLFEAVVALIKNR 120  
Db 220 DFILVLRHRYRSPVQIYEIEBEHKIETWREIYLGCCFKPLVISPNDLSLFEAVVALIKNR 279  
Qy 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE 339  
Qy 181 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOQYTNHLDMSVGEALRQR 240  
Db 340 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOQYTNHLDMSVGEALRQR 399  
Qy 241 TLCLEGLVSCQPHEIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALVLSGAGI 300  
Db 400 TLCLEGLVSCQPHEIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALVLSGAGI 459  
Qy 301 DALGA 305  
Db 460 DALGA 464  
RESULT 12  
US-11-075-134-4  
; Sequence 4, Application US/11075134  
; Publication No. US20050208551A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for



Qy 61 DFILVLRHYRSPVQIYIEIQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNR 120  
Db 220 DFILVLRHYRSPVQIYIEIEBEHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNR 279  
Qy 121 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE 339  
Qy 181 TAPILTALDIFVDRRVSALPVNCEGQVGLYSRFDVHLLAAQOTYNHLDMSVGEALRQR 240  
Db 340 TAPILTALDIFVDRRVSALPVNCEGQVGLYSRFDVHLLAAQOTYNHLDMSVGEALRQR 399  
Qy 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETHLGVVSLSDILOALVLSPAGI 300  
Db 400 TLCLEGVLSQCPHETLGEVIDRIAREQVHRLVLDVDETHLGVVSLSDILOALVLSPAGI 459  
Qy 301 DALGA 305  
Db 460 DALGA 464

RESULT 15  
US-11-075-134-8  
; Sequence 8, Application US/11075134  
; Publication No. US20050208551A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for  
; TITLE OF INVENTION: Reproductive  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/11/075,134  
; PRIOR FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: US/09/950,022  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-11-075-134-8

Query Match 97.1%; Score 1506; DB 6; Length 464;  
Best Local Similarity 96.7%; Pred. No. 1.1e-143;  
Matches 295; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMILTIT 60  
Db 160 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMILTIT 219  
Qy 61 DFILVLRHYRSPVQIYIEIQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNR 120  
Db 220 DFILVLRHYRSPVQIYIEIEBEHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNR 279  
Qy 121 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE 339  
Qy 181 TAPILTALDIFVDRRVSALPVNCEGQVGLYSRFDVHLLAAQOTYNHLDMSVGEALRQR 240  
Db 340 TAPILTALDIFVDRRVSALPVNCEGQVGLYSRFDVHLLAAQOTYNHLDMSVGEALRQR 399  
Qy 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETHLGVVSLSDILOALVLSPAGI 300

Db 400 TLCLEGVLSQCPHETLGEVIDRIAREQVHRLVLDVDETHLGVVSLSDILOALVLSPAGI 459  
Qy 301 DALGA 305  
Db 460 DALGA 464  
Search completed: January 24, 2006, 22:30:57  
Job time : 68.4252 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:02:17 ; Search time 29.5657 Seconds  
(without alignments)  
1510.014 Million cell updates/sec

Title: US-10-070-794A-30  
Perfect score: 2403  
Sequence: 1 MSFLEQNSSWSPAVTSS.....LSDILOALVLSPPAGIDALGA 464

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1028	42.8	330	2 T10759	AMP-activated prot
2	488	20.3	478	2 T25899	hypothetical prote
3	457	19.0	322	1 RBYC3	regulatory protein
4	375.5	15.6	274	2 S67444	probable 5'-AMP-ac
5	243.5	10.1	331	2 B86222	hypothetical prote
6	222	9.2	443	2 T25854	hypothetical prote
7	215.5	9.0	460	2 T24248	hypothetical prote
8	214	8.9	379	2 T10371	Pv42 protein - kid
9	198	8.2	424	2 T46197	hypothetical prote
10	197	8.2	629	2 T18227	hypothetical prote
11	189.5	7.9	352	2 F86287	hypothetical prote
12	179	7.4	399	2 D96832	hypothetical prote
13	163	6.8	447	2 B96720	hypothetical prote
14	163	6.8	527	2 S46088	hypothetical prote
15	161.5	6.7	392	2 G75056	dehydrogenase PAB0
16	155.5	6.5	392	2 D71175	hypothetical prote
17	149	6.2	280	1 H64452	conserved hypotet
18	148.5	6.2	250	2 C90449	conserved hypotet
19	148	6.2	92	2 T50087	probable 5'-AMP-ac
20	146	6.1	313	1 E69030	conserved hypotet
21	141.5	5.9	157	1 F69185	yhcV homolog WTH64
22	139	5.8	152	2 AF2282	hypothetical prote
23	139	5.8	300	1 S08244	conserved hypotet
24	138.5	5.8	421	2 C64475	hypothetical prote
25	138	5.7	485	1 JC4998	IMP dehydrogenase
26	137	5.7	284	2 S64355	conserved hypotet
27	136.5	5.7	527	2 S64060	probable membrane
28	134	5.6	1286	2 A12195	two-component hybr
29	130.5	5.4	792	2 A84308	chloride channel [

30	129.5	5.4	1344	2 AD2103	two-component hybr
31	126.5	5.3	168	1 A64478	hypothetical prote
32	126	5.2	486	1 E71456	IMP dehydrogenase
33	125.5	5.2	157	2 AF3344	IMP dehydrogenase
34	123.5	5.1	287	2 F72780	hypothetical prote
35	122	5.1	282	2 C75148	hypothetical prote
36	120.5	5.0	223	2 T36952	conserved hypotet
37	120.5	5.0	278	2 A72781	probable acetoin u
38	120.5	5.0	284	1 H69232	YJ1225-related pro
39	119	5.0	122	2 B69119	yhcV homolog WTH18
40	119	5.0	485	2 E75015	IMP dehydrogenase
41	116.5	4.8	382	2 AD2762	conserved hypotet
42	116.5	4.8	382	2 C97543	hypothetical prote
43	115.5	4.8	285	1 C71188	conserved hypotet
44	115.5	4.8	895	2 T03446	probable transcript
45	115	4.8	482	2 C72264	IMP dehydrogenase

ALIGNMENTS

RESULT 1

T10759  
AMP-activated protein kinase (EC 2.7.1.1-) gamma chain - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T10759  
R;Woods, A.; Cheung P, C.F.; Smith, F.C.; Davison, M.D.; Scott, J.; Beri, R.K.; Carling, J. Biol. Chem. 271, 10282-10290, 1996  
A;Title: Characterization of AMP-activated protein kinase beta and gamma subunits: Assem  
A;Reference number: 206738; MUID:96215327; PMID:8626596  
A;Accession: T10759  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-330 <WOO>  
A;Cross-references: UNIPROT:P80385; UNIPARC:UPI00001250B4; EMBL:X95578; NID:g1185270; PI  
A;Experimental source: strain Wistar  
C;Complex: heterotrimer; alpha, beta and gamma chains  
C;Function:  
A;Description: is responsible for the regulation of fatty acid synthesis by phosphorylat  
A;Superfamily: CAT3 protein  
C;Keywords: fatty acid biosynthesis; phosphotransferase

Query Match 42.8%; Score 1028; DB 2; Length 330;  
Best Local Similarity 62.3%; Pred. No. 1.4e-73;  
Matches 197; Conservative 56; Mismatches 63; Indels 0; Gaps 0;

QY	140	APPKLGWDELLKPGAQIYMRFMQEHCTCYDAMATSSKLVIFDTMLEIKKAPFALVANGV	199
DB	9	APAPENEHSQETPESNSSVYTTFMKSHRCVDLIPTSSKLVVFTSLQVKKAFALVTNGV	68
QY	200	RAAPLWDSKKQSPVGMLTITDFTLVLRHYVRSPLVQIYEIQHKIETWRIYLQCGCFKL	259
DB	69	RAAPLWDSKKQSPVGMLTITDFTLVLRHYKSAVQIYELEEHKIEIETWRSVYLDQSFKL	128
QY	260	VSISPNDLSFEAVYTLIKRIHRLPVLDVPVSGNVLHILTKRLKLFHIFGSLLPSPFL	319
DB	129	VCISPNASLFDVSSLIIRNKIHRLPVIDPESGNTLVILTKRLKLFKLFITFPKPEFM	188
QY	320	YRTIQDLGTGTRDLAVLLETAPILTALDIFVDRRSALPVPVNECGQVGLYRFRDVIHL	379
DB	189	SKSLEELQIGTVANIAMVRITTPVYVALGIFVQHRVSALPVPVDEKGRVDIYKFDVINL	248
QY	380	AAQOTVNHLDMSVGEALRORTLCLEGLVSCOPHESIGEVIDRIARQVHRLVLVDEQHL	439
DB	249	AAEKTNNLDVSVTKALQHRSHYFEGVLKCYLHLEAIINRLVVEAVHRLVVDHVV	308
QY	440	LGWVSLSDILQALVLS	455
DB	309	KGIVSLSDILQALVLT	324

RESULT 2

submitted to the EMBL Data Library, June 1993

A:Description: Correct end of the ORF for the CDC20 gene of *Saccharomyces cerevisiae*.  
A:Reference number: S48507  
A:Accession: S48508  
A:Molecule type: DNA  
A:Residues: 1-21 <DOI>  
A:Cross-references: UNIPARC:UPI0000168851; EMBL:D16506; NID:g391938; PIDN:CAA03958.1; PFI:  
R:Laquin, G.  
submitted to the Protein Sequence Database, May 1996  
A:Reference number: S64122  
A:Accession: S64125  
A:Molecule type: DNA  
A:Residues: 1-322 <LAU>  
A:Cross-references: UNIPARC:UPI0000052F23; EMBL:272637; NID:g13222666; PIDN:CAA96823.1; PFI:  
A:Experimental source: strain S288C  
C:Genetics:  
A:Gene: SGD:SNF4; CAT34; MIPS:YGL115W  
A:Cross-references: SGD:S0003083; MIPS:YGL115W  
A:Map position: 7L  
C:Function:  
A:Description: involved in derepression of glucose-repressed genes  
C:Superfamily: CAT3 protein  
C:Keywords: nucleus; transcription regulation

Query Match 19.0%; Score 457; DB 1; Length 322;  
Best Local Similarity 34.2%; Pred. NO. 1.8e-28;  
Matches 106; Conservative 66; Mismatches 108; Indels 30; Gaps 6;

Qy	161	RPMQEHICYDAMWSSKLIVIFDTMLEIKAPFALVANGVRAAPLWDSKKQSFVGMITITD	220
Db	24	KFLNSKTSYDVLPLVSYRIVLIDTSLVKKSLNVLQNSIVSAPLWDSKTSRFAGLITTD	83
Qy	221	FILVLHRYRSPLOVQIYEIQHKIETWREIYLGCGFKPL-----VSIQNSDLF	269
Db	84	FINVIQYFSPN-----DKFLVDVKLQDQ-LKDIERALGVDDQLDTASIHPSRPLF	133
Qy	270	EAVYTLIKNRIRHRLPVLDPVSGN-----VHLIUTHKRLKPLHIFGSLLRPS-FLYRTIQ	324
Db	134	EACLKMLSESRGRIPLIDQDETHREIVVSVLTQYRILKFV----ALNCRETHFLKIPIG	189
Qy	325	DLGTGTFDLAVLETAPILTALDIFVDRRVSLPWNCGGVGLYSRFDVTHLAAQQT	384
Db	190	DLNITIQDNMSQMTTFVIDVIQMLTQGRVSSVPIIDENGYLINVEAYDVGLIKGGI	249
Qy	385	YNHLDMVSGEALRQRTLCLEGLVLSQPHESLGEVIDRIAREQVHRLVLVDETHLLGVWS	444
Db	250	YNDLSLSGEALMRSDDFEGYVTCCKDKLSTIMDNIRKARVHRFFVVDVGLVGLT	309
Qy	445	LSDIQLQALVL 454	
Db	310	LSDIQLKYILL 319	

RESULT 4  
S67444  
probable 5'-AMP-activated, gamma subunit family - fission yeast (*Schizosaccharomyces pombe*)  
C:Species: *Schizosaccharomyces pombe*  
C:Date: 20-Jul-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C:Accession: T38059; S67444  
R:McLean, J.; Harris, D.; Barrrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, March 1996  
A:Reference number: Z21766  
A:Accession: T38059  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-274 <MC2>  
A:Cross-references: UNIPARC:UPI000016207F; EMBL:Z69944; NID:g1217974; PIDN:CAA93805.1; F  
C:Genetics:  
A:Map position: 1  
A:Introns: 12/3; 54/1; 173/3; 226/1  
C:Superfamily: CAT3 protein

Query Match 15.6%; Score 375.5; DB 2; Length 274;

[illegible]

Matches	86; Conservative	73; Mismatches	140; Indels	83; Gaps	15;	
QY	121	ECELEGLLEBPALCLSPQAPPKLGWDE	-----LRKPGAQI	-----	158	
Db	81	ECNVEAVYDLR	-----DKAHAF	-----YDDNGPRPRSRNSDDLILRKTSRPISFNVGVG	131	
QY	159	-----YRPMQHTCYDAMATSSKLVIPDTMLEIKKAPFALVANGVRAAPLWDSKKQS	211			
Db	132	IDQKTDPHYQMSVVDVYELCPNNKSVIIIDASTPTTRAFRIMRDHNTITLIVWDSAR	191			
QY	212	FV--GMLTITDIFLVHRYRSPVQIVYEIQHKIETWREIYLOGCFKPLVSPNDLSF	269			
Db	192	HVKENILITDCLNAIRN--ETPPADQGVLRASDI	-----LSG--NQLVSVSISSKIL	240		
QY	270	EAVYTLIKRIHRLPVLDPVSGNVHLHILTKRLKFLHIFGSLLPFRSFLYRTIQDLGIG	329			
Db	241	DLCEELHQNLRHVVVLDLDAK--EVNIIISVRVIAAHKQNRSLHFAQWLSKSGMSAIG	299			
QY	330	TFRDLAVVLETAPILTALDIFVDRRYSALPVNCEGVVGLYSRFDVTHLAAQTYNHL	388			
Db	300	TWENVAVISQNETYRAMEDMLGFHYSALPVVDKQNVIGVITKDICKALPR	---NFIE	356		
QY	389	-----DMSVGEALRQRTLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQ	-----	437		
Db	357	PKRWLOETKVSIDLH--ICKSQL--ISSADSVQVLDTL	-----LAGDTQSAFAI	403		
QY	438	---HLLGVVSDIQLQALVLP	456			
Db	404	HNGKAIGVISLTDFLSHLRSP	425			
RESULT 8						
T10971						
Pv42 protein - kidney bean						
C:Species: Phaseolus vulgaris (kidney bean)						
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004						
C:Accession: T10971						
R:Abc, H.						
submitted to the EMBL Data Library, November 1995						
A:Reference number: Z17236						
A:Accession: T10971						
A:Status: preliminary; translated from GB/EMBL/DBJ						
A:Molecule type: mRNA						
A:Residues: 1-379 <AB>						
A:Cross-references: UNIPROT:Q41108; UNIPARC:UPI00000ACD11; EMBL:U40713; NID:g1113940; PI						
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Best Local Similarity						
Matches						
QY	163	MOHTCYDAMATSSKLVIPDTMLEIKKAPFALVANGVRAAPL	-----W	-----DS	207	
Db	17	LKEKKVKDMVGKKRLVEVPYTASLAQIMNTLVANKIVAVPVAAPPQGWIGAGGSMIVES	76			
QY	208	KQOS	-----FVGMLTITDILV	-----HRYRSPVQIVYEIQHKIETWREIY	---LQG	254
Db	77	DKQTAVKRYHGMVMTDILAHAGDHLSCGDNIQ	---DLDQMSDSVSIIGHSEF	134		
QY	255	CFKPLVISPNDLSLFEAVYTLIKNRHRLPVLDPVSG	---NV	-----LHILTH	299	
Db	135	L--SLWTLNPNTSMLDCEVFSKG--VHRAMV--PVDGLEENVASGVELTESASSYQMLTQ	189			
QY	300	KRLKFLHIFGSLLPFRSFLYRTTQDLGIGTRDLAVVLETAPILTALDIFVDRRYSALP	359			
Db	190	MDMLKFLGGGAEL--HSTLSRSVDLGADTVQIYAIT--DRTKLVHAIKCLKAAMLNAPV	246			
QY	360	VV	-----NECGOVVGLYSRFDV--THLAAQTYNHL--MSVGEALRQRTL	401		
Db	247	IVRATGVGDHDKQLINGRCRKLITGFSATDURGCHISLSKSWLGSALAFTEEVRSPL	306			
QY	402	CLEG	-----VLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGLVSVSDILQ	450		
Db	307	YSESDMQNRGSRRELVTCTYAESPLSEVIEKAVTSHVHRVWVDVQEGLLVGVVSLTDVIR	366			

Qy	451	AL	452		
Db	367	VI	368		
RESULT 9					
T46197					
hypothetical protein T8P19.40 - Arabidopsis thaliana					
C:Species: Arabidopsis thaliana (mouse-ear cress)					
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004					
C:Accession: T46197					
R:Choine, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa					
submitted to the Protein Sequence Database, December 1999					
A:Reference number: Z23008					
A:Accession: T46197					
A>Status: preliminary					
A:Molecule type: DNA					
A:Residues: 1-424 <CHO>					
A:Cross-references: UNIPROT:Q9S7W6; UNIPARC:UPI00000AB74A; EMBL:AL133315					
A:Experimental source: cultivar Columbia; BAC clone T8P19					
C:Genetics:					
A:Map position: 3					
A:Introns: 69/1; 126/3; 178/3; 270/3; 325/2					
A:Note: T8P19.40					
Query Match					
Best Local Similarity					
Matches					
Qy	137	SPOAPPFKLG	-----WDELKPKGAQIYMRFMQHTCYDAMATSSKLVIPDTM--LEIK	188	
Db	23	SPEA	---KLGMRVEDLWDEQ--KPQLSPNEKL---NACPESIPVSAPPLSSDSQDIERS	74	
Qy	189	-----KAPFALVANGVRAAPLWD	-----SKQSFGVGMILTITDIFIL-VLHRY	---RS	231
Db	75	DTSLAEAVQTLSPKPKVLSAPVVDVADPADASWIDRYTIGIVEFGVIVWLLHQLEPPSPRS	134		
Qy	232	PLVQIYIEIQH	-----KISTWREIY	-----LQGCFK--PLVSI	262
Db	135	PAVAASNGFSGHDFTTDVLNDGDSAVTSGNFEVITSSELYKNTKVRDISGTFRWAPPLAL	194		
Qy	263	SPNDSLFEAVYTLIKNRHRLPVLDPVSGNVHLTHKRLKFLHIFGSLLPFRSFLYRT	322		
Db	195	QKENSFLTMILLLSKYKMKSPVVDLGVAKIENITQSGVIHMLAEACAGLLWFEDWGKT	254		
Qy	323	IQDLGIGTFR--DLAVVLETAPILTALDIFVDRVSNALPVNCEGV--VGLYSRFDV	---IH	378	
Db	255	LSEVGLPIMSKDHIKIYEDFVLQAPFKLMRRKRIGGIPVIERNSEKPEVGNISLRDVQFL	314		
Qy	379	LAAQOTYN	-----HLDMSVGEALRQRTL	---L	423
Db	315	LTAPEIYHDSYRSITTKNPLVSVRSHLEK---CGDTSAPIMSGVIACNTKNTLKEILLMD	371		
Qy	424	REQVHRLVLDVETQHLGLVSVSDILQALVLSAPG	458		
Db	372	AEKHRIYVVDVDFGNLEGLITLRDILARLVHEPSG	406		
RESULT 10					
Ti8227					
hypothetical protein - yeast (Candida albicans)					
C:Species: Candida albicans					
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004					
C:Accession: Ti8227					
R:Barrell, B.G.; Rajandream, M.A.					
submitted to the EMBL Data Library, November 1998					
A:Reference number: Z18831					
A:Accession: Ti8227					
A>Status: preliminary; translated from GB/EMBL/DBJ					
A:Molecule type: DNA					
A:Residues: 1-629 <BAR>					
A:Cross-references: UNIPROT:Q94035; UNIPARC:UPI0000069ECC; EMBL:AL033501; NID:el1341022;					



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Db      313  -LPNLALEFVEKIPRTLFLFTAARTSGRELVTCHVTSTLAQVITHMTTKRVHRVWVVDQN 371
QY      437  QHLGLVSVSLSDIILQALVLS 455
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Db      372  GGIQGLVSLTDII-AVRS 389

RESULT 13
B96720
hypothetical protein T17F3.17 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B96720
R:Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96720
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-447 <STO>
A:Cross-references: UNIPROT:Q9CAR3; UNIPARC:UPI000000A79F9; GB:AE005173; NID:g6358813;
C:Genetics:
A:Gene: T17F3.17
A:Map position: 1

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Query Match	6.8%;	Score 163;	DB 2;	Length 447;
Best Local Similarity	25.5%;	Pred. No. 4.9e-05;		
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Qy	237	YEI----	EQHKIETWRIYI	QCGCFPLVSI
		:	:	SPNDLSFEAVYTLIKRIHPLVLD
		:	:	PVSGN 292
Db	194	YEVILQEP	EPFKSTTVRTILKS	FRWAPFLPVSTESSMLSVMLLSKYRLRNPV
		:	:	IKTGEPD 253
Qy	293	VLHILTHKRLK	-----FLHIFGSL	LPSPFLYRTIQDLGCTGFRDLAV
		:	:	-LETA 341
Db	254	IKNTVTQSA	VGHLEGGCKGRDWF	DI--SALP-----ISDLGLPFMSFNEVISIESE
		:	:	303
Qy	342	P-IITALD	IFDVRVSALPVVNECG	-QVWGLYSRFDVIHLAAQO-----TYNHLD
		:	:	390
Db	304	ELLLEAFK	MRDNNIGGLPVVEGLNKKIVG	NSMRDIRYLLLOQPEVFSNFRQLTKVSFAT
		:	:	363
Qy	391	SVG	EARLORTILCLEGLVSCQPHES	CGEVIDRIAREQVHRL--VLVDETHQLLGVVSLSDIL
		:	:	449
Db	364	KIATAGEE	YGLAIPAI--TCRPDSTLGS	VINSLASRSVHRVYVVAAGDENELYGVITLRDVI
		:	:	422
Qy	450	QALV	LSP 456	
		:	:	
Db	423	SCFV	SEP 429	
		:	:	

RESULT 14

S46088  
hypothetical protein YBR214w - yeast (*Saccharomyces cerevisiae*)  
N:Alternate names: hypothetical protein YBR1501  
C:Species: *Saccharomyces cerevisiae*  
C:Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 05-Oct-2004  
C:Accession: S46088; S46090  
R:Rieger, M.  
submitted to the Protein Sequence Database, August 1994  
A:Reference number: S45734  
A:Accession: S46088  
A:Molecule type: DNA  
A:Residues: 1-527 <RIE>  
A:Cross-references: UNIPROT:P38314; UNIPARC:UPI000013A25A; EMBL:Z36083; NID:G536599; PIR:  
A:Experimental source: strain S288C

R;Dubois, E.; El Baktoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.;  
submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45782  
A;Accession: S46090  
A;Molecule type: DNA  
A;Residues: 114-527 <DUB>  
A;Cross-references: UNIPARC:UPI00001799DD; EMBL:Z36083; MIPS:YBR214W  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: SGD:SDS24  
A;Cross-references: SGD:S0000418  
A;Map position: 2R  
C;Superfamily: uncharacterized conserved protein

Query Match	6.8%;	Score 163;	DB 2;	Length 527;
Best Local Similarity	21.7%;	Pred. No. 6.2e-05;		
Matches	95;	Conservative	63;	Mismatches 181;
			Indels	98;
			Gaps	17;
Qy	46	PPGGGEGPRGRPTAESTGL--EATFPKTTPLAQADPAG-----VGTPPTGMDCLPSDCT	97	
Db	9	PPSQSNSNNLPTSRHASIVEMLSTPPLPHVQVNDTDDKEQPEESTPT-----AT	60	
Qy	98	ASAGSSTDDVEILATERPATEWCELEGLLEERPALCLS---POAPFPKLG-----W	147	
Db	61	AAAPGPGC---AATPAP-----LRDERPQFKLSAVPMQTQSCLSCSVHAQKW	105	
Qy	148	DDELRKPCAQIYMFMOEHCTCYDAMATSSKLVIPTDMLKIKKAPFALVANGVRAAPLWDS	207	
Db	106	-----QHPLSQLIEQNKLIFVPGSISVEAFNTLIKYHLNSIPV-----	145	
Qy	208	KKQSFGVGMJLTIDF-----ILVHRYRSPVLQIYETEQHKIETWREIYLOGCFKP	258	
Db	146	--ESFPGDMNCFTFDYNDLNSYLLLVNLKINTSVSNKQLTADQNGKFPVPGVMVKLTTPNP	203	
Qy	259	LVSTSPNDSLFEAVYTLIKRIHRLPVLDPVSGVNLHILTHKRLKFL---HIFGSLLP	314	
Db	204	FYKUPENESL--STWGIIIGSGVHRVAITNEEMTKVKGILSORRLIKYLDWNARSTSLP	262	
Qy	315	RPSELYRTIQDLGIG-----TFRDIAV--VLETAPILTALDIFVDRRVASALPVNNEC	364	
Db	263	--LLNSSQLDLHGVLNMIQSKPTSRQSRVSIQGEPELIMGLYQHWHERISSIAVIDKQ	319	
Qy	365	GOVVGLYSRFDVHLLAAQNTYHLDMS---VGEALRORTLCLE---GVLSCQPHESLG	416	
Db	320	GNLGNISVTDVKHWRTSQPPLHKTRHFISVILNSRGLETGKDSFPFIHVYESSLA	379	
Qy	417	EVIDRIAREQVHRLVLV	433	
Db	380	RTLAKLVATKSHRLWIV	396	

RESULT 15  
G75056  
dehydrogenase PAB0961 - Pyrococcus abyssi (strain Orsay)  
C.Species: Pyrococcus abyssi  
C.Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C.Accession: G75056  
R.anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A.Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str  
A.Reference number: A75001  
A.Accession: G75056  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-392 <RAW>  
A.Cross-references: UNIPROT:Q9UYR4; UNIPARC:UPI000003454F; GB:AJ248287; GB:AL096836; NI  
A.Experimental source: strain Orsay  
C.Genetics:  
A.Gene: PAB0961

Query Match	6.7%	Score 161.5;	DB 2;	Length 392;
Best Local Similarity	23.4%;	Pred. No. 5.4e-05;		
Matches 63: Conservative	54;	Mismatches 103;	Indels 49;	Gaps 12;



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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2006, 21:54:27 ; Search time 127.313 Seconds  
(without alignments)  
1601.338 Million cell updates/sec

Title: US-10-070-794A-30  
Perfect score: 2403  
Sequence: 1 MSFLEQENSSWSPAVTSS.....LSDILQALVLSFAGIDALGA 464

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378791 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2403	100.0	464	AAE00223	Aae00223 Human AMP
2	2403	100.0	464	ADP43223	Adp43223 Human AMP
3	2403	100.0	489	ADF50310	Adf50310 Human AMP
4	2398	99.8	489	AB47679	Aab47679 PRKAG3.1
5	2398	99.8	489	AAE32034	Aae32034 Human kin
6	2398	99.8	489	ADP87617	Adp87617 Human NOV
7	2391	99.5	489	ABP43929	Abp43929 AMP activ
8	2376	98.9	489	AAE38410	Aae38410 Human Prk
9	2376	98.9	489	ADP50314	Adf50314 Human AMP
10	2372	98.7	492	ADP87619	Adp87619 Human NOV
11	2372	98.7	492	AE669187	Aeb669187 Human mod
12	2013	83.8	464	AAE22985	Aae22985 Pig PRKAG
13	2011	83.7	464	AAE00222	Aae00222 Pig AMPK
14	2011	83.7	464	AAE22984	Aae22984 Pig wild-
15	2011	83.7	514	AAE00224	Aae00224 Sus scrof
16	2010	83.6	464	AAE22987	Aae22987 Pig PRKAG
17	2010	83.6	489	ADP43210	Adp43210 Mouse AMP
18	2007	83.5	464	AAE22988	Aae22988 Pig PRKAG
19	2005	83.4	464	AAE22986	Aae22986 Pig PRKAG
20	2000	83.2	489	ADF50312	Adf50312 Murine AM
21	1989	82.8	489	ADP87682	Adp87682 AMPK rat
22	1551	64.5	305	AAE00221	Aae00221 Human AMP
23	1550	64.5	305	AAE00329	Aae00329 Human Prk
24	1547	64.4	305	AAE00328	Aae00328 Human Prk

25	1507	62.7	305	4	AAE00220	Aae00220 Pig AMPK
26	1506	62.7	305	4	AAE00226	Aae00226 Sus scrof
27	1503	62.5	305	4	AAE00225	Aae00225 Sus scrof
28	1093	45.5	569	8	ADP43207	Adp43207 Human AMP
29	1093	45.5	569	8	ADP43217	Adp43217 Human AMP
30	1093	45.5	569	9	AE669186	Aeb669186 Human mod
31	1092	45.4	414	9	AD280782	Adz80782 Amino aci
32	1082.5	45.0	352	5	AAO18495	Aao18495 Human ins
33	1082.5	45.0	352	8	ADP43208	Adp43208 Human AMP
34	1080.5	45.0	328	2	AAW88438	Aaw88438 Disease a
35	1080.5	45.0	328	4	AAE93432	Aab93432 Human pro
36	1080.5	45.0	328	5	AAO18496	Aao18496 Human ins
37	1080.5	45.0	328	8	ADP87611	Adp87611 Human NOV
38	1080.5	45.0	328	8	ADP87613	Adp87613 Human AMP
39	1076.5	44.8	328	8	ADP87694	Adp87694 Human AMP
40	1075.5	44.8	328	8	ADP87615	Adp87615 Human NOV
41	1050	43.7	391	8	ABM83420	Abm83420 Human dia
42	1028	42.8	330	7	AD62621	Ad62621 Rat Prote
43	1028	42.8	330	8	ADP43225	Adp43225 Rat AMPK
44	1017	42.3	331	2	AAW29817	Aaw29817 Mammalian
45	1017	42.3	331	5	AAO18497	Aao18497 Human ins

ALIGNMENTS

RESULT 1

AAE00223  
ID AAE00223 standard; protein; 464 AA.

XX AAE00223;

DT 13-JUN-2001 (first entry)

DE Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3.

XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;  
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;  
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;  
KW cystathione beta synthase; CBS; cardiant; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 172..225

FT /label= CBS

FT /note= "Cystathione beta synthase domain"

FT Misc-difference 200

FT /note= "RN- mutation site"

FT Domain 253..307

FT /label= CBS

FT /note= "Cystathione beta synthase domain"

FT Domain 329..382

FT /label= CBS

FT /note= "Cystathione beta synthase domain"

FT Domain 400..453

FT /label= CBS

FT /note= "Cystathione beta synthase domain"

XX WO200120003-A2.

XX 22-MAR-2001.

XX 11-SEP-2000; 2000WO-EP009896.

XX 10-SEP-1999; 99EP-00402236.

XX 18-MAY-2000; 2000EP-00401388.

XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.

XX (ANDE/) ANDERSSON L.

XX (LOOF/) LOOFT C.

XX (KALM/) KALM E.

XX

PI Anderson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;  
PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;  
DR WPI; 2001-244810/25.  
DR N-PSDB; AAD03320.  
XX  
XX New variants of the gamma subunit of vertebrate adenosine monophosphate-  
PT activated kinase for diagnosis or treatment of disorders associated with  
PT energy metabolism such as diabetes, obesity, and myopathy.  
XX  
XX Claim 5; Fig 3; 71pp; English.  
XX  
XX The present sequence is human adenosine monophosphate (AMP)-activated  
CC kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3.  
CC Mutation in Prkag3 results in an altered regulation of carbohydrate  
CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as  
CC therapeutic for treating carbohydrate metabolism disorders such as  
CC diabetes, obesity, and disorders associated with muscle metabolism such  
CC as myopathy and cardiovascular diseases, to modulate AMPK activity, and  
CC for restoring a normal AMPK function. PRKAG3 sequence and its  
CC functionally altered mutants are useful for the diagnostic evaluation,  
CC genetic testing and prognosis of a metabolic disorder, preferably a  
CC carbohydrate metabolism disorder. Primers that can detect a genetic  
CC polymorphic marker linked to a sequence encoding PRKAG3, are useful for  
CC detecting a dysfunction of carbohydrate metabolism resulting from the  
CC expression of a functionally altered allele of PRKAG3. Transgenic animal  
CC and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting  
CC of PRKAG3 or its mutant, are useful for screening compounds able to  
CC modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for  
CC detecting mutations in a Prkag3 gene, or in a sequence encoding the first  
CC cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene  
CC therapy  
XX  
XX

Sequence 464 AA;

Query Match	100.0%;	Score 2403;	DB 4;	Length 464;
Best Local Similarity	100.0%;	Pred. No. 3.9e-240;		
Matches 464;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MSFLEQENSSWSPSPAVTSSSIRIGKRAKALRWTRQSVKEGEPGQGGPRSRPTAE 60  
DB 1 MSFLEQENSSWSPSPAVTSSSIRIGKRAKALRWTRQSVKEGEPGQGGPRSRPTAE 60  
QY 61 STGLEATPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 120  
DB 61 STGLEATPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 120  
QY 121 ECELEGLLEERPALCLSPQAPPKLGWDELRKPKAQIYMRPMOHTCYDAMATSSKLVI 180  
DB 121 ECELEGLLEERPALCLSPQAPPKLGWDELRKPKAQIYMRPMOHTCYDAMATSSKLVI 180  
QY 181 FDTMLEIKKAFALVANGRAAPLWDSKKQSFVGMLTITDFILVHLRYRSPVQIYBIE 240  
DB 181 FDTMLEIKKAFALVANGRAAPLWDSKKQSFVGMLTITDFILVHLRYRSPVQIYBIE 240  
QY 241 QHKTETWEIYVQGCFFKPLVSPNDLSIFEAVYTLIKRIRHLVPLDVPVSGNVLHLTHK 300  
DB 241 QHKTETWEIYVQGCFFKPLVSPNDLSIFEAVYTLIKRIRHLVPLDVPVSGNVLHLTHK 300  
QY 301 RLLKFLHIFGSLPRPSFLYRTIQLDGLGTFRDLAVLETPALTALDI FVDRRVSLPVP 360  
DB 301 RLLKFLHIFGSLPRPSFLYRTIQLDGLGTFRDLAVLETPALTALDI FVDRRVSLPVP 360  
QY 361 VNECCQVGLYSRFDVIHLAAQTYNHLDMVSGEALRQRTLCLEGLVSCQPHEISGEVID 420  
DB 361 VNECCQVGLYSRFDVIHLAAQTYNHLDMVSGEALRQRTLCLEGLVSCQPHEISGEVID 420  
QY 421 RIARQVHRLVLDVDTQHLGLGVVSLDIIQALVLS PAGIDALGA 464  
DB 421 RIARQVHRLVLDVDTQHLGLGVVSLDIIQALVLS PAGIDALGA 464

RESULT 2

ADP43223  
ID ADP43223 standard; protein; 464 AA.  
XX  
XX AC ADP43223;  
XX  
XX DT 09-SEP-2004 (first entry)  
XX  
XX DE Human AMPK gamma-3 subunit.  
XX  
XX KW cardiovascular; neuroprotective; dermatological; cytostatic;  
KW AMPK modulator; AMPK agonist; gene therapy;  
KW adenosine monophosphate-activated protein kinase; AMPK;  
KW cardiovascular disorder; neurological disorder; metabolic disorder;  
KW dermatological disorder; neoplastic disorder; age-associated disorder;  
XX geriatric disorder.  
XX OS Homo sapiens.  
XX PN WO2004050898-A2.  
XX PD 17-JUN-2004.  
XX PF 04-DEC-2003; 2003WO-US038628.  
XX PR 04-DEC-2002; 2002US-0430804P.  
XX PR 18-JUL-2003; 2003US-0488261P.  
XX PA (ELIX-) ELIXIR PHARM INC.  
XX PI Apfeld J, O'connor G;  
XX DR WPI; 2004-450740/42.  
XX  
XX Evaluating a compound, useful for treating e.g., age-related disorder,  
PT comprises contacting a polypeptide at least 85% identical to e.g., alpha  
PT adenosine monophosphate-activated protein kinase (AMPK) subunit with a  
PT test compound.  
XX  
XX Disclosure; SEQ ID NO 26; 160pp; English.  
XX  
XX The invention relates to a method of evaluating a compound by contacting  
CC a polypeptide comprising a sequence at least 85% identical to alpha, beta  
CC or gamma adenosine monophosphate-activated protein kinase (AMPK) subunit  
CC or a functional domain in vitro with a test compound, evaluating  
CC interaction between compound and polypeptide, contacting a cell or  
CC organism that produces the polypeptide with test compound, and evaluating  
CC a rate of aging of the cell or organism. A method comprising providing a  
CC modulator of the AMPK pathway to the subject is useful for treating or  
CC preventing a disease or disorder in a subject, preferably a  
CC cardiovascular disorder, a neurological disorder, a metabolic disorder, a  
CC dermatological disorder, a neoplastic disorder, an age-associated  
CC disorder, or a geriatric disorder. A compound that alters the expression  
CC or activity of an AMPK pathway component is useful for altering lifespan  
CC regulation in a cell or organism. This sequence represent a protein  
CC sequence of an AMPK pathway member or its homologue used in the method of  
CC the invention.  
XX  
XX Sequence 464 AA;  
QY Query Match 100.0%; Score 2403; DB 8; Length 464;  
DB Best Local Similarity 100.0%; Pred. No. 3.9e-240;  
Matches 464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSFLEQENSSWSPSPAVTSSSIRIGKRAKALRWTRQSVKEGEPGQGGPRSRPTAE 60  
DB 1 MSFLEQENSSWSPSPAVTSSSIRIGKRAKALRWTRQSVKEGEPGQGGPRSRPTAE 60  
QY 61 STGLEATPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 120  
DB 61 STGLEATPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 120  
QY 121 ECELEGLLEERPALCLSPQAPPKLGWDELRKPKAQIYMRPMOHTCYDAMATSSKLVI 180  
DB 121 ECELEGLLEERPALCLSPQAPPKLGWDELRKPKAQIYMRPMOHTCYDAMATSSKLVI 180

Db 121 ECELEGLLEERPALCLSPQAPFPKLGWDDDELKFKGAQIYMRFMQEHCTCYDAMATSSKLI 180  
 Qy 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHLHRYRSPVQIYIE 240  
 Db 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHLHRYRSPVQIYIE 240  
 Qy 241 QHKIETWREIYLOGCFKPLVSIISNDLSLFEAVYTLIKNRHRLPVLDPVSGNVLHILTHK 300  
 Db 241 QHKIETWREIYLOGCFKPLVSIISNDLSLFEAVYTLIKNRHRLPVLDPVSGNVLHILTHK 300  
 Qy 301 RLLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALPV 360  
 Db 301 RLLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALPV 360  
 Qy 361 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHESLGEVID 420  
 Db 361 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHESLGEVID 420  
 Qy 421 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPPAGIDALGA 464  
 Db 421 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPPAGIDALGA 464

RESULT 3

ADP50310  
 ID ADP50310 standard; protein; 489 AA.

AC ADP50310;

DT 12-FEB-2004 (first entry)

XX Human AMP-activated protein kinase (AMPK)-gamma 3 protein subunit.

XX human; transgenic; AMP-activated protein kinase gamma 3 subunit; Prkg3;  
 KW AMPK; energy metabolism; obesity; dyslipidaemia;  
 KW insulin resistance syndrome; type 2 diabetes; antidiabetic; anorectic;  
 KW antilipaemic.

XX Homo sapiens.

XX WO2003063586-A1.

XX 07-AUG-2003.

XX 31-JAN-2003; 2003WO-IB000912.

XX 01-FEB-2002; 2002US-0353430P.

XX (AREX-) AREXIS AB.

XX Andersson L, Marklund S;

XX WPI; 2003-663404/62.

XX N-PSDB; ADF50309.

XX New transgenic non-human animals expressing an AMP-activated protein  
 PT kinase gamma 3 subunit, useful as models for improving treatment,  
 PT prevention or diagnosis of diseases related to energy metabolism, e.g.  
 PT obesity or type 2 diabetes.

PS Claim 3; SEQ ID NO 2; 46pp; English.

XX This invention relates to novel transgenic non-human animals expressing  
 CC an AMP-activated protein kinase (AMPK)-gamma 3 subunit. Specifically, it  
 CC relates to the transgene Prkg3 gene that encodes the AMPK gamma3 subunit  
 CC or a variant thereof, where the nucleic acid is operably linked to a  
 CC regulatory element. AMPK is involved in the regulation of energy  
 CC metabolism in eukaryotic cells, and is recognised as a major regulator of  
 CC lipid biosynthetic pathways due to its role in the phosphorylation and  
 CC inactivation of key enzymes such as acetyl-CoA carboxylase. The present  
 CC invention describes transgenic animals expressing AMPK-gamma 3 to be used  
 CC as models for energy metabolism diseases and also methods for the  
 CC development of drugs for the treatment or prevention of obesity,

CC dyslipidaemia, insulin resistance syndrome or type 2 diabetes.  
 CC Accordingly, the compositions of this invention have various activities  
 CC including antidiabetic, anorectic and antilipaemic. This polypeptide  
 CC sequence is the human AMPK-gamma3 protein subunit of the invention.  
 SQ Sequence 489 AA;

Query Match 100.0%; Score 2403; DB 7; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-240;  
 Matches 464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFLEQBNSSWSPSPAVTSSSERIRGRRAKALRWTRQKSVBEGEPGQGGSPRSPTAE 60  
 Db 26 MSFLEQBNSSWSPSPAVTSSSERIRGRRAKALRWTRQKSVBEGEPGQGGSPRSPTAE 85  
 Qy 61 STGLEATFPKTTPLAQADPAGVTPPTGWDCLPSDCTASAGSSTDVDELATEFPATEAW 120  
 Db 86 STGLEATFPKTTPLAQADPAGVTPPTGWDCLPSDCTASAGSSTDVDELATEFPATEAW 145  
 Qy 121 ECELEGLLEERPALCLSPQAPFPKLGWDDDELKFKGAQIYMRFMQEHCTCYDAMATSSKLI 180  
 Db 146 ECELEGLLEERPALCLSPQAPFPKLGWDDDELKFKGAQIYMRFMQEHCTCYDAMATSSKLI 205  
 Qy 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHLHRYRSPVQIYIE 240  
 Db 206 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHLHRYRSPVQIYIE 265  
 Qy 241 QHKIETWREIYLOGCFKPLVSIISNDLSLFEAVYTLIKNRHRLPVLDPVSGNVLHILTHK 300  
 Db 266 QHKIETWREIYLOGCFKPLVSIISNDLSLFEAVYTLIKNRHRLPVLDPVSGNVLHILTHK 325  
 Qy 301 RLLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALPV 360  
 Db 326 RLLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALPV 385  
 Qy 361 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHESLGEVID 420  
 Db 386 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHESLGEVID 445  
 Qy 421 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPPAGIDALGA 464  
 Db 446 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPPAGIDALGA 489

RESULT 4

AAB47679

ID AAB47679 standard; protein; 489 AA.

AC AAB47679;

DT 21-JAN-2002 (first entry)

DE PRKAG3.

KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;  
 KW metabolic disease; diabetes; obesity; substitution; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 71

FT /note= "Possible variation point P71A"

FT Misc-difference 340

FT /note= "Possible variation point R340W"

XX WO200177305-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-SE000765.

XX 07-APR-2000; 2000US-0195665P.

XX



CC compounds for effectiveness as agonist or antagonist of the polypeptides,  
CC or in altering the expression of the target polynucleotide and compounds  
CC that specifically bind to or modulate the activity of the polypeptide.  
CC The microarray is useful in monitoring or measuring protein-protein  
CC interactions, drug-target interactions, and gene expression profiles. KPP  
CC DNA is used in gene therapy. The present sequence is human KPP protein  
XX  
SQ Sequence 489 AA;

Query Match 99.8%; Score 2398; DB 6; Length 489;  
Best Local Similarity 99.8%; Pred. No. 1.4e-239;  
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFLEQNSSWSPSPAVTSSSIRIGKRAKALRWTRQKSVGEPPGQEGPRSRPTAE 60  
Db 26 MSFLEQNSSWSPSPAVTSSSIRIGKRAKALRWTRQKSVGEPPGQEGPRSPAEE 85

Qy 61 STGLEATFPKTTPLAQADPAGVCTPTGWDCLPSDCTASAGSSTDVELATFPATEAW 120  
Db 86 STGLEATFPKTTPLAQADPAGVCTPTGWDCLPSDCTASAGSSTDVELATFPATEAW 145

Qy 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLKRPQAGIYMRFMQHTCYDAMATSSKLV 180  
Db 146 ECELEGLLEERPALCLSPQAPFPKLGWDDLKRPQAGIYMRFMQHTCYDAMATSSKLV 205

Qy 181 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFILVHRYRSPVLQIYEIE 240  
Db 206 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFILVHRYRSPVLQIYEIE 265

Qy 241 QHKIETWREIYLGCCFKPLVSPNDLSLFEAVNTLKNRHLRPLVDPVSGNVLHILTHK 300  
Db 266 QHKIETWREIYLGCCFKPLVSPNDLSLFEAVNTLKNRHLRPLVDPVSGNVLHILTHK 325

Qy 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRRVSALPV 360  
Db 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRRVSALPV 385

Qy 361 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCEGLVSLQCPHESLGEVID 420  
Db 386 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCEGLVSLQCPHESLGEVID 445

Qy 421 RIAREQVHRLVLDVETQHLGVVLSLSDILQALVLSPPAGIDALGA 464  
Db 446 RIAREQVHRLVLDVETQHLGVVLSLSDILQALVLSPPAGIDALGA 489

## RESULT 6

ADP87617  
ID ADP87617 standard; protein; 489 AA.

AC ADP87617;

XX 23-SEP-2004 (first entry)

XX Human NOVX polypeptide, NOV10a.

XX anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;  
KW insulin resistance; hybridization probe; chromosome mapping;  
KW tissue typing; preventive medicine; pharmacogenomics; NOVX; human.

XX Homo sapiens.

XX WO2004056961-A2.

XX 08-JUL-2004.

XX 27-OCT-2003; 2003WO-US034114.

XX 25-OCT-2002; 2002US-0421239P.

PR 28-OCT-2002; 2002US-0421700P.

PR 31-OCT-2002; 2002US-0422776P.

PR 13-NOV-2002; 2002US-0426197P.

PR 20-DEC-2002; 2002US-0435498P.

PR 20-DEC-2002; 2002US-0435510P.  
PR 20-DEC-2002; 2002US-0435568P.  
PR 21-MAR-2003; 2003US-0456812P.  
XX (CURA-) CURAGEN CORP.  
XX Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;  
XX WPI; 2004-500293/47.  
XX N-PSDB; ADP87616.  
XX New NOVX nucleic acid molecules and polypeptides useful for preventing or  
PT treating NOVX-associated disorders, e.g. diabetes, insulin resistance or  
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.  
XX Claim 3; SEQ ID NO 74; 570pp; English.

CC The invention relates to a novel isolated nucleic acid molecule  
CC comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base  
CC pairs) fully defined in the specification; or encodes any of the amino  
CC acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the  
CC specification. The invention further comprises an isolated polypeptide  
CC comprising any of the amino acid sequences cited above; a method for  
CC identifying compounds that modulate target polypeptide activity; an  
CC antibody that immunospecifically binds to the target polypeptide, where  
CC the target polypeptide comprises any of the above-mentioned amino acid  
CC sequences, an amino acid sequence that is at least 95% identical to the  
CC above amino acid sequences, an amino acid sequence of at least one domain  
CC of the above-mentioned amino acid sequences, or an amino acid sequence  
CC that is at least 95% identical to the domain of the above amino acid  
CC sequences; a method for identifying a potential therapeutic agent for use  
CC in treatment of a pathology, where the pathology is related to aberrant  
CC expression or aberrant physiological interactions of a target polypeptide  
CC; and a method of screening for a modulator of activity of or of latency  
CC or predisposition to a pathology associated with a target polypeptide.  
CC The modulating compounds have anorectic and antidiabetic activities. The  
CC nucleic acid sequences of the invention may be used in gene therapy to  
CC treat disorders. The proteins of the invention may be used in creating a  
CC vaccine. The composition and methods of the invention may be used in identifying compounds  
CC that modulate protein activity or for diagnosing, preventing or treating  
CC diverse pathological conditions, such as obesity, diabetes or insulin  
CC resistance. The nucleic acids are also used as hybridization probes, in  
CC chromosome mapping, tissue typing, preventive medicine, and  
CC pharmacogenomics. This sequence represents a NOVX polypeptide of the  
CC invention.

XX Sequence 489 AA;

Query Match 99.8%; Score 2398; DB 8; Length 489;

Best Local Similarity 99.8%; Pred. No. 1.4e-239;

Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFLEQNSSWSPSPAVTSSSIRIGKRAKALRWTRQKSVGEPPGQEGPRSRPTAE 60

Db 26 MSFLEQNSSWSPSPAVTSSSIRIGKRAKALRWTRQKSVGEPPGQEGPRSPAEE 85

Qy 61 STGLEATFPKTTPLAQADPAGVCTPTGWDCLPSDCTASAGSSTDVELATFPATEAW 120

Db 86 STGLEATFPKTTPLAQADPAGVCTPTGWDCLPSDCTASAGSSTDVELATFPATEAW 145

Qy 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLKRPQAGIYMRFMQHTCYDAMATSSKLV 180

Db 146 ECELEGLLEERPALCLSPQAPFPKLGWDDLKRPQAGIYMRFMQHTCYDAMATSSKLV 205

Qy 181 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFILVHRYRSPVLQIYEIE 240

Db 206 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFILVHRYRSPVLQIYEIE 265

Qy 241 QHKIETWREIYLGCCFKPLVSPNDLSLFEAVNTLKNRHLRPLVDPVSGNVLHILTHK 300

Db 266 QHKIETWREIYLGCCFKPLVSPNDLSLFEAVNTLKNRHLRPLVDPVSGNVLHILTHK 325

Qy 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRRVSALPV 360

Db 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETPALITLALDIFVDRVSALPV 385  
Qy 361 VNECGQVVGYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLGVLSQOPHESLGEVID 420  
Db 386 VNECGQVVGYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLGVLSQOPHESLGEVID 445  
Qy 421 RIAREQVHRLVLDVDETOHLLGVWSLSLQALVLSPPAGIDALGA 464  
Db 446 RIAREQVHRLVLDVDETOHLLGVWSLSLQALVLSPPAGIDALGA 489

RESULT 7  
ABP43929  
ID ABP43929 standard; protein; 489 AA.  
AC ABP43929;  
XX 26-FEB-2003 (first entry)  
XX AMP activated protein kinase gamma 3 subunit.  
XX Neuroprotective; immunomodulator; cancer; chromosome 2; cytostatic;  
KW anti-inflammatory; gene therapy; nutritional supplement; wound; burn;  
KW ulcer; Alzheimer's disease; Huntington's disease;  
KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;  
KW vulvarey.  
XX Homo sapiens.  
OS  
XX WO200231111-A2.  
XX 18-APR-2002.  
XX 11-OCT-2001; 2001WO-US027760.  
XX 12-OCT-2000; 2000US-00687527.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
XX WPI; 2002-426278/45.  
DR N-PSDB; ABQ61173.  
XX New polypeptides and their encoded proteins, useful as nutritional  
PT sources or supplements, or in gene therapy, particularly for treating  
PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or  
PT inflammation.  
XX Claim 20; SEQ ID # 832; 357pp + Sequence Listing; English.  
XX The invention relates to 446 newly isolated polynucleotide sequences. The  
CC activity of polynucleotides of the invention may be described as,  
CC vulvarey, neuroprotective, immunomodulator, cytostatic and anti-  
CC inflammatory. Compositions comprising nucleic acids of the invention are  
CC useful for treating a mammalian subject, or as nutritional sources or  
CC supplements. These are useful in gene therapy, particularly for treating  
CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,  
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or  
CC inflammation. The nucleic acids and polypeptides are also useful in  
CC diagnostic and research methods. The sequences given in records ABP43544-  
CC ABP43999 represent polypeptides encoded by polynucleotides of the  
CC invention. NOTE: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 489 AA;

Query Match 99.5%; Score 2391; DB 5; Length 489;  
Best Local Similarity 99.4%; Pred. No. 7.4e-239;  
Matches 461; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFLEQENSSWPSPAVTSSSRIRGKRAKALRWTRQKSVGEPPGQGEGRSPRTAE 60  
Db 26 MSFLEQENSSWPSPAVTSSSRIRGKRAKALRWTRQKSVGEPPGQGEGRSPRTAE 85  
Qy 61 STGLEATFPKTTPLAQAADPAGVGTPTGWDCLPDSCTASAAAGSSTDDVELATEFPATEAW 120  
Db 86 STGLEATFPKTTPLAQAADPAGVGTPTGWDCLPDSCTASAAAGSSTDDVELATEFPATEAW 145  
Qy 121 ECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQHTCYDAMATSSKLVI 180  
Db 146 ECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQHTCYDAMATSSKLVI 205  
Qy 181 FDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDIFILVLRHYVSPVQIYEIE 240  
Db 206 FDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDIFILVLRHYVSPVQIYEIE 265  
Qy 241 QHKIETWREIYLOQCFKPLVISISPNDSLFEAVTTLIKNRIHRLPVLDPVSGNVLHILTHK 300  
Db 266 QHKIETWREIYLOQCFKPLVISISPNDSLFEAVTTLIKNRIHRLPVLDPVSGNVLHILTHK 325  
Qy 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETPALITLALDIFVDRVSALPV 360  
Db 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETPALITLALDIFVDRVSALPV 385  
Qy 361 VNECGQVVGYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLGVLSQOPHESLGEVID 420  
Db 386 VNECGQVVGYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLGVLSQOPHESLGEVID 445  
Qy 421 RIAREQVHRLVLDVDETOHLLGVWSLSLQALVLSPPAGIDALGA 464  
Db 446 RIAREQVHRLVLDVDETOHLLGVWSLSLQALVLSPPAGIDALGA 489

RESULT 8  
AAE38410  
ID AAE38410 standard; protein; 489 AA.  
XX AAE38410;  
XX 20-NOV-2003 (first entry)  
XX Human Prkag3 protein.  
XX Human; Prkag3; transcription; therapy; prevention; energy metabolism;  
KW obesity; dyslipidaemia; insulin resistance syndrome; type II diabetes;  
KW anorectic; antilipaeamic; antidiabetic.  
XX Homo sapiens.  
XX WO2003064465-A2.  
XX 07-AUG-2003.  
XX 31-JAN-2003; 2003WO-IB000762.  
XX 01-FEB-2002; 2002US-0353429P.  
XX (AREX-) AREXIS AB.  
XX Svensson T;  
XX WPI; 2003-636796/60.  
DR N-PSDB; AAD58250.  
XX Novel isolated nucleic acid encoding human Prkag3 promoter capable of  
PT directing transcription of a heterologous coding sequence, useful for  
PT screening compounds which modulate human Prkag3 promoter activity.  
XX Disclosure; Page 52-53; 53pp; English.  
XX The present invention relates to novel human Prkag3 promoter capable of  
CC directing transcription of a heterologous coding sequence, useful for

CC screening compounds which modulate human Prkg3 promoter activity. The  
 CC invention is useful for treating or preventing diseases related to energy  
 CC metabolism e.g. obesity, dyslipidaemia, insulin resistance syndrome or  
 CC type II diabetes. The present sequence is human Prkg3 protein  
 XX  
 SQ Sequence 489 AA;

Query Match 98.9%; Score 2376; DB 7; Length 489;  
 Best Local Similarity 98.9%; Pred. No. 2.7e-237;  
 Matches 459; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSFLEQENSSWSPAVTSSSERIRGKRKALRWTRQKSVEEGPPGQGGPRSRPTAE 60  
 DB 26 MSFLEQENSSWSPAVTSSSERIRGKRKALRWTRQKSVEEGPPGQGGPRSRPAE 85  
 QY 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 120  
 DB 86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 145  
 QY 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 180  
 DB 146 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 205  
 QY 181 FDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLRHYRSPVQIYEIE 240  
 DB 206 FDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLRHYRSPVQIYEIE 265  
 QY 241 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRHRLPVLPVSGNVLIHLTHK 300  
 DB 266 QHKIETWREIYLOGCFKPLVSIISPNDLFEAVYTLIKNRHRLPVLPVSGNVLIHLTHK 325  
 QY 301 RLLKFLHIFGSLPRPSFLVRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALPV 360  
 DB 326 RLLKFLHIFGSLPRPSFLVRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALPV 385  
 QY 361 VNECGQVGLYSRFDVHILAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 420  
 DB 386 VNECGQVGLYSRFDVHILAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 445  
 QY 421 RIAREQVHRLVLDVETQHLGVVSLSDILQALVLSAPAGIDALGA 464  
 DB 446 RIAREQVHRLVLDVETQHLGVVSLSDILQALVLSAPAGIDALGA 489

RESULT 9  
 ADF50314  
 ID ADF50314 standard; protein; 489 AA.

XX AC ADF50314;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Human AMPK-gamma 3 protein subunit (seqid 6).

XX human; transgenic; AMP-activated protein kinase gamma 3 subunit; Prkg3;  
 KW AMPK; energy metabolism; obesity; dyslipidaemia;  
 KW insulin resistance syndrome; type 2 diabetes; antidiabetic; anorectic;  
 KW antilipaeamic.

XX OS Homo sapiens.

XX KW WO2003063586-A1.

XX PD 07-AUG-2003.

XX PF 31-JAN-2003; 2003WO-IB0000912.

XX PR 01-FEB-2002; 2002US-0353430P.

XX PA (AREX-) AREXIS AB.

XX PI Andersson L, Marklund S;

XX DT 23-SEP-2004 (first entry)

XX

DR WPI; 2003-663404/62.  
 DR N-PSDB; ADF50313.

PT New transgenic non-human animals expressing an AMP-activated protein  
 PT kinase gamma 3 subunit, useful as models for improving treatment, e.g.  
 PT prevention or diagnosis of diseases related to energy metabolism, e.g.  
 PT obesity or type 2 diabetes.

XX Example 1; SEQ ID NO 6; 46pp; English.

XX This invention relates to novel transgenic non-human animals expressing  
 CC an AMP-activated protein kinase (AMPK)-gamma 3 subunit. Specifically, it  
 CC relates to the transgene Prkg3 gene that encodes the AMPK gamma3 subunit  
 CC or a variant thereof, where the nucleic acid is operably linked to a  
 CC regulatory element. AMPK is involved in the regulation of energy  
 CC metabolism in eukaryotic cells, and is recognised as a major regulator of  
 CC lipid biosynthetic pathways due to its role in the phosphorylation and  
 CC inactivation of key enzymes such as acetyl-CoA carboxylase. The present  
 CC invention describes transgenic animals expressing AMPK-gamma 3 to be used  
 CC as models for energy metabolism diseases and also methods for the  
 CC development of drugs for the treatment or prevention of obesity,  
 CC dyslipidaemia, insulin resistance syndrome or type 2 diabetes.  
 CC Accordingly, the compositions of this invention have various activities  
 CC including, antidiabetic, anorectic and antilipaeamic. This polypeptide  
 CC sequence is the human AMPK-gamma3 protein subunit of the invention.

XX Sequence 489 AA;

Query Match 98.9%; Score 2376; DB 7; Length 489;  
 Best Local Similarity 98.9%; Pred. No. 2.7e-237;  
 Matches 459; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSFLEQENSSWSPAVTSSSERIRGKRKALRWTRQKSVEEGPPGQGGPRSRPTAE 60  
 DB 26 MSFLEQENSSWSPAVTSSSERIRGKRKALRWTRQKSVEEGPPGQGGPRSRPAE 85  
 QY 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 120  
 DB 86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 145  
 QY 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 180  
 DB 146 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 205  
 QY 181 FDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLRHYRSPVQIYEIE 240  
 DB 206 FDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLRHYRSPVQIYEIE 265  
 QY 241 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRHRLPVLPVSGNVLIHLTHK 300  
 DB 266 QHKIETWREIYLOGCFKPLVSIISPNDLFEAVYTLIKNRHRLPVLPVSGNVLIHLTHK 325  
 QY 301 RLLKFLHIFGSLPRPSFLVRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALPV 360  
 DB 326 RLLKFLHIFGSLPRPSFLVRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALPV 385  
 QY 361 VNECGQVGLYSRFDVHILAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 420  
 DB 386 VNECGQVGLYSRFDVHILAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 445  
 QY 421 RIAREQVHRLVLDVETQHLGVVSLSDILQALVLSAPAGIDALGA 464  
 DB 446 RIAREQVHRLVLDVETQHLGVVSLSDILQALVLSAPAGIDALGA 489

RESULT 10  
 ADP87619

ID ADP87619 standard; protein; 492 AA.

XX AC ADP87619;

XX DT 23-SEP-2004 (first entry)

XX

DE	Human NOVX polypeptide, NOV10b.	
XX	anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;	
KW	insulin resistance; hybridization probe; chromosome mapping;	
KW	tissue typing; preventive medicine; pharmacogenomics; NOVX; human.	
XX	Homo sapiens.	
XX	W02004056961-A2.	
XX	08-JUL-2004.	
XX	27-OCT-2003; 2003WO-US034114.	
XX	25-OCT-2002; 2002US-0421239P.	
PR	28-OCT-2002; 2002US-0421700P.	
PR	31-OCT-2002; 2002US-0422776P.	
PR	13-NOV-2002; 2002US-0426197P.	
PR	20-DEC-2002; 2002US-0435498P.	
PR	20-DEC-2002; 2002US-0435510P.	
PR	20-DEC-2002; 2002US-0435568P.	
PR	21-MAR-2003; 2003US-0456812P.	
XX	(CURA-) CURAGEN CORP.	
XX	Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;	
PI	WPI; 2004-500293/47.	
DR	N-PSDB; ADP87618.	
DR	New NOVX nucleic acid molecules and polypeptides useful for preventing or	
XX	treating NOVX-associated disorders, e.g. diabetes, insulin resistance or	
PT	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.	
PT	Claim 3; SEQ ID NO 76; 570pp; English.	
PS	The invention relates to a novel isolated nucleic acid molecule	
XX	comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base	
CC	pairs) fully defined in the specification; or encodes any of the amino	
CC	acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the	
CC	specification. The invention further comprises: an isolated polypeptide	
CC	comprising any of the amino acid sequences cited above; a method for	
CC	identifying compounds that modulate target polypeptide activity; an	
CC	antibody that immunospecifically binds to the target polypeptide; where	
CC	the target polypeptide comprises any of the above-mentioned amino acid	
CC	sequences, an amino acid sequence that is at least 95% identical to the	
CC	above amino acid sequences, an amino acid sequence of at least one domain	
CC	of the above-mentioned amino acid sequences, or an amino acid sequence	
CC	that is at least 95% identical to the domain of the above amino acid	
CC	sequences; a method for identifying a potential therapeutic agent for use	
CC	in treatment of a pathology, where the pathology is related to aberrant	
CC	expression or aberrant physiological interactions of a target polypeptide	
CC	; and a method of screening for a modulator of activity of or of latency	
CC	or predisposition to a pathology associated with a target polypeptide.	
CC	The modulating compounds have anorectic and antidiabetic activities. The	
CC	nucleic acid sequences of the invention may be used in gene therapy to	
CC	treat disorders. The proteins of the invention may be used in creating a	
CC	vaccine. The composition and methods are useful for identifying compounds	
CC	that modulate protein activity or for diagnosing, preventing or treating	
CC	diverse pathological conditions, such as obesity, diabetes or insulin	
CC	resistance. The nucleic acids are also used as hybridization probes, in	
CC	chromosome mapping, tissue typing, preventive medicine, and	
CC	pharmacogenomics. This sequence represents a NOVX polypeptide of the	
XX	invention.	
SQ	Sequence 492 AA;	
XX	Query Match 98.7%; Score 2372; DB 8; Length 492;	
XX	Best Local Similarity 98.7%; Pred. No. 7.1e-237;	
XX	Matches 457; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	
XX	1 MSFLEQENSSWPSPAVTSSSIRIGKRRAKALRWTRQKSVGEPPGQEGPRSRPAE 60	
QY		

Db	26	MSFLEQENSSWPSPAVTSSSIRIGKRRAKALRWTRQKSVGEPPGQEGPRSRPAE	85
QY	61	STGLEATFPKTTPLAQADPAGVCTPTGWDCLSDCTASAGSSTDDVELATFPATEAW	120
Db	86	STGLEATFPKTTPLAQADPAGVCTPTGWDCLSDCTASAGSSTDDVELATFPATEAW	145
QY	121	ECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYNRFMOEHTCYDAMATSSKLVI	180
Db	146	ECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYNRFMOEHTCYDAMATSSKLVI	205
QY	181	FTMLETIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDILVHLHYRSPLVQIYEIE	240
Db	206	FTMLETIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDILVHLHYRSPLVQIYEIE	265
QY	241	QHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRTHRLPVLDPVSGNVLHILTHK	300
Db	266	QHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRTHRLPVLDPVSGNVLHILTHK	325
QY	301	RLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPAIIITALDIFVDRRSALPV	360
Db	326	RLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPAIIITALDIFVDRRSALPV	385
QY	361	VNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQPHESLGEVID	420
Db	386	VNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQPHESLGEVID	445
QY	421	RIAREQVHRLVLDVDETHLLGVVSLSDILQALVLSPPAGIDALG	463
Db	446	RIAREQVHRLVLDVDETHLLGVVSLSDILQALVLSPPAGIDPFG	488
RESULT 11			
AE69187			
ID	AE69187	standard; protein; 492 AA.	
XX	AC	AE69187;	
XX	DT	20-OCT-2005 (first entry)	
XX	DE	Human modulator of IGFR pathway polypeptide #4.	
XX	KW	Screening; insulin growth factor receptor; IGFR; diagnosis; cancer;	
XX	OS	neoplasm; cytostatic.	
XX	PN	Homo sapiens.	
XX	PD	WO2005073723-A1.	
XX	PF	11-AUG-2005.	
XX	PR	27-JAN-2005; 2005WO-US002638.	
XX	PR	28-JAN-2004; 2004US-0539837P.	
XX	PR	12-MAR-2004; 2004US-0552634P.	
XX	PR	21-JUN-2004; 2004US-0581696P.	
XX	PA	(EXEL-) EXELIXIS INC.	
XX	PA	(NICO/) NICOLL M.	
XX	PI	Nicoll M, Friedman L, Francis-Lang H, Parks A, Shaw KJ, Zhang H;	
XX	PI	Bjerke LM, Adamkiewicz J, Hitz BC, Lickteig K, Jin Y;	
XX	DR	WPI; 2005-582573/59.	
XX	DR	N-PSDB; AEB69127.	
XX	PT	Identifying a candidate insulin growth factor receptor (IGFR) pathway	
XX	PT	modulating agents useful for diagnosing or treating, for e.g. cancer,	
XX	PT	comprises screening for agents that modulate the activity of a modifier	
XX	PS	of IGFR (MIGFR).	
XX	PS	Example; SEQ ID NO 64; 334pp; English.	
XX	CC	The invention relates to a method of identifying a candidate insulin	



growth factor receptor (IGFR) pathway modulating agent comprising screening for agents that modulate the activity of a modifier of IGFR (MIGFR). The method comprises providing an assay system comprising an MIGFR polypeptide or polynucleotide, contacting the assay system with a test agent under conditions where, but for the presence of the test agent, the system provides a reference activity and detecting a test agent-biased activity of the assay system, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate IGFR pathway modulating agent. The invention also relates to methods for modulating an IGFR pathway of a cell or in a mammalian cell and a method for diagnosing a disease in a patient. The methods are useful for diagnosing or treating cancer or for identifying modulators of an IGFR pathway, which may be utilized as therapeutic targets for disorders associated with defective IGFR function, such as cancer. This sequence represents a human modulator of IGFR pathway polypeptide of the invention.

Query Match	98.7%;	Score 2372;	DB 9;	Length 492;
Best Local Similarity	98.7%;	Pred. No. 7.1e-237;		
Matches 457;	Conservative 3;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	MSFLEQNSSSWPSPAVTSSSERIRGKRAKALRWTRQKSYVEEGEPPOGQSGPRSPRAE	60	
Db	26	MSFLEQNSSSWPSPAVTSSSERIRGKRAKALRWTRQKSYVEEGEPPOGQSGPRSPRAE	85	
Qy	61	STGLEATFPKTTPLAQADPAGVGTPPTGWCDCLPDCTASAAGSSTDDVELATEPPATEAW	120	
Db	86	STGLEATFPKTTPLAQADPAGVGTPPTGWCDCLPDCTASAAGSSTDDVELATEPPATEAW	145	
Qy	121	ECELEGLEERPALCLSPQAPFPKLGWDDELKPKGAQIYMFMOEHTCYDAMATSSKLI	180	
Db	146	ECELEGLEERPALCLSPQAPFPKLGWDDELKPKGAQIYMFIEBHTCYDAMATSSKLI	205	
Qy	181	FTDMLETKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYRSPLVQIYE	240	
Db	206	FTDMLETKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYRSPLVQIYE	265	
Qy	241	OHKIETWREIYLQCCFKPLYSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK	300	
Db	266	OHKIETWREIYLQCCFKPLYSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK	325	
Qy	301	RLLKFLHIFGSLPRPSFLVRTIOQLGIGTFRDLAVLETAPIITALDIFVDRRVSALPV	360	
Db	326	RLLKFLHIFGSLPRPSFLVRTIOQLGIGTFRDLAVLETAPIITALDIFVDRRVSALPV	385	
Qy	361	VNECGQVVGLYSRFDVTHLAAQQTNYNHLDMVSGEALRQRTICLREGVLSQCPHESIGE	420	
Db	386	VNECGQVVGLYSRFDVTHLAAQQTNYNHLDMVSGEALRKRCTLCLGVLSCQPHESIGE	445	
Qy	421	RIAREQVRLVLVDETOHLLGVWSLSDIQLALVISPAGIDALG	463	
Db	446	RIAREQVRLVLVDETOHLLGVWSLSDIQLALVISPAGIDPSG	488	

RESULT	12
AAE22985	
ID	AAE22985 standard; protein; 464 AA.
XX	
XX	AAE22985;
AC	
XX	
DT	09-AUG-2002 (first entry)
XX	
DE	Pig PRKAG3 polymorphic variant (PRKAG3-30).
XX	
KW	AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KM	screening; meat quality; single nucleotide polymorphism; SNP; Pig;
KW	variant.
XX	
XX	
OS	Sus scrofa.
XX	
Key	Location/Qualifiers
FX	
FF	

FT	Misc-difference 30	
FT	/note= "Wild type Asn is substituted with Thr due to	
FT	single nucleotide polymorphism (SNP) "	
XX		
XX	W0200220850-A2.	
PN		
XX		
PD	14-MAR-2002.	
XX		
XX	10-SEP-2001; 2001WO-US028283.	
XX		
PR	08-SEP-2000; 2000US-0231045P.	
PR	08-JAN-2001; 2001US-0260239P.	
PR	18-JUN-2001; 2001US-0299111P.	
XX		
PA	(IOWA ) UNIV IOWA STATE RES FOUND INC.	
XX		
XX	Rothschild MF, Ciobanu DC, Malek M, Plastow G;	
PI		
XX	WPI; 2002-393850/42.	
DR	N-PSDB; AAD36457.	
DR		
XX		
PT	Screening animals to determine those likely to produce larger litters and	
PT	improved meat quality traits involves assaying for the presence of	
PT	polymorphisms in the AMP activated protein kinase regulatory gamma	
PT	subunit gene.	
XX		
PS	Disclosure; Page 91-93; 109pp; English.	
XX		
CC	The invention relates to a method for screening animals to determine	
CC	those more likely to produce large litters and improved meat quality	
CC	traits. The method involves assaying for the presence of a genotype in	
CC	the sample of genetic material obtained from animal. The genotype is	
CC	characterised by polymorphism(s) in the AMP activated protein kinase	
CC	regulatory gamma subunit (PRKAG3) gene. The method is used for screening	
CC	animals e.g., pigs to determine those most likely to exhibit improved	
CC	meat quality traits and to produce larger litters. The present sequence	
CC	is pig PRKAG3 polymorphic variant (PRKAG3-30)	
XX		
SQ	Sequence 464 AA;	

Query Match	83.8%;	Score 2013;	DB 5;	Length 464;
Best Local Similarity	86.0%;	Pred. No. 1.3e-199;		
Matches 400;	Conservative 19;	Mismatches 44;	Indels 2;	Gaps 2;
QY	1	MSFLEQENSSWSPSAVTTSSSERIRGKRRAKALRWTRQKSVESGEPGQEGPGRSRRTAE	60	
DB	1	MSFLEQESRSPSAVTTSSSRSHGDOGTKASRWTQEDVESGGPPGREGQSRPVAE	60	
QY	61	STGLEATFPKTTPLAQADP-AGVGTPTGTGDCULPDSCTASAAAGSTDDVELATEFPATEA	119	
DB	61	STGQEATFPKATPLAQAAPLAEVNDNPETTERDILPSCAASASDNTDHLGLGIEFSAA	120	
QY	120	WECELEGLLEERPALCLSPQAPPKLGWDDELKPKGAQIYMRFMQHTCYDAMATSSKL	179	
DB	121	SGDEL-GLVEEKAPCPSEVLLPRLGWDELQKPGAQVYHMFQHTCYDAMATSSKL	179	
QY	180	IFDTMLLEIKAPFALVANGVRAAPLWDSKKQSPVGMLTITDFILVLHRYRSPLVQIYEI	239	
DB	180	IFDTMLLEIKAPFALVANGVRAAPLWDSKKQSPVGMLTITDFILVLHRYRSPLVQIYEI	239	
QY	240	EQHKIETWREIYLQGCFKPLVSI SPNDSLFEAVYTLIKRIHRLPVLDPVSGNVLHLTTH	299	
DB	240	EEHKIETWREIYLQGCFKPLVSI SPNDSLFEAVYTLIKRIHRLPVLDPVSGNVLHLTTH	299	
QY	300	KRLLKFLHIFGSLPRPSFLYRTIQDLGIGTTFRDLAWLLETAPILTALDIFVDRRVSALP	359	
DB	300	KRLLKFLHIFGTLPRPSFLYRTIQDLGIGTTFRDLAWLLETAPILTALDIFVDRRVSALP	359	
QY	360	VVNECCQVGLYSRPFVVIHLAQOQTNHLDMSVGEALRORTLCLEGVLSQCPHESIGEVI	419	
DB	360	VVNETQVVGLYSRPFVVIHLAQOQTNHLDNMVGEALRORTLCLEGVLSQCPHETLGEVI	419	
QY	420	DRTARSOVHRLVLDTEQHLIGVVSITDILQALVLSPAGIDALGA	464	

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Db      420 DRIVREQVHRLVLDVDETHQLLGVVSLSDILQALVLSFAGIDALGA 464
|||||
RESULT 14
AAE00222
ID      AAE00222 standard; protein; 464 AA.
AC      AAE00222;
XX
XX      13-JUN-2001 (first entry)
XX
XX      Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
XX
XX      Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
XX      PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
XX      genetic testing; carbohydrate metabolism disorder; skeletal muscle;
XX      cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
XX      chromosome 15.
XX
XX      Sus scrofa.
XX
XX      Key      Location/Qualifiers
XX      Domain   172..225
XX              /label= CBS
XX              /note= "Cystathione beta synthase domain"
XX      Misc-difference 200
XX              /note= "RN- mutation site"
XX      Domain   253..307
XX              /label= CBS
XX              /note= "Cystathione beta synthase domain"
XX      Domain   329..382
XX              /label= CBS
XX              /note= "Cystathione beta synthase domain"
XX      Domain   400..453
XX              /label= CBS
XX              /note= "Cystathione beta synthase domain"
XX
XX      WO200120003-A2.
XX
XX      22-MAR-2001.
XX
XX      11-SEP-2000; 2000WO-EP009896.
XX
XX      10-SEP-1999; 99EP-00402236.
XX      18-MAY-2000; 2000EP-00401388.
XX
XX      (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX      (ANDE/) ANDERSSON L.
XX      (LOOF/) LOOFT C.
XX      (KALM/) KALM E.
XX
XX      Andersson L, Loof C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX      Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
XX      WPI; 2001-244810/25.
XX      NP-PSDB; AAD03319.
XX
XX      New variants of the gamma subunit of vertebrate adenosine monophosphate-
XX      activated kinase for diagnosis or treatment of disorders associated with
XX      energy metabolism such as diabetes, obesity, and myopathy.
XX
XX      Claim 5; Fig 3; 7lpp; English.
XX
XX      The present sequence is pig adenosine monophosphate (AMP)-activated
XX      kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3.
XX      Prkag3 gene is located in the RN locus of chromosome 15. Mutation in
XX      Prkag3 results in an altered regulation of carbohydrate metabolism,
XX      particularly in skeletal muscle. PRKAG3 is useful as therapeutic for
XX      treating carbohydrate metabolism disorders such as diabetes, obesity, and
XX      disorders associated with muscle metabolism such as myopathy and
XX      cardiovascular diseases, to modulate AMPK activity, and for restoring a
XX      normal AMPK function. PRKAG3 sequence and its functionally altered

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CC      mutants are useful for the diagnostic evaluation, genetic testing and
CC      prognosis of a metabolic disorder, preferably a carbohydrate metabolism
CC      disorder. Primers that can detect a genetic polymorphic marker linked to
CC      a sequence encoding PRKAG3, are useful for detecting a dysfunction of
CC      carbohydrate metabolism resulting from the expression of a functionally
CC      altered allele of PRKAG3. Transgenic animal and host cell transformed
CC      with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant,
CC      are useful for screening compounds able to modulate AMPK activity.
CC      Nucleic acid encoding PRKAG3 is useful for detecting mutations in a
CC      Prkag3 gene, or in a sequence encoding the first cystathione beta
CC      synthase (CBS) domain of PRKAG3 and is useful in gene therapy
XX
XX      SQ      Sequence 464 AA;
XX
XX      Query Match      83.7%; Score 2011; DB 4; Length 464;
XX      Best Local Similarity 86.0%; Pred. No. 2.2e-199;
XX      Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;
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XX      Qy      1 MSFLEQENSSSWPSPAVTSSSRIRKRAKALRWTRQKSVEEGPPGQGGPRSRPTAE 60
XX      Db      1 MSFLEQGESRSWFSRAVTTSSRSRSHGQGNKASRWTRQEDVEEGPPGREGPQSRPVAE 60
XX
XX      Qy      61 STGLEATFPKTTPLAQADP-AGVGTPTPTGMDCLPSPDCTASAAGSSTDDELATFPATEA 119
XX      Db      61 STGQEAATFPKATPLAQAAPLAEVDNPPPTERDILPSCDAASASDNTDHLDIGIEFSAA 120
XX
XX      Qy      120 WECELEGLLEERPALCLSPQAPPKLGWDDDELKPKGAQIYMRFMQEHCTCYDAMATSSKLV 179
XX      Db      121 SGDEL-GLVEEKAPAPCPSPPEVLPRLGWDDDELQKGAQVYMHFMQEHCTCYDAMATSSKLV 179
XX
XX      Qy      180 IFDTMLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEI 239
XX      Db      180 IFDTMLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEI 239
XX
XX      Qy      240 EOHKIETWREIYLQGCCKPLVSPNDLSLFEAVVTILKNRIHRPLVDLPVSGNVHLILTH 299
XX      Db      240 EEHKIETWREIYLQGCCKPLVSPNDLSLFEAVVTILKNRIHRPLVDLPVSGNVHLILTH 299
XX
XX      Qy      300 KRLKFLHIFGSLPRPSFLYRTTQDLGIGCTFRDLAVVLETPILTALDIFVDRRVSAIP 359
XX      Db      300 KRLKFLHIFGTLPRPSFLYRTTQDLGIGCTFRDLAVVLETPILTALDIFVDRRVSAIP 359
XX
XX      Qy      360 VVNECGOVVGLYSRFDVHILAAQQTYNHLDMSVGEALRQRTLCLGVLSCOPHESLGEVI 419
XX      Db      360 VVNETGVVGLYSRFDVHILAAQQTYNHLDNVGEALRQRTLCLGVLSCOPHETLGEVI 419
XX
XX      Qy      420 DRIAREQVHRLVLDVDETHQLLGVVSLSDILQALVLSFAGIDALGA 464
XX      Db      420 DRIVREQVHRLVLDVDETHQLLGVVSLSDILQALVLSFAGIDALGA 464
XX
XX      RESULT 14
XX      AAE22984
XX      ID      AAE22984 standard; protein; 464 AA.
XX      AC      AAE22984;
XX      XX      09-AUG-2002 (first entry)
XX      DE      Pig wild-type PRKAG3 protein.
XX      KW      AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
XX      screening; meat quality; single nucleotide polymorphism; SNP; pig.
XX      OS      Sus scrofa.
XX      Key      Location/Qualifiers
XX      Misc-difference 30
XX      /note= "Wild type Asn is replaced with Thr during single
XX      nucleotide polymorphism (SNP)"
XX      Misc-difference 52
XX      /note= "Wild type Gly is replaced with Ser during single
XX      nucleotide polymorphism (SNP)"
XX      FT

```



```
Query Match      83.7%; Score 2011; DB 4; Length 514;
Best Local Similarity 86.0%; Pred.No. 2.5e-199;
Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;

Qy      1 MSFLEQENSSSPSPAVTSSSERIRGRKRAKALRWTRQKSVEEGEPGQGEGRSRPTAE 60
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      51 MSFLEQGESRWPBRVNTTSSERHGGQGNKASRWTRQEDVEEGCPGPGREGQSPRVAE 110
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      61 STGLEATFPKTPPLAQADP-AGVCTPPTGMDCLPSCDCTASAGSSSTDDELATEFPATEA 119
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      111 STGQEAFFPKATPLAQAPLAEVNDPPTERDILPFDCAASASDNTDHLDLGIEFSASAA 170
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      120 WECLEGLLEERPALCLSPQAPFPKLGWDDDELKKGGAQIYMRFMQEHCTCYDAMATSSKLV 179
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      171 SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDDELQKPGAQVYMHFMQEHCTCYDAMATSSKLV 229
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      180 IFDTMLEIKKAPFAFVANGVRAAPLWDSKKQSFVGMLTITDFILVLRHYRSPVLQIYEI 239
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      230 IFDTMLEIKKAPFAFVANGVRAAPLWDSKKQSFVGMLTITDFILVLRHYRSPVLQIYEI 289
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      240 EOHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      290 EHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 349
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      300 KRLKFLHIFGSLIPRPSFLYRTIQDLGIGTFRDLAVVLETPAPILTALDIFVDRRVSAIP 359
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      350 KRLKFLHIFGTLIPRPSFLYRTIQDLGIGTFRDLAVVLETPAPILTALDIFVDRRVSAIP 409
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      360 VVNECGQVVGLYSRFDVTHLAAQOQTYNHLDMVGEALRQRTLCEGLVSCOPHESLGEVI 419
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      410 VVNETGVVVGLYSRFDVTHLAAQOQTYNHLDMVGEALRQRTLCEGLVSCOPHETLGEVI 469
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      420 DRIAREQVHRLVLDVDETQHLGLGWSLSDILOALVLSPAGIDALGA 464
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      470 DRIVEQVHRLVLDVDETQHLGLGWSLSDILOALVLSPAGIDALGA 514
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: January 24, 2006, 22:08:49  
Job time : 128.313 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 26, 2006, 03:26:13 ; Search time 709.948 Seconds  
(without alignments)  
356.862 Million cell updates/sec

Title: US-10-070-794A-4

Perfect score: 1551

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Searched: 6059551 seqs, 415333918 residues

Total number of hits satisfying chosen parameters: 12119102

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	1002	64.6	1628	8	US-11-136-527-2210
2	500.5	32.3	1321	7	US-10-750-185-28770
3	500.5	32.3	1321	7	US-10-750-623-28770
4	461.5	29.8	568	8	US-11-128-061-330
5	461.5	29.8	568	8	US-11-128-061-3972
6	461.5	29.8	568	8	US-11-128-049-330
7	461.5	29.8	568	8	US-11-128-049-3972

8	229.5	14.8	1500	8	US-11-041-776-79	Sequence 79, Appl
9	107.5	6.9	1494	7	US-10-467-657-5005	Sequence 5005, Ap
c 10	95.5	6.2	170837	8	US-11-121-086-97	Sequence 97, Appl
c 11	91.5	5.9	3061	7	US-10-793-626-4134	Sequence 4134, Ap
c 12	89.5	5.8	1467	7	US-10-793-626-2307	Sequence 2307, Ap
c 13	89.5	5.8	2980	7	US-10-793-626-4242	Sequence 4242, Ap
c 14	89.5	5.8	3980	7	US-10-793-626-4013	Sequence 4013, Ap
c 15	87	5.6	2862	8	US-11-156-953-6	Sequence 6, Appli
c 16	86.5	5.6	1641	8	US-11-055-822-945	Sequence 945, Ap
c 17	86.5	5.6	5100	8	US-11-136-527-4000	Sequence 4000, Ap
c 18	86	5.5	1400	8	US-11-136-527-4370	Sequence 4370, Ap
c 19	86	5.5	6021	8	US-11-136-527-274	Sequence 274, App
c 20	85.5	5.5	574	8	US-11-055-822-947	Sequence 947, App
c 21	85.5	5.5	1131	7	US-10-467-657-8227	Sequence 8227, Ap
c 22	85.5	5.5	1431	8	US-11-143-980-17	Sequence 17, Appl
c 23	85.5	5.5	1662	7	US-10-467-657-8239	Sequence 8239, Ap
c 24	85.5	5.5	116856	8	US-11-143-980-1	Sequence 1, Appli
c 25	84.5	5.4	4716	8	US-11-156-953-4	Sequence 4, Appli
c 26	83.5	5.4	1832	8	US-11-136-527-3815	Sequence 3815, Ap
c 27	83	5.4	1400	8	US-11-128-061-6939	Sequence 6939, Ap
c 28	83	5.4	3030	8	US-11-128-061-3297	Sequence 3297, Ap
c 29	83	5.4	3030	8	US-11-128-049-3297	Sequence 3297, Ap
c 30	83	5.4	3030	8	US-11-128-049-3297	Sequence 3297, Ap
c 31	82.5	5.3	1212	7	US-10-821-234-638	Sequence 638, App
c 32	82.5	5.3	1311	8	US-11-000-888-494	Sequence 494, App
c 33	82.5	5.3	1677	7	US-10-750-185-60961	Sequence 60961, A
c 34	82.5	5.3	1677	7	US-10-750-623-60961	Sequence 60961, A
c 35	82.5	5.3	35997	7	US-10-895-561-13301	Sequence 13301, A
c 36	81.5	5.3	7396	8	US-11-136-527-2724	Sequence 2724, Ap
c 37	80.5	5.2	960	7	US-10-873-528-275	Sequence 275, App
c 38	80.5	5.2	1963	8	US-11-038-981A-28	Sequence 28, Appl
c 39	80.5	5.2	6406	7	US-10-821-234-311	Sequence 311, App
c 40	80	5.2	4914	7	US-10-947-249-163	Sequence 163, App
c 41	80	5.2	5270	8	US-11-136-527-2161	Sequence 2161, Ap
c 42	80	5.2	160170	8	US-11-121-086-32	Sequence 32, Appl
c 43	79.5	5.1	2147	7	US-10-750-185-32313	Sequence 32313, A
c 44	79.5	5.1	2147	7	US-10-750-623-32313	Sequence 32313, A
c 45	79	5.1	987	8	US-11-128-061-971	Sequence 971, App

## ALIGNMENTS

RESULT 1

US-11-136-527-2210  
; Sequence 2210, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136, 527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574, 294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2210  
; LENGTH: 1628  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-2210

Alignment Scores:					
Pred. No.:	2.59e-107	Length:	1628		
Score:	1002.00	Matches:	191		
Percent Similarity:	82.65%	Conservative:	52		
Best Local Similarity:	64.97%	Mismatches:	51		
Query Match:	64.60%	Indels:	0		
DB:	8	Gaps:	0		

US-10-070-794A-4 (1-305) x US-11-136-527-2210 (1-1628)

```

Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
Db 127 TTTATGAAGTCTATCCTGCTATGACTGATGCCACAGCTCCAGCTGGTGGTATT 186
Qy 23 AspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAla 42
Db 187 GATATCTCGCTGCAGGTAAAGAAAGCCTCTTTGCCCTGGTGACTAAACGGTGTTCGTGCT 246
Qy 43 AlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 247 GCCCTTTGTGGGATAGTAAGAACAGACAGCTTTGTGGGCATGCTGCACCATCAGCTTC 306
Qy 63 IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGln 82
Db 307 ATCAATATCTGCAACCATCTACAGTACGCCCTGGTGACATCTATGACTGGAGGAG 366
Qy 83 HisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSer 102
Db 367 CACAAGATAGAGACTTGGAGAGAGTCTACCTGCAAGACTCCTTTAAGCCACTTGTCTGC 426
Qy 103 IleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHis 122
Db 427 ATTTCTCAATGCCAGCTTGTTCGATGCTGTCTTTCATTAATTCGAAATAAGATCCAC 486
Qy 123 ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArg 142
Db 487 AGGTTCCAGTATTGACCCGAGTACAGGCAACCTTTGTACATCTTACTCACAGCGG 546
Qy 143 LeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg 162
Db 547 ATCTCAAGTCTTCTCAAGTGTGTTATCATCTAGTTCGCCAAGCGGAATTCATGCTAAG 606
Qy 163 ThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAla 182
Db 607 TCTCTGGAAGAGCTACAGATTGGCACCTTACGCCCAATATTGCCATGGTCCGTACCACATACA 666
Qy 183 ProfileLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProValVal 202
Db 667 CTTGCTATGCTGCTGCTGGGATCTTTGTACAGCACCGAGTCTCGCCCTTGCCTTGGTGTG 726
Qy 203 AsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAlaAla 222
Db 727 GATGAGAAAGGGCGTGTGGTGCATCTACTTCCAAAGTTTGATGTGATTAATTTGGCAGCA 786
Qy 223 GlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242
Db 787 GAAAAGACATACAAACACTAGATGTCTGTGACAAAAGCCCTACAGCCCGGTCCACAC 846
Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 262
Db 847 TACTTCGAGGGGTGTTCTCAAGTCTTACCTACATGAGACTCTAGAACCAATCATCATAGA 906
Qy 263 IleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeuGly 282
Db 907 CTGGTGGAGCAGAGGTTCCCGTCTGGTGGTGGTGAATGAACATGACGTGCTCAGGGC 966
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 967 ATTTGATCGCTGCTGACATCTTACAGGCTCTGGTGTCTGCACAA 1008

```

# RESULT 2

```

US-10-750-185-28770
; Sequence 28770, Application US/10750185
; Publication NO. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

```

```

; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28770
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Bovine 19866880603844
US-10-750-185-28770

Alignment Scores:      2,42e-48      Length:      1321
Pred. No.:            500,50          Matches:     136
Score:                53,27%          Conservative: 43
Percent Similarity:    40,48%          Mismatches:  89
Best Local Similarity: 32,27%          Indels:      69
Query Match:          7               Gaps:       5
DB:

US-10-070-794A-4 (1-305) x US-10-750-185-28770 (1-1321)

Qy 9 CysTyrAspAlaMetAlaThrSerSerLysLeuValIlePheAspThrMetLeuGluIle 28
Db 101 TGCTATGACCTGAGTCTCCAAAGCTCCCAATTTGGTTGTATTGTCTACTTCCCTGCAGGTA 160
Qy 29 LysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAlaAlaProLeu-TrpAspSe 48
Db 161 TACAAG-----TTGCCCTCTCTGGGATAC 184
Qy 48 rLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisAr 68
Db 185 TAAAGCAAGGACTTGTGGCATGTGATTAATCAACCAATTTTCATCAATATCTGCCTA 244
Qy 68 gTyrTyrArgSerProLeuVal-GlnIleTyrGluIleGluGlnHisLysIleGluThr 88
Db 245 TTACTATATGACCTTGGTTCCAGAGCTATGAGCTGGAAGAATACAAAATAGAAACTT 304
Qy 88 rPArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIleSerProAsnAspS 108
Db 305 GAAAGGAGGTGTATATACAGGACTTCTTAAACCACTTGTCTGCATTTCTTCTAATGCCA 364
Qy 108 erLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuA 128
Db 365 ACTTGTATTATGCTGCTCTTTTCATTAATTCAGAACAGATCCACAGGCTGCCAGTTGTG 424
Qy 128 spProValSerGlyAsnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuH 148
Db 425 ACCCAGAATCAAGCAACATCTTGTACACCCCTCACCCCAAGTGCATTTCTCATGTTCCTCA 484
Qy 148 isIlePheGlySerLeuLeuProArgProSerPheLeuTyrArgThr-IleGlnAspLeu 167
Db 485 AAGTGTATTATCAGTACGCTCTT-AAAGCAGAAATTCATGCTTAAGTCTAATAGAAGAT--- 540
Qy 168 GlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAlaProIleLeuThrAla 187
Db 541 -----TAGCTTCTATGCCAGATTCATGTTCTGCACATATGACCCCACTGACAGGCT 594
Qy 188 LeuAspIlePheValAspArgValSerAlaLeuProValValAsnGluCysGlyGln 207
Db 595 CTGGGCATC-----TCTGTACAGGATCTGCCA---GTGAATGAGAGAGGTGAG 639
Qy 208 ValValGlyLeuTyrSerArgPhe----- 215
Db 640 GTGGTGAACATCTATTTCACATTTGATGTTATCTGTGCTAAGTCACTTCAGTCAGTCACGTC 699
Qy 215 ----- 215
Db 700 ACTCTTTGGGATCCTCTGAGCTGTAGCCGCTCAGGCTTCTCTGTCCATGGGAGTTCACGAG 759
Qy 216 -----AspValIleHisLeuAlaAla 222

```

```
Db 760 GCAGAACACATAGAGTGGGTTACCATTTCTTCTCAGTGAATGTTATCCATCAGGAGCA 819
Qy 223 GlnGlnThrTyraAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242
Db 820 TAAAGAGTCTACCAACACCTAGATGCTGCTAGTCAAGCCCTGAAATTCGATCAG 879
Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGluValIleAspArg 262
Db 880 TACTTTAAATGTAGCTTCAAGTGCAGCTGCTGATGAGGCTCTGGAGACCTTTCTCAGCAG 939
Qy 263 IleAlaArgGluGlnValHisArgLeuValValAspGluThrGlnHisLeuLeuGly 282
Db 940 CTAGTGAACAGGAGTACCCACTCTGCTGCTGATGAGATGATGTGATCAAGGGA 999
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 1000 ACTGTATCACCATCTGTCATCTCTGTAGACCTGGTGTCTACA 1041

RESULT 3
US-10-750-623-28770
; Sequence 28770, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750, 623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28770
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Bovine 19866880603844
US-10-750-623-28770

Alignment Scores:
Pred. No.: 2,42e-48 Length: 1321
Score: 500.50 Matches: 136
Percent Similarity: 53.27% Conservative: 43
Best Local Similarity: 40.48% Mismatches: 89
Query Match: 32.27% Indels: 69
DB: Gaps: 5

US-10-070-794A-4 (1-305) x US-10-750-623-28770 (1-1321)
Qy 9 CysTyraAspAlaMetAlaThrSerSerLysLeuValIlePheAspThrMetLeuGluIle 28
Db 101 TGCTATGACCTGAGTCTCAACAGCTCCAAATTTGTTGTTATTTGCTACTTCCCTGCAGGTA 160
Qy 29 LysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAlaAlaProLeu-Trpaspse 48
Db 161 TACAAG-----TTGCCCTCTCTGTGATAC 184
Qy 48 rLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisar 68
Db 185 TAAAGACAGGACTTGTGGCATGTGGATATACCAATTTCAATCAATATCTCTGACTA 244
Qy 68 gTyTyraArgSerProLeuVal-GlnIleTyrgluIleGluGlnHisLysIleGluThr 88
Db 245 TTACTATATCTGACCTTGGTCTCCAGAGCTATGAGTGGAGAAATACAAATAGAACTT 304
Qy 88 rpargGluIleTyLeuGlnGlyCysPheLysProLeuValSerIleSerProAsnAspS 108
Db 305 GAAAGGAGGTATATACAGGACTTCTTTAAACCACTTGTCTGCATTTCTTAAATGCCA 364
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Qy 108 erLeuPheGluAlaValTyThrLeuIleLysAsnArgIleHisArgLeuProValLeuA 128
Db 365 ACTTGTTTAATGCTGCTTTTCAATTAATTCAGAACAGATCCACAGGCTGCCAGTTGTTG 424
Qy 128 spProValSerGlyAnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuH 148
Db 425 ACCAAGATCAAGCAACATCTTTGTACACCTTCACCCCAAGTGCATTTCTCATGTCTCTCA 484
Qy 148 istlePheGlySerLeuLeuProArgProSerPheLeuTyArgThr-IleGlnAspLeu 167
Db 485 AGTGTTTATCACTGAGCTCTT-AAAGCAGATTCATGTCTAAGTCTAATAGAAGAT--- 540
Qy 168 GlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAlaProIleLeuThrAla 187
Db 541 -----TAGCTTCTATGCCAGCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594
Qy 188 LeuAspIlePheValAspArgValSerAlaLeuProValValAsnGluCysGlyGln 207
Db 595 CTGGGCATC-----TCTGTACAGGATCTGCCA---GTGAATGAGGAAGGTGAG 639
Qy 208 ValValGlyLeuTySerArgPhe----- 215
Db 640 GTGGTGAACATCTATTCACATTTGATTTATCTGTCTAAGTCACTTCACTCAGTCACGTCCA 699
Qy 215 ----- 215
Db 700 ACTCTTTGGGATCCTCTGAGCTGTAGCCGTGAGGCTTCTCTGCTGCTGCTGCTGCTGCT 759
Qy 216 -----AspValIleHisLeuAlaAala 222
Db 760 GCAGAACACATAGAGTGGGTTACCATTTCTTCTCAGTGAATGTTATCCATCAGGAGCA 819
Qy 223 GlnGlnThrTyraAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242
Db 820 TAAAGATCTACCAACCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 879
Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGluValIleAspArg 262
Db 880 TACTTTAAATGTAGCTTCAAGTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 939
Qy 263 IleAlaArgGluGlnValHisArgLeuValValAspGluThrGlnHisLeuLeuGly 282
Db 940 CTAGTGAAGAGGAGGAGTCAACGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 999
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 1000 ACTGTATCACCATCTGTCATCTCTGTAGACCTGGTGTCTACA 1041

RESULT 4
US-11-128-061-330
; Sequence 330, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 330
; LENGTH: 568
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; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-061-330

Alignment Scores:
Pred. No.: 2,69e-44 Length: 568
Score: 461.50 Matches: 104
Percent Similarity: 59.32% Conservative: 36
Best Local Similarity: 44.07% Mismatches: 40
Query Match: 29.75% Indels: 57
DB: 8 Gaps: 2

US-10-070-794A-4 (1-305) x US-11-128-061-330 (1-568)
Qy 62 PheileLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 81
Db 3 TTTATCAACATCTCGACCGGATATATAAGTCGCGCTTGGTGACAGATCTATGAACCTGAA 62
Qy 82 GlnHisIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 101
Db 63 GAACACAAAGATAGAACTTGGAGAGGTATACCTACAGGACTCTTTAAGCCCTTGTC 122
Qy 102 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 121
Db 123 TGCATTCTCCAAATGC-CAGATCACTGAG----- 151
Qy 122 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 141
Db 151 ----- 151
Qy 142 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 161
Db 152 -----TTCCCAAGCCGACGAATTCATGCT 175
Qy 162 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 181
Db 176 AAGTCTCTGGAGAGCTACAGATTGGCACCTATGCCAACATTTGCTATGGTCCGTACTACC 235
Qy 182 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 201
Db 236 ACACCTGTCTATGTGCTCTAGGCATCTTTGTACAGCACCGAGTCTCTGCGCTCGCTGTG 295
Qy 202 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle-HisLeuAl 221
Db 296 GTGGATGAG-----AAGAATTGGC 316
Qy 221 aAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgTh 241
Db 317 AGCAGAAAGACCTATAACACCTGGATATATCTGTGACAAAGCTCTACACACCGGTC 376
Qy 241 rLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAs 261
Db 377 TCACCTACTTGGGGGTGTTCTCAAGTGCTATCTACAGGAGACTCTGGAGACTATCATTA 436
Qy 261 pArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLe 281
Db 437 TAGACTGTGGAGACGAGAGGTTCACCGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 496
Qy 281 uGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 497 GGGCATGTATGCTGTCCGATATCTCGAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 542

RESULT 5
US-11-128-061-3972
; Sequence 3972, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
```



Db 497 GGGCATCGTATCGCTGTCCGATATCTCGCAGGCTCTGGTGTCTACA 542

RESULT 6

US-11-128-049-330

Sequence 330, Application US/11128049

Publication No. US20060010513A1

GENERAL INFORMATION:

APPLICANT: Melville, Mark W.

APPLICANT: Charlesbois, Timothy S.

APPLICANT: Mounts, William M.

APPLICANT: Hann, Louane E.

APPLICANT: Sinacore, Martin S.

APPLICANT: Leonard, Mark W.

APPLICANT: Brown, Eugene L.

APPLICANT: Miller, Christopher P.

TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR

FILE REFERENCE: 01997.027700

CURRENT APPLICATION NUMBER: US/11/128,049

CURRENT FILING DATE: 2005-05-11

PRIOR FILING DATE: 2004-05-11

NUMBER OF SEQ ID NOS: 7285

SOFTWARE: PatentIn version 3.3

SEQ ID NO 330

LENGTH: 568

TYPE: DNA

ORGANISM: Cricetulus griseus

US-11-128-049-330

Alignment Scores:

Pred. No.: 2,69e-44 Length: 568

Score: 461.50 Matches: 104

Percent Similarity: 59.32% Conservative: 36

Best Local Similarity: 44.07% Mismatches: 40

Query Match: 29.75% Indels: 57

DB: 8 Gaps: 2

US-10-070-794A-4 (1-305) x US-11-128-049-330 (1-568)

Qy 62 PheileuValLeuHisArgTyrArgSerProLeuValGlnIleTyrGluIleGlu 81

Db 3 TTTATCAACATCTCGCAGGATATCTAAGTCGCGCTTGGTGAGACTATGAAGTGA 62

Qy 82 GlnHisIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 101

Db 63 GAACACAGATAGAACTTGGAGAGGTATACCTACAGACTCTTTAGCCCTTGTCT 122

Qy 102 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 121

Db 123 TGCATTTCTCCAAATGC-CAGATCACTGAG----- 151

Qy 122 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 141

Db 151 ----- 151

Qy 142 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 161

Db 152 -----TTCCCAAGCCAGATTCATGTCT 175

Qy 162 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 181

Db 176 AAGTCTCGGAAGAGCTACAGATTGGCACCTATGCCAACATTTGTATGTCGCTACTACC 235

Qy 182 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 201

Db 236 ACACCTGTCTATGTGGCTTAGGCATCTTTGTACAGACCAGAGTCTCTGCCCTGCTGTG 295

Qy 202 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle-HisLeuAl 221

Db 296 GTGATGAG-----AAAGAAATTTGGC 316

Qy 221 aAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyAlaLeuArgGlnArgTh 241

Db 317 AGCAGAAAGACCTATAACAACTGGATATATCTGTGACAAAAGCTCTACAACACCGGTCTC 376

Qy 241 xLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAs 261

Db 377 TCACTACTTTGAGGGTGTCTCAAGTGTATCTACAGGAGACTCTGGAGACTATCATAA 436

Qy 261 pArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLe 281

Db 437 TAGACTGGTGAAGCAGAGGTTTCAACGCTCTGGTGGTGGATGAGAAACGACGTTGGTCAA 496

Qy 281 uGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296

Db 497 GGGCATCGTATCGCTGTCCGATATCTCGCAGGCTCTGGTGTCTACA 542

RESULT 7

US-11-128-049-3972

Sequence 3972, Application US/11128049

Publication No. US20060010513A1

GENERAL INFORMATION:

APPLICANT: Melville, Mark W.

APPLICANT: Charlesbois, Timothy S.

APPLICANT: Mounts, William M.

APPLICANT: Hann, Louane E.

APPLICANT: Sinacore, Martin S.

APPLICANT: Leonard, Mark W.

APPLICANT: Brown, Eugene L.

APPLICANT: Miller, Christopher P.

TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR

FILE REFERENCE: 01997.027700

CURRENT APPLICATION NUMBER: US/11/128,049

CURRENT FILING DATE: 2005-05-11

PRIOR FILING DATE: 2004-05-11

NUMBER OF SEQ ID NOS: 7285

SOFTWARE: PatentIn version 3.3

SEQ ID NO 3972

LENGTH: 568

TYPE: DNA

ORGANISM: Cricetulus griseus

US-11-128-049-3972

Alignment Scores:

Pred. No.: 2,69e-44 Length: 568

Score: 461.50 Matches: 104

Percent Similarity: 59.32% Conservative: 36

Best Local Similarity: 44.07% Mismatches: 40

Query Match: 29.75% Indels: 57

DB: 8 Gaps: 2

US-10-070-794A-4 (1-305) x US-11-128-049-3972 (1-568)

Qy 62 PheileuValLeuHisArgTyrArgSerProLeuValGlnIleTyrGluIleGlu 81

Db 3 TTTATCAACATCTCGCAGGATATCTAAGTCGCGCTTGGTGAGACTATGAAGTGA 62

Qy 82 GlnHisIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 101

Db 63 GAACACAGATAGAACTTGGAGAGGTATACCTACAGACTCTTTAGCCCTTGTCT 122

Qy 102 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 121

Db 123 TGCATTTCTCCAAATGC-CAGATCACTGAG----- 151

Qy 122 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 141

Db 151 ----- 151

Qy 142 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 161

Db 152 -----TTCCCAAGCCAGATTCATGTCT 175



; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 5005  
; LENGTH: 1494  
; TYPE: DNA  
; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-5005

Alignment Scores:  
Pred. No.: 0.0609 Length: 1494  
Score: 107.50 Matches: 36  
Percent Similarity: 48.91% Conservative: 31  
Best Local Similarity: 26.28% Mismatches: 57  
Query Match: 6.93% Indels: 13  
DB: 7 Gaps: 4

US-10-070-794A-4 (1-305) x US-10-467-657-5005 (1-1494)

Qy 170 GlyThrPheArgAspLeuAlaValLeuGluThrAlaProIleLeuThrAlaLeuAsp 189  
Db 304 GCGTGTGTCAGAACCGGTAACCGTTCGCGGACACGCTCATCCGCGAAGTCTTGGAA 363  
Qy 190 IlePheValAsp-----ArgArgValSerAlaLeuProValValAenGluCysGlyGln 207  
Db 364 ATGCGCGCGAGCGCAACGCAAAATGTCGGCGCTGCGCGTCTGTT---GAAACGCGCAAA 420  
Qy 208 ValValGlyLeuThrSerArgPheAspValIleHisLeuAlaGlnThrThrAsn 227  
Db 421 GTCTGCGGATCGTAACCAACCGGACCTG-----CGTTTGGAAAC 462  
Qy 228 HisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeuCysLeuGluGlyVal 247  
Db 463 CGCGTGTATTTGCGGTTTCGCGCATATGACCCCGCGC-----GAACGTCGT 510  
Qy 248 LeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArgIleAlaArgGluGln 267  
Db 511 GTTACCTCCCGAAGGCACAGCATAGACGCGCGAAGCTGATGCACACGTACAAA 570  
Qy 268 ValHisArgLeuValLeuValAspGluThrGlnHisLeuLeuGlyValValSerLeuSer 287  
Db 571 GTCGACGCGTTTGGTCTGGAAGAAAAGACGAGCTTAAAGCGCTTGATTCATTTAA 630  
Qy 288 AspileLeuGlnAlaLeuValLeuSerProAlaGlyIleAspAlaLeuGly 304  
Db 631 GATATTTTAAACCCAGCGAGTTTCCCAATGCCCAACAAAGACTCCGGAAGGC 681

RESULT 10

US-11-121-086-97/c  
; Sequence 97, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 97  
; LENGTH: 170837  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-11-121-086-97

Alignment Scores:  
Pred. No.: 1.98e+03 Length: 170837  
Score: 95.50 Matches: 68  
Percent Similarity: 38.78% Conservative: 46  
Best Local Similarity: 23.13% Mismatches: 92  
Query Match: 6.16% Indels: 88  
DB: 8 Gaps: 18

US-10-070-794A-4 (1-305) x US-11-121-086-97 (1-170837)

Qy 27 GluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAla-----AlaPro 44  
Db 39144 GAATGGAAAAAATACTTTTAAAGCTCATATGGAACCAAAAAAGAGCCGCATGCCAAG 39085  
Qy 45 LeuTipAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIleLeu 64  
Db 39084 TCATCTCTAGCCCAAAAGAACAAA---GTGGAGGCATCAGCTACCTGACTTCTACTA 39028  
Qy 65 ValLeuHisArgTyrTyrArgSerProLeuValGlnIle-----TyrGluIleGluGln 82  
Db 39027 -----TACTACAAGGCTACAGTAACCAACCAACAGCATGGTACTGTACCAAAAC 38980  
Qy 83 HisLysIleGluThrTrpArgGluIle-----TyrLeuGlnGlyCysPheLys 98  
Db 38979 AGAGATATAGCAACCAATGGAACAGACAGAGCCCTCAGAAAATAATACCAATCTACAAC 38920  
Qy 99 ProLeuValSerIleSerPro-----AsnAspSerLeuPheGlu 111  
Db 38919 TACCTGATCTTTGACAAACCTGACAAAAACAAGAAATGGGAAATGATTCCTTATTAA 38860  
Qy 112 -----AlaValTyrThrLeuIleLysAsnArgIleHisArg 123  
Db 38859 AAATGCTGTGGGAAACTGGCTAGCATATGTACAAAGCTGAA----- 38815  
Qy 124 LeuProValLeuAspProValSerGlyAsnVal-LeuHisIleLeuThrHisLysArgLe 143  
Db 38814 -----CTGGATCCCTTCTTAAACACCTTACACAAATTT-----AATCAAGATG 38770  
Qy 143 uLeuLysPheLeuHisIlePheGlySerLeuLeuProArg---ProSerPheLeuTyrAr 162  
Db 38769 GATTAAGACTTACATGTTAGACTTAAACCATAAACCCCTAGAGAAAACCTAGAGCAA 38710  
Qy 162 gThrIleGlnAspLeuGlyIleGly-----ThrPheArgAspLeuAl 176  
Db 38709 TACCATTCAGACATAGGATGGCAAGGACTTCATGTCTGAAACACCAAAATCAATGGC 38650  
Qy 176 aVal-----ValLeuGluThrAlaProIleLeuThrAlaLe 188  
Db 38649 AACAGAAGCCAAAATTCACAAATGGGATCTAATTAACCTAAAGAGCTTTTGCACAGCAA 38590  
Qy 188 uAspIlePheValAspArgValSerAlaLeuProValValAsnGluCysGlyGlnVa 208  
Db 38589 AGAAACTATGATC-----AGAGTGAACAGGCAACCT-----ACAGAATGGGAGAAAT 38542  
Qy 208 lValGlyLeuTyrSerArgPheAspValIleHisLeuAlaAlaGlnGlnThrTyrAsnHi 228  
Db 38541 TTTTGAATCTACTCATCTGCACAA-----GGGCTAATTCAGAAATCTACAAAGAACTC 38488  
Qy 228 sLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeuCysLeuGlyValLe 248  
Db 38487 AAACACATTTACA-----AGAAAAAAA----- 38466  
Qy 248 uSerCysGlnProHisGluSerLeuGlyGluValIleAsp----- 261  
Db 38465 -----CAACCCCATCAAAAATTTGGCAAGAGATATGAATAGACTTCTCTCAAAAGAAG 38413  
Qy 262 -ArgIleAlaArgGluGlnValHisArgLeuValLeuVal 274  
Db 38412 ACATTATGCGCCACACACATCATGAAAAAATGCTCATC 38373

RESULT 11

```

US-10-793-626-4134/c
; Sequence 4134, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4134
; LENGTH: 3061
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4134

Alignment Scores:
Pred. No.: 13.8 Length: 3061
Score: 91.50 Matches: 52
Percent Similarity: 41.08% Conservative: 24
Best Local Similarity: 28.11% Mismatches: 70
Query Match: 5.90% Indels: 40
DB: 7 Gaps: 10

US-10-070-794A-4 (1-305) x US-10-793-626-4134 (1-3061)
Qy 61 AspPheLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 2401 AATCTCAATTTGGTAATCCATCGTCAATAC-----ATTCTATGGTAGAGATG 2354
Qy 81 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 2353 CACGCAATAT-CTTGATCACTGTCGTCGTACAGTTGACAA-----TTG 2310
Qy 101 ValSerIleSerProAsnAspSerLeuPhe-----GluAlaValIleThr 115
Db 2309 TTGGAGCGAATCCGATGAAGTAATATTACAGTGTGTCACAGATCGAATAACACT 2250
Qy 116 LeuLeuLysAsnArgIleHisArgLeuProValLeuAspProValSerGlyAsnValLeu 135
Db 2249 GCTATTAAAGGATTAGTGAAGCGGAATGAACAATTA-----GGTAAT- 2208
Qy 136 HisIleLeuThrHisLys--ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeu 154
Db 2207 CATATTATTACTACCAAAATTTGAACACCATTCAGTATTACACGTATATGACAACTTGA 2148
Qy 155 ProArgPro--SerPheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArg 173
Db 2147 AAAGAAGGTTATGATCTTACGTATCTAGATGATAGTATGCTGGTGA-----GTT 2097
Qy 174 AspLeuAlaValLeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAsp 193
Db 2096 GATTTAGACCAATTAAGAAACAAATTAATGATAGAACAAATTTTA----- 2052
Qy 194 ArgArgValSerAlaLeuProValValAsnGluCysGlyGlnValValGlyLeuTyrSer 213
Db 2051 -----GTATCAATATTATGTTGTAATAATAGATTTGGAACAGTACAAAATTTATGAT 1998
Qy 214 ArgPheAspValIle-----HisLeuAlaAlaGlnGlnThrTyr 226
Db 1997 ATTGAAGATATTATTGGAGACACTCATCGTTATTCCATGTTGATGCTGTTCAACCAATT 1938
Qy 227 AsnHisLeuAspMet 231
Db 1937 GCACATTTTAGATTTA 1923

, RESULT 12

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US-10-793-626-2307
; Sequence 2307, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2307
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-2307

Alignment Scores:
Pred. No.: 7.84 Length: 1467
Score: 89.50 Matches: 71
Percent Similarity: 40.75% Conservative: 59
Best Local Similarity: 22.26% Mismatches: 122
Query Match: 5.77% Indels: 67
DB: 7 Gaps: 15

US-10-070-794A-4 (1-305) x US-10-793-626-2307 (1-1467)
Qy 22 PheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyValArg 41
Db 37 TTCAGCAGCTGTACTCATCTCCAGCTGCATCAGATGTTTACCACGCGATTTGACTTA 96
Qy 42 AlaAlaProLeuTyrAspSerLysLysGlnSerPhe-----ValGlyMetLeu 57
Db 97 AGTGTCAAATATCAGATAGATCAAGTTAAACATTCCTGTTATCTCAGCAGGTATGGAT 156
Qy 58 ThrIleThrAspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIle 77
Db 157 ACAGTAACCTGAATCAAAATGGCAATTGCTATGCTCGACAAAGCGGTTTAGGTGTTATT 216
Qy 78 TyrGlu-----IleGluGlnHisLysIleGluThrTyrArg--GluIleTyrLeu 93
Db 217 CATAGAATATGGCGTCGAAGACGAGCTGATGAGTACAAAGGTTTAAACGTTTCAGAA 276
Qy 94 GlnGlyCysPheLysProLeuValSerIleSerProAsnAspSerLeuPheGluAlaVal 113
Db 277 AATGTTGTTATTTCTAACCCGTTCTTTTACACCGGAGAAAGTGTGTATGAGGCTGAA 336
Qy 114 TyrThrLeuLysAsnArgIleHisArgLeuProValLeuAsp--ProValSerGly 132
Db 337 GCATTAAATGGTAAATACCGTATCTCTGCTGATCCCATTTGCGATAATCAAGAGGATCGC 396
Qy 133 AsnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuHisIlePheGlySer 152
Db 397 AAGTTGATTGGGATTTTAAACAANTCGTGATTAA----- 429
Qy 153 LeuLeuProArgProSerPheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPhe 172
Db 430 -----CGTTTTATTGAAGATTTTCAATT---AAAATA 459
Qy 173 ArgAspLeuAlaValVal-----LeuGluThrAlaProIleLeuThrAlaLeuAsp--- 189
Db 460 TCAGATGAATGACGAAAGATAAATTTAATAACAGCTCCAGTTGGTACGACTTTAGATGAA 519
Qy 190 -----IlePheValAspArgValSerAlaLeuProValValAsnGlyCysGly 206
Db 520 GCCGAGGCTATTCTTCAAAAACATAAGATTGAGAAACTTCCATTAGTA---GAAATGGT 576
Qy 207 GlnValValGlyLeuTyrSerArgPheAspVal-----IleHisLeuAla 221

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Db 577 GGTITAGAGGATTAATCACTATTAAAGATATTGAAAAAGTACTTGTAATCCCATATGCA 636  
 Qy 222 AlaGlnGlnThrTyAsnHisLeu-  
 Db 637 GCTAAGATGACATGCGAGATCTTACTAGCTGCGCAGCAATCGTACGTCTAAGATACT 696  
 Qy 236 AlaLeuArgGlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSer 255  
 Db 697 GAAATTCGTGCACAAAACTAGTTGAAGCTGGCGTA-  
 Qy 256 LeuGlyGluValIleAspArgIleAlaArgGluGlnValHisArgLeuValLeuValAsp 275  
 Db 739 TTA-  
 Qy 276 GluThrGlnHisLeu-  
 Db 784 CAACTTAACACATCAAGAAACATATCCTGAATTAATCTGTCGCTGCTAAGCTAGCG 843  
 Qy 286 LeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAspAlaLeuGly 304  
 Db 844 ACTGCAGAGGCAACACGCTGCTTTATTTGAAGCGGTCGCGATGTTGTTAAAGTAGGT 900

## RESULT 13

US-10-793-626-4242  
 ; Sequence 4242, Application US/10793626  
 ; Publication No. US20050255478A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMMERLY, WILLIAM JOHN  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 ; FILE REFERENCE: PU3480US  
 ; CURRENT APPLICATION NUMBER: US/10/793,626  
 ; PRIOR FILING DATE: 2004-03-04  
 ; PRIOR APPLICATION NUMBER: 60/164,258  
 ; PRIOR FILING DATE: 1999-11-09  
 ; NUMBER OF SEQ ID NOS: 4472  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 4242  
 ; LENGTH: 2980  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: nucleic acid sequence  
 US-10-793-626-4242

Alignment Scores:  
 Pred. No.: 22.8 Length: 2980  
 Score: 89.50 Matches: 71  
 Percent Similarity: 40.75% Conservative: 59  
 Best Local Similarity: 22.26% Mismatches: 122  
 Query Match: 5.77% Indels: 67  
 DB: 7 Gaps: 15

## US-10-070-794A-4 (1-305) x US-10-793-626-4242 (1-2980)

Qy 22 PheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyValArg 41  
 Db 653 TTCGACGACGTGTACTCATTCACGCTGCATCAGATGTTTACCAGCGATGTGACTTA 712  
 Qy 42 AlaAlaProLeuTrpAspSerLysLysGlnSerPhe-  
 Db 713 AGTGCAAAATTCAGATAAGATCAAGTTAAACATTCCTGTTATCTCAGCAGGTATGGAT 772  
 Qy 58 ThrIleThrAspPheIleLeuValLeuHisArgTyTyArgSerProLeuValGlnIle 77  
 Db 773 ACAGTAACCTGAATCAAAATGGCAATTCGATGCTCGACAGCGGTGTAGGTGTTATT 832  
 Qy 78 TyrGlu-  
 Db 833 CATAGAATATGGCGCTCGAAGACAGCTGATGAGGTACAAAAGGTAAACGTTACAGAA 892  
 Qy 94 GlnGlyCysPheLysProLeuValSerIleSerProAsnAspSerLeuPheGluAlaVal 113

Db 893 AATGGTGTATTATTCTTAACCCGTTCTTCTTAACCCGGAAGAAAGTGTGTATGAGGCTGAA 952  
 Qy 114 TyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuAsp-  
 Db 953 GCATTAAATGGGTAAATACCGTATCTCTGGGTATCCCATTCGATTCGATANTCAAGAGGATCGC 1012  
 Qy 133 AsnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuHisIlePheGlySer 152  
 Db 1013 AAGTTGATTGGGATTTTAACAAAATCGTGATTTA-  
 Qy 153 LeuLeuProArgProSerPheLeuTyArgThrIleGlnAspLeuGlyIleGlyThrPhe 172  
 Db 1046 -  
 Qy 173 ArgAspLeuAlaValVal-  
 Db 1076 TCAGATGTAATGACGAAGAAGATAATTAATCAACAGCTCCAGTTGGTAGACTTTAGATGAA 1135  
 Qy 190 -  
 Db 1136 GCCGAGGCTATTCTCAAAAACATAAGATTGAGAAACTTCCATTAGTA-  
 Qy 207 GlnValValGlyLeuTySerArgPheAspVal-  
 Db 1193 CGTTTGAAGGATTAATCACTATTAAAGATATTGAAAAAGTACTTGAATTCCTCATATGCA 1252  
 Qy 222 AlaGlnGlnThrTyAsnHisLeu-  
 Db 1253 GCTAAGATGAACATGCGCAGATGTTAGCTGCGCAGCAATCGTACGTCTTAAGATACT 1312  
 Qy 236 AlaLeuArgGlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSer 255  
 Db 1313 GAAATTCGTGCACAAAACTAGTTGAAGCTGGCGTA-  
 Qy 256 LeuGlyGluValIleAspArgIleAlaArgGluGlnValHisArgLeuValLeuValAsp 275  
 Db 1355 TTA-  
 Qy 276 GluThrGlnHisLeu-  
 Db 1400 CAAGTTAAACACATCAAGGAAACATATCTCGAAATTAATCTGTCGCTGCTAAGCTAGCG 1459  
 Qy 286 LeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAspAlaLeuGly 304  
 Db 1460 ACTGCAGAGGCAACACGCTGCTTTATTTGAAGCGGTCGCGATGTTGTTAAAGTAGGT 1516

## RESULT 14

US-10-793-626-4013  
 ; Sequence 4013, Application US/10793626  
 ; Publication No. US20050255478A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMMERLY, WILLIAM JOHN  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 ; FILE REFERENCE: PU3480US  
 ; CURRENT APPLICATION NUMBER: US/10/793,626  
 ; CURRENT FILING DATE: 2004-03-04  
 ; PRIOR APPLICATION NUMBER: 60/164,258  
 ; PRIOR FILING DATE: 1999-11-09  
 ; NUMBER OF SEQ ID NOS: 4472  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 4013  
 ; LENGTH: 3840  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: nucleic acid sequence  
 US-10-793-626-4013

Alignment Scores: 33.3 Length: 3840  
 Pred. No.: 89.50 Matches: 71  
 Score:

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Percent Similarity: 40.75%      Conservative: 59
Best Local Similarity: 22.26%   Mismatches: 122
Query Match: 5.77%             Indels: 67
DB: 7                           Gaps: 15

US-10-070-794A-4 (1-305) x US-10-793-626-4013 (1-3840)

Qy 22 PhaAspThrMetLeuGluLeuLysLysAlaPheAlaLeuValAlaAsnGlyValArg 41
Db 1501 TTCAGCAGCGTGTACTCAITTCAGCTGCATCAGATGTTTTTACCAGCGATGTTGACTTA 1560
Qy 42 AlaAlaProLeuTrpAspSerLysLysGlnSerPhe-----ValGlyMetLeu 57
Db 1561 AGTGCTCAAAATTCAGATAGATCAAGTTAAATTCCTGCTGCAGCAAGCGGTTTGGTGTATT 1620
Qy 58 ThrIleThrAspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIle 77
Db 1621 ACAGTAAGTCAAAATGCAATGCTATGCTGCAGCAAGCGGTTTGGTGTATT 1680
Qy 78 TyrGlu-----IleGluGlnHisLysLysIleGluThrTrpArg---GluIleTyrLeu 93
Db 1681 CATAAAGATATGGCGTCGAGAGCAAGCTGATGAGGTACAAAGGTTTAAACGTTTCAGAA 1740
Qy 94 GlnGlyCysPheLysProLeuValSerIleSerProAsnAspSerLeuPheGluAlaVal 113
Db 1741 AATGGTGTATTCTTCAACCGCTTCTTTACACCGGAGAAAGTGTGTATGAGGCTGAA 1800
Qy 114 TyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuAsp---ProValSerGly 132
Db 1801 GCATTAAATGGTAAATACCGTATCTCTGGTGTACCCATTCGATGATCAAGAGGATCGC 1860
Qy 133 AsnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuHisIlePheGlySer 152
Db 1861 AAGTTGATGGATTTTAAACAAATCGTGAATTA-----1893
Qy 153 LeuLeuProArgProSerPheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPhe 172
Db 1894 -----CGTTTATTTGAAGATTTTTCATTT-----AAATA 1923
Qy 173 ArgAspLeuAlaValVal-----LeuGluThrAlaProIleLeuThrAlaLeuAsp---189
Db 1924 TCAGATGTAATGACGAAAGATAATTTAATAACAGCTCCAGTTCGATGATGATGAA 1983
Qy 190 -----IlePheValAspArgValSerAlaLeuProValValAsnGlyCysGly 206
Db 1984 GCCGAGGCTATTCTTCAAAAAACATAAGATTCAGAAACTTCCATTAGTA--GAAATAGGT 2040
Qy 207 GlnValValGlyLeuTyrSerArgPheAspVal-----IleHisLeuAla 221
Db 2041 CGTTTAGAAGATTAATCACTATTAAAGATTTGAAAAGTACTTGAATTCCTCATATGCA 2100
Qy 222 AlaGlnGlnThrTyrAsnHisLeu-----AspMetSerValGlyGlu 235
Db 2101 GCTAAAGATGAACATGGCAGATTGTTAGCTGCGGCAGCAATCGGTACGCTTAAAGATACT 2160
Qy 236 AlaLeuArgGlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSer 255
Db 2161 GAAATTCGTGCACAAAAACTAGTTGAAGCTGGCGTA-----GATGCA 2202
Qy 256 LeuGlyGluValIleAspArgIleAlaArgGluGlnValHisArgLeuValLeuValAsp 275
Db 2203 TTA-----ATTATTGAT-----ACAGCTCATGTGTCATCTTAAAGGCGTTATTAT 2247
Qy 276 GluThrGlnHisLeu-----LeuGlyValValSer 285
Db 2248 CAAGTTAAACACATCAAGGAAACATATCTCTGAAATTAATCTGTTGTCGCTGTTAAACGTAGC 2307
Qy 286 LeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAspAlaLeuGly 304
Db 2308 ACTGCAGAGGCAACACGTGCTTTTATTGAAGCGGTGCGGATGTTGTTTAAAGTAGGT 2364

RESULT 15
US-11-156-953-6/C

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```

; Sequence 6, Application US/11156953
; Publication NO. US20060003051A1
; GENERAL INFORMATION:
; APPLICANT: Cleary, Joseph
; APPLICANT: Coleman, Russell
; APPLICANT: Harding, Nancy
; APPLICANT: Patel, Yamin
; TITLE OF INVENTION: GENETICALLY PURIFIED GELLAN GUM
; FILE REFERENCE: G12047.00029
; CURRENT APPLICATION NUMBER: US/11/156,953
; CURRENT FILING DATE: 2005-06-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2862
; TYPE: DNA
; ORGANISM: Sphingomonas elodea
US-11-156-953-6

Alignment Scores: 42.2      Length: 2862
Pred. No.: 37.00      Matches: 70
Score: 37.94%      Conservative: 37
Percent Similarity: 24.82%      Mismatches: 99
Best Local Similarity: 5.61%      Indels: 77
Query Match: 8      Gaps: 14
DB:

US-10-070-794A-4 (1-305) x US-11-156-953-6 (1-2862)
Qy 55 GlyMetLeuThrIleThrAspPheIleLeuValLeuHisArgTyrTyrArgSerProLeu 74
Db 1607 GGCCTGGACAGTCATCTAGACTTCTCCCTGCTTCCTCCGG-----GAAACCCCGAG 1557
Qy 75 ValGlnIleTyrGluIleGluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGln 94
Db 1556 CCCGATGTCATTGTAGAACCGGAGATGGACTTACAACTGCTGTATGAT-----CAA 1506
Qy 95 GlyCysPheLysProLeuValSerIleSerProAsnAspSerLeuPheGluAlaValTyr 114
Db 1505 TCCTGTCCATCGGCTTTGGCCAGATAGTCTGCGACATG-CATCTCGAGAGCGG-----1453
Qy 115 ThrLeuIleLysAsnArgIleHisArgLeuProValLeuAspProValSer-----131
Db 1452 -----CGACACGGTGCCTCGAACTCGAACTCGAACTCGGCTCGCTCTCGTA 1408
Qy 132 -----GlyAsnValLeuHisIleLeuThrHisLysArg 142
Db 1407 GAGATGTTCCGGTTCGGCATTTGGCGCGCGGAGCAGCTTCACCTTGCTCGTAGAGCGC 1348
Qy 143 LeuLeuLysPheLeuHisIlePheGlySerLeuLeuPro---ArgProSerPheLeuTyr 161
Db 1347 GTCGACCCAG---CGTGAGAACCGGCGGCTCGCTCCGATTTTCCGCTCCAGCTTTGG 1291
Qy 162 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 181
Db 1290 GATCCGACACAGGATCAGGTATGAAAGCGCGGTGCGATGCGGAGATAGTCCGCGCAC 1231
Qy 182 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 201
Db 1230 CCG-----CGCTTCGCGCGCACGCGCTT 1207
Qy 202 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle-----218
Db 1206 GAACGAGAAAGCGGCGGCGCCCTTCAGCATTTCCGACACAGGATCTCGCGCGCCCGG 1147
Qy 219 -----HisLeuAlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAla 236
Db 1146 GATCGGACACCTGGCAGGACGCGCACGCGGCGGCTCTCTCGACCGGATAGTCCGTGAGGCG 1087
Qy 237 LeuArgGlnArgThrLeuCysLeuGluGly-----246
Db 1086 GAAAGAGCCCGCGA-----GAGGGTGGCGGTGCTTCGGGCCCGGCTTCGGCACAG 1036

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Qy 247 -----ValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg---Ile 263
Db 1035 CCACGTGTGTACGTGCCCCAGCCG-----GTCGCGCGCATAGTCGACCGGCGCGTT 985
Qy 264 AlaArgGluGlnValHisArgLeuVal---LeuValAspGluThrGlnHisLeuLeuGly 282
Db 984 GAGCGCGAGCACGTCCATCTTCTCCCGCATCAGGTCGATGAGGGCAG----- 937
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAspAla 302
Db 936 -----GAACAGCTGGCGGTTGAGCCCGTCCTTGTAGAGATC 901
Qy 303 LeuGly 304
Db 900 CTTGGG 895

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Search completed: January 26, 2006, 08:30:07  
Job time : 767.948 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 25, 2006, 21:43:01 ; Search time 4086.76 Seconds  
(without alignments)  
4242.296 Million cell updates/sec

Title: US-10-070-794A-4

Perfect score: 1551

Sequence: 1 MRFMBHTCYDAMATSSKLV.....LSDILQALVLSPIGADALGA 305

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*  
1: gb.ba.\*  
2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1551	100.0	1470	6 AX814738	AX814738 Sequence
2	1551	100.0	1597	8 BC098255	BC098255 Homo sapi
3	1551	100.0	1597	8 BC098277	BC098277 Homo sapi

4	1551	100.0	1597	8	BC098306	BC098306 Homo sapi
5	1551	100.0	1599	8	BC098102	BC098102 Homo sapi
6	1551	100.0	1647	6	AX281582	AX281582 Sequence
7	1551	100.0	2109	6	AX099776	AX099776 Sequence
8	1551	100.0	2115	6	AX099802	AX099802 Sequence
9	1551	100.0	2115	8	AF214519	AF214519 Homo sapi
10	1525	98.3	2290	8	HS249977	HS249977 Homo sapi
11	1507	97.2	1867	6	AX099774	AX099774 Sequence
12	1507	97.2	1873	6	AX099800	AX099800 Sequence
13	1507	97.2	1873	6	AX398331	AX398331 Sequence
14	1507	97.2	1873	6	AX398333	AX398333 Sequence
15	1507	97.2	1873	6	AX398335	AX398335 Sequence
16	1507	97.2	2022	6	AX099804	AX099804 Sequence
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19	1506	97.1	1873	6	AX398337	AX398337 Sequence
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24	1376	88.7	1322	4	AY376689	AY376689 Equus cab
25	1275	82.2	1570	6	CQ714782	CQ714782 Sequence
26	1250	80.6	1777	5	DQ079815	DQ079815 Gallus ga
27	1250	80.6	1788	5	DQ079814	DQ079814 Gallus ga
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29	1184	76.3	2679	5	CT025503	CT025503 xenopus t
30	1068	68.9	2192	9	AY348864	AY348864 Mus muscu
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32	1068	68.9	2484	9	BC097267	BC097267 Rattus no
33	1067	68.8	3132	9	BC015283	BC015283 Mus muscu
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ALIGNMENTS

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DEFINITION	AX814738	Sequence 1 from Patent WO03063586.				
ACCESSION	AX814738	Sequence 1 from Patent WO03063586.				
VERSION	AX814738.1	GI:39103937				
KEYWORDS						
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
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		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
		Hominidae; Homo.				
REFERENCE	1	Andersson, L. and Marklund, S.				
AUTHORS		Transgenic animals expressing prkag3				
TITLE		Patent: WO 03063586-A 1 07-AUG-2003;				
JOURNAL		Arexis AB (SE)				
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CDS						



Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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 GSLLPSPFLYRTIDQIGICTFDLAVLETAPLTALDIFVDRVRSALPVNCEGQV  
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#### gene

#### CDS

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Qy	141	LyArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160
Db	992	AAAGCGCTGCTCAAGTTCTTGTGCACTCTTTGGTTCCTGCTGCCCGGCGCTCTTCTCTC	1051
Qy	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu	180
Db	1052	TACCGCACTATCAAGATTGGGCATCGGCACATCCGAGACTTGGCTGTGGTGTGGAG	1111
Qy	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	200
Db	1112	ACAGCACCCATCTGACTGCACTGGACATCTTTGTGACCGCGCTGTGTCTGCACTGCT	1171
Qy	201	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	220
Db	1172	GTGGTCAACGAATGTGGTCAAGTGTGGGCTCTTATTCCTGCTTTGAATGATTCACCTG	1231
Qy	221	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	240
Db	1232	GCTGCCAGCAACCTACAACACCTGGACATGAGTGTGGAGAGCCCTGAGCAGAGG	1291
Qy	241	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle	260
Db	1292	ACACTATGCTGGAGGAGTCTCTTCTGTCAGCCGCCACGAGAGCTTGGGGAGTATC	1351
Qy	261	AspArgIleAlaArgGlnGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	280
Db	1352	GACAGATTGCTCGGAGCAGGTACACAGGCTGGTGTAGTGGACGAGACCCAGCATCTC	1411
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Qy	301	AspAlaLeuGlyAla	305
Db	1472	GATGCCCTCGGGGCC	1486

#### RESULT 3

#### BC098277

#### LOCUS

#### DEFINITION

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

1597 bp mRNA linear PRI 02-JUL-2005  
 Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic  
 subunit, mRNA (cdna clone MGC:119344 IMAGE:40005886), complete cds.

BC098277

BC098277.1 GI:67514270

MGC.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

1 (bases 1 to 1597)

Klausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Altshuler, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahney, J., Hellon, E., Kettman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,

Schmurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

#### CONSTRM

Mammalian Gene Collection Program Team

#### ORIGIN

#### Alignment Scores:

Pred. No.: 1.81e-131 Length: 1597  
 Score: 1551.00 Matches: 305  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-070-794A-4 (1-305) x BC098255 (1-1597)

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Qy	41	ArgAlaAlaProLeuTyrPheSerLysLysGlnSerPheValGlyMetLeuThrIleThr	60
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Qy	61	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	80
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## RESULT 5

LOCUS BC098102 1599 bp mRNA linear PRI 23-JUN-2005  
 DEFINITION Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit, mRNA (CDNA clone MGC:119342 IMAGE:40005880), complete cds.

ACCESSION BC098102

VERSION BC098102.1 GI:66990059

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1599)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.I., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Mammalian Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1599)

JOURNAL PUBMED

NIH MGC Project

Direct Submission

Submitted (03-JUN-2005) National Institutes of Health, Mammalian

Gene Collection (MGC), Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgs.nci.nih.gov>

Contact: MGC help desk

Email: [c9apbs-remail.nih.gov](mailto:c9apbs-remail.nih.gov)

Tissue Procurement: Baylor Human Genome Sequencing Center

cDNA Library Preparation: Baylor Human Genome Sequencing Center

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),  
 Gaithersburg, Maryland:  
 Web site: <http://www.nisc.nih.gov/>

Contact: nisc\_mgc@nigri.nih.gov  
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
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 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
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 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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## CDS

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## ORIGIN

Alignment Scores:  
 Pred. No.: 1.81e-131 Length: 1599  
 Score: 1551.00 Matches: 305  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-070-794A-4 (1-305) x BC098102 (1-1599)

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Db 812 GAACAACATAAGATTGAGACTGGAGGAGATCTACTGTCGACAGCTGCTTCAAGCTCTG 871
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Db 872 GTCTCCATCTCTCTAATGATAGCTGTTTGAAGCTGTACACCTCATCAAGAACCGG 931
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisLysLeuThrHis 140
Db 932 ATCCATCGCTGCTGCTGTTTGAACCGGTGTGAGCAACGTACTCCATCTCTCACAC 991
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 992 AAACGCTGCTCAAGTTCCTGCACATCTTGTGTTCCCTGCTGCCCGGCTCTCTCTC 1051
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
Db 1052 TACCGCATATCCAAAGATTGGGCAATCGGCACATTCGACACTTGGCTGTGGTCTGAG 1111
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
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Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
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Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1232 GCTGCCAGCAACCTACACCACTGACATGATGATGTGGAGAACCTGAGGACAGG 1291
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1292 ACATATGTCTGGAGGAGTCTTTCTTCTGCGAGCCCTTTCAGGAGCTTGGGGGAGT 1351
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
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Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1412 TTGGCGTGTCTCCCTCTCGACATCTTCAGGCACTTGTGGTCTCAGCCCTGCTGGCATC 1471
Qy 301 AspAlaLeuGlyAla 305
Db 1472 GATGCCCTCGGGCC 1486

RESULT 6
AX281582 LOCUS AX281582 1647 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 5 from Patent WO0177305.
ACCESSION AX281582
VERSION AX281582.1 GI:16608833
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini,
Hominidae; Homo.
1
REFERENCE
AUTHORS Andersson, L., Luthman, H. and Marklund, S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit.
JOURNAL Patent: WO 0177305-A 5 18-OCT-2001;
Arexix AB (SE)
FEATURES
source
location/Qualifiers
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## ORIGIN

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Alignment Scores:
Pred. No.: 1.88e-131 Length: 1647
Score: 1551.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-070-794A-4 (1-305) x AX281582 (1-1647)
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Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 632 ATCTTGACACCATGCTGGAGATCAAGAAGCGCTTCTTCTGCTGGCGCAACGGTGTG 691
Qy 41 ArgAlaAlaProLeuThrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 692 CGGCGACGCCCTCTATGGGACAGCAAGACAGAGCTTTTGTGGGATGTGACCATCACT 751
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 752 GACTTCATCTCGGTGCTGCACTGCTACTACAGTCCCTCCCTGGTCCAGATCTATGAGATT 811
Qy 81 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 812 GAACAACATAAGATTGAGACTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCTCTG 871
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 872 GTCTCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGG 931
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisLysLeuThrHis 140
Db 932 ATCCATCGCTGCTGCTGTTTGAACCGGTGTGAGCAACGTACTCCATCTCTCACAC 991
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 992 AAACGCTGCTCAAGTTCCTGCACATCTTGTGTTCCCTGCTGCCCGGCTCTCTCTC 1051
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
Db 1052 TACCGCATATCCAAAGATTGGGCAATTCGACACTTGGCTGTGGTCTGAG 1111
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1112 ACAGCACCATCTCTGACTGCACTGAGCATCTTTGTGACCGGTGTGTCTGCACTGCT 1171
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1172 GTGGTCAACGATGTGTGAGTCTGAGTCTGAGGCTCTATTCCCGCTTTGATGATTCAC 1231
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240

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Db      1292  AACTATGTCTGGAGGAGTCTTTCTCTGTCAGCCACAGAGCTTGGGGAGAGTGATC 1351
Qy      261   AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db      1352  GACAGGATTCCTGGGAGCAGGTACACAGGCTGGTGTAGTGACAGAGACCCAGCATCTC 1411
Qy      281   LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db      1412  TTGGCGTGTCTCTCTCTCGACATCTTCAGGCACTGTGTCTCAGCCCTGTGTGGATC 1471
Qy      301   AspAlaLeuGlyAla 305
Db      1472  GATGCCCTCGGGGCC 1486

RESULT 7
AX099776
LOCUS      AX099776      2109 bp      DNA      linear      PAT 02-APR-2001
DEFINITION Sequence 3 from Patent WO0120003.
ACCESSION AX099776
VERSION    AX099776.1 GI:13538810
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS    Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
            Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
            Chardon,P.
TITLE      Variants of the gamma chain of ampk, dna sequences encoding the
            same, and uses thereof
JOURNAL    Patent: WO 0120003-A 3 22-MAR-2001;
            INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
            Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
FEATURES    Location/Qualifiers
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CDS
Alignment Scores:
Pred. No.:      2,53e-131      Length:      2109
Score:          1551.00      Matches:      305
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels: 0
DB:              6      Gaps: 0

US-10-070-794A-4 (1-305) x AX099776 (1-2109)

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Db      592  CGGGCAGCCCTCTAT7GGGACAGCAAGAAGCAGAGCTTTGTGGGATGCTGACATCACT 651
Qy      61   AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db      652  GACTTCATCTGTGTGTGTCATCGCTACTACAGTCCCCCTGTCCTCAGATCTATGAGATT 711
Qy      81   GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db      712  GAACAACAATAAGATTGAGACCTGGAGGAGATCTAGCTGCAAGGCTGCTTCAAGCCCTCTG 771
Qy      101  ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db      772  GTCTCCATCTCTCTAATGATAGCCCTGTTTGAAGCTGTGTACACCCCTCATCAAGAACCGG 831
Qy      121  IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db      832  ATCCATCGCCTGCTGCTGTTCTTGACCCGGTGTGAGGCAACGTACTCCACATCTCCACAC 891
Qy      141  LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db      892  AAAGCGCTGCTCAAGTTCCTGTCACATCTTTGGTTCCTGCTGCCCGCGCTCTCTCTCTC 951
Qy      161  TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
Db      952  TACCGCATCTATCCAAGATTGGGCGATCGGCACATTCGAGACTTGGCTGTGGTGTGGAG 1011
Qy      181  ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
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Qy      221  AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
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Qy      261  AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
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Qy      281  LeuGlyValValSerLeuSerAspIleGlnAlaLeuValLeuSerProAlaGlyIle 300
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Qy      301  AspAlaLeuGlyAla 305
Db      1372  GATGCCCTCGGGGCC 1386

RESULT 8
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LOCUS      AX099802      2115 bp      DNA      linear      PAT 02-APR-2001
DEFINITION Sequence 29 from Patent WO0120003.
ACCESSION AX099802
VERSION    AX099802.1 GI:13538836
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS    Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
            Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and

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## ORIGIN

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Pred. No.: 2,54e-131 Length: 2115  
Score: 1551.00 Matches: 305  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-10-070-794A-4 (1-305) x AF214519 (1-2115)

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Db	538	ATCTTCGACACCATGCTGAGATCAAGAAGCCCTCTTTGCTCTGTTGGCCCAACGGGTG	597
Qy	41	ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	60
Db	598	CGGCGAGCCCTCATGCGACAGCAAGAACAGAGCTTTGTGGGGATGCTGCACCATCACT	657
Qy	61	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	80
Db	658	GACTTCATCTGGGTGCTCATCGCTACTACAGGTCCGCCCTGGTCCAGATCTATGAGATT	717
Qy	81	GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	718	GAACAACATAGATTGACCTCGAGGGGAGATCTACCTGCAAGCTGCTTCAAGCCCTG	777
Qy	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120
Db	778	GTCCTCATCTCTCTAATAGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGG	837
Qy	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleIleThrHis	140
Db	838	ATCCATCGCCCTGCCCTGTTCTTGACCCGGTGTGAGCAACGACTCCATCTCACACAC	897
Qy	141	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160
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Qy	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	180
Db	958	TACCGCATATCCAGATTGCGGCATCGGCATCCGACATTCGAGACTTGGCTGTGTGTGGAG	1017
Qy	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgAtqValSerAlaLeuPro	200
Db	1018	ACAGACCCATCTCTGACGTGACATGACATCTTTGTGGACCGCGGTGTCTGCACCTGCT	1077
Qy	201	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	220
Db	1078	GTGGTCAACGAATGGTTCAGTCTGGGCTCTATTCCGCTTTGATGTGATTCACCTG	1137
Qy	221	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	240
Db	1138	GCTGCCACGCAACACCTACAACACCTGACATGAGTGTGGGAGAACGCCCTGAGGCAGAGG	1197
Qy	241	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle	260

Db	1198	ACACTATGTCGGAGGAGTCTTTTCTCTGCGACGCCACGAGAGCTTGGGGAGTGCATC	1257
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Db	1258	GACAGGATTCTCGGGAGCAGGTACACAGGCTGTGTAGTGGACGAGACCCAGCATCTC	1317
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Db	1318	TTGGCGCTGTGTCTCCCTCTCCGACATCTTCAGGACCTGGTGCTCAGCCCTGCTGGCATC	1377
Qy	301	AspAlaLeuGlyAla	305
Db	1378	GATGCCCTCGGGGCC	1392

## RESULT 10

HSA249977

## LOCUS

HSA249977

## DEFINITION

Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit

(AMPK gamma 3 gene).

## ACCESSION

AJ249977.1

GI:6688200

## KEYWORDS

AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

## REFERENCE

1

Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D.

Characterization of AMP-activated protein kinase gamma-subunit

isoforms and their role in AMP binding

Biochem. J. 346 Pt 3, 659-669 (2000)

## JOURNAL

PUBMED

10698692

## REFERENCE

2 (bases 1 to 2290)

Carling, D.

## AUTHORS

Direct Submission

Submitted (12-OCT-1999)

Carling D., Cellular Stress Group, MRC

Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,

London, W12 0NN, UNITED KINGDOM

## FEATURES

Location/Qualifiers

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## ORIGIN

## Alignment Scores:

Pred. No.: 6,53e-129 Length: 2290  
Score: 1525.00 Matches: 299  
Percent Similarity: 99.34% Conservativity: 3  
Best Local Similarity: 98.36% Mismatches: 2

Query Match: 98.32% Indels: 0  
DB: 8 Gaps: 0  
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QY 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
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DB 1354 GACAGGATGCTCGGAGGAGGTACACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1413  
QY 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
DB 1414 TTGGGCTGTGCTCTCTCTCTCGACATCTTCAGGCTGTGTGTGTGTGTGTGTGTGTGTG 1473  
QY 301 AspAlaLeuGly 304  
DB 1474 GATCCCTCGGG 1485

RESULT 11  
AX099774  
LOCUS  
DEFINITION Sequence 1 from Patent WO0120003.

AX099774  
AX099774.1 GI:13538808  
Sus scrofa (pig)  
Sus scrofa  
Sus scrofa  
Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof  
Patent: WO 0120003-A 1 22-MAR-2001;  
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;  
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)  
location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Alignment Scores:  
Pred. No.: 2,22e-127 Length: 1867  
Score: 1507.00 Matches: 296  
Percent Similarity: 98.36% Conservative: 4  
Best Local Similarity: 97.05% Mismatches: 5  
Query Match: 97.16% Indels: 0  
DB: 6 Gaps: 0  
US-10-070-794A-4 (1-305) x AX099774 (1-1867)

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DB 532 ATCTTCGACACCATGCTGGAGATCAGAGAGCCCTCTTTGCCCTGTGGTGGCCAGCGGTC 591  
QY 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
DB 592 CGAGCGGACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGATGCTGACCATCACA 651  
QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
DB 652 GACTTCATCTTGTGTGTCACCGCTATTACAGGTCCCGCTGCTGCTGCTGCTGCTGCTGCT 711  
QY 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
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QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
DB 772 GTCTCCATCTCTCCCAATGACAGCTGTTTGAAGCTGTCTACGCCCTCATCAAGAACCGG 831  
QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisLysLeuThrHis 140  
DB 832 ATCCACCGCTGCTGGTCTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891

Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
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Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
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Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
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Qy 301 AspAlaLeuGlyAla 305  
Db 1372 GATGCCCTCGGGGCC 1386

RESULT 12  
AX099800  
LOCUS AX099800  
DEFINITION Sequence 27 from Patent WO0120003.  
ACCESSION AX099800  
VERSION AX099800.1 GI:13538834  
KEYWORDS  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.

REFERENCE 1  
AUTHORS Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,  
Rogei-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and  
Chardon,P.  
TITLE Variants of the gamma chain of ampk, dna sequences encoding the  
same, and uses thereof  
JOURNAL Patent: WO 0120003-A 27 22-MAR-2001;  
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;  
Andersson, Lelf (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)  
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ORIGIN  
Alignment Scores:  
Pred. No.: 2.23e-127 Length: 1873  
Score: 1507.00 Matches: 296  
Percent Similarity: 98.36% Conservative: 4  
Best Local Similarity: 97.05% Mismatches: 5  
Query Match: 97.16% Indels: 0  
Gaps: 0  
DB: 6

US-10-070-794A-4 (1-305) x AX099800 (1-1873)

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Qy 41 ArgAlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
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Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleThrGluIle 80  
Db 658 GACTTCATCTTGTGTGCTGCACCGCTATTACAGGTCCCGCCCTGGTCCAGATCTACGAGATT 717  
Qy 81 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db 718 GAAGAACATAGATTGAGACCTGGAGGAGATCTACCTTTCAAGGCTGCTTCAAGCCTCTG 777  
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 Qy 301 AspAlaLeuGlyAla 305  
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## RESULT 13

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 LOCUS AX398331 1873 bp DNA linear PAT 27-MAY-2002  
 DEFINITION Sequence 1 from Patent WO0220850.  
 ACCESSION AX398331  
 VERSION AX398331.1 GI:21261106  
 KEYWORDS  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 Sus.

## REFERENCE

1 Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.  
 Novel prkag3 alleles and use of the same as genetic markers for  
 reproductive and meat quality traits  
 JOURNAL Patent: WO 0220850-A 1 14-MAR-2002;  
 Iowa State University Research Foundation, Inc. (US)

## FEATURES

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## ORIGIN

Alignment Scores:  
 Pred. No.: 2,23e-127 Length: 1873  
 Score: 1507.00 Matches: 296  
 Percent Similarity: 98.36% Conservative: 4  
 Best Local Similarity: 97.05% Mismatches: 5  
 Query Match: 97.16% Indels: 0  
 DB: 6 Gaps: 0

US-10-070-794A-4 (1-305) x AX398331 (1-1873)

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 Db 538 ATCTTCGACACCATGCTGGAGATCAGAAGCCCTTCTGCCCTGGTGGCCAAACGGCGTC 597  
 Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
 Db 598 CGAGCGGCACCTTGTGGGACAGCAGCAGAGAGCTTCGTGGGATGCTGACCATCA 657  
 Qy 61 AspPheIleLeuValLeuHisArgTyTyArgSerProLeuValGlnIleTyGluIle 80  
 Db 658 GACTTCATCTGGTGTGCACCGCTATTACAGGTCCCGCTGGTCCAGATCTACGAGATT 717  
 Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyArgGlnGlyCysPheLysProLeu 100  
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 Db 838 ATCCACCGCCTGCGGGTCTGGACCCCTGTCTCCGGGGCTGTGTCTCCACATCTCTCACAT 897  
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RESULT 14  
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 DEFINITION Sequence 3 from Patent WO0220850.  
 ACCESSION AX398333  
 VERSION AX398333.1 GI:21261108  
 KEYWORDS  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 Sus.

REFERENCE 1  
 Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.  
 Novel prkag3 alleles and use of the same as genetic markers for  
 reproductive and meat quality traits  
 JOURNAL Patent: WO 0220850-A 3 14-MAR-2002;  
 Iowa State University Research Foundation, Inc. (US)

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## ORIGIN

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Alignment Scores: 2.23e-127 Length: 1873  
Pred. No.: 1507.00 Matches: 296  
Score: 1507.00 Matches: 296  
Percent Similarity: 98.36% Conservative: 4  
Best Local Similarity: 97.05% Mismatches: 5  
Query Match: 97.16% Indels: 0  
DB: 6 Gaps: 0  
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DB GAAGAACATAAGATTGAGACCTTGGAGGAGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777  
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LOCUS  
DEFINITION Sequence 5 from Patent WO0220850.  
ACCESSION AX398335  
VERSION AX398335.1 GI:21261110  
KEYWORDS  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.  
REFERENCE 1  
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.  
TITLE Novel prkag3 alleles and use of the same as genetic markers for  
reproductive and meat quality traits  
JOURNAL Patent: WO 0220850-A 5 14-MAR-2002;  
Iowa State University Research Foundation, Inc. (US)  
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## ORIGIN

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Alignment Scores: 2.23e-127 Length: 1873  
Pred. No.: 1507.00 Matches: 296  
Score: 1507.00 Matches: 296  
Percent Similarity: 98.36% Conservative: 4  
Best Local Similarity: 97.05% Mismatches: 5  
Query Match: 97.16% Indels: 0  
DB: 6 Gaps: 0  
US-10-070-794A-4 (1-305) x AX398335 (1-1873)  
QY 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20  
DB 478 ATGCATTCATGCAGGACACACCTGCTACGATGCCATGCCAGCAGCTCCAACTGGTC 537  
QY 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
DB 538 ATCTTCGACACCATGCTGGAGATCAAGAGGCTCTTTGGCCCTGGTGGCAACGGGCTC 597  
QY 41 ArgAlaAlaProLeuTyrAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60  
DB CGAGCGGCACCTTTGTGGGACAGCAGCAAGAGCTTCGTGGGGATGCTGACCATCACA 657
```

Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
Db |||||  
658 GACTTCATCTTGGTGTGACCGCTATTACAGGTCCCGCTGGTCCAGATCTACGAGATT 717  
Qy 81 GluGlnHisIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db |||||  
718 GAAGACATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777  
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
Db |||||  
778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTAAGCCCTCATCAAGACCGG 837  
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db |||||  
838 ATCCACCGCCTGCCGCTCTGGACCTGTCTCCGGGGCTGTGCTCCACATCCTCACACAT 897  
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db |||||  
898 AAGCGGCTTCTCAAGTTCTCTGCACATCTTTGGCACCCTGTGCTGCCCGCCTCCTTCCTC 957  
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180  
Db |||||  
958 TACCGCACCATCCAGATTGGGCATCGGCACATTCGAGACTTGGCCGTGGTCTGAA 1017  
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200  
Db |||||  
1018 ACGCGGCCCATCTGACCGCATCTGACATCTTCGTGACCGCGTGTGCTGCGCTGCCT 1077  
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
Db |||||  
1078 GTGGTCAACGAACTGGACAGGTAGTGGGCTCTACTCTCGCTTGTATGTGATCCACTG 1137  
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
Db |||||  
1138 GCTGCCCAACAAACATACACACCTCGACATGATGTGGAGAGAGCCCTGAGCGACCGG 1197  
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260  
Db |||||  
1198 ACCTGTGTCTGGAAGGCTCTTCTCTGCGCAGCCCGCAGACCTTGGGGGAAGTCATT 1257  
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
Db |||||  
1258 GACCGGATTGTCCGGGAACAGGTGCACCGCTGTGCTCGTGATGAGACCCAGACCTT 1317  
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
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1318 CTGGCGTGTGTCTCTCTGACATCTTCAGGCTCTGTGCTCAGCCCTGTGGAATT 1377  
Qy 301 AspAlaLeuGlyAla 305  
Db |||||  
1378 GATGCCCTCGGGCC 1392

Search completed: January 26, 2006, 01:18:01  
Job time : 4102.76 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 25, 2006, 20:40:11 ; Search time 469.2 Seconds  
(without alignments)

4332.332 Million cell updates/sec

Title: US-10-070-794A-4

Perfect score: 1551

Sequence: 1 MRFQHEHTCYDAMATSKLV.....LSDIQLVLSPAGIDALGA 305

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Zgapop 6.0 , Zgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 21: \*  
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3: Geneseqn2000s: \*  
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8: Geneseqn2003as: \*  
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11: Geneseqn2003ds: \*  
12: Geneseqn2004as: \*  
13: Geneseqn2004bs: \*  
14: Geneseqn2005s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1551	100.0	1470	10	ADF50309 Human prk
2	1551	100.0	1647	5	Aah43685 PRKAG3 CD
3	1551	100.0	1647	12	Adp87616 Human NOV
4	1551	100.0	2109	4	Aad03296 Human AMP

5	1551	100.0	2115	4	AAD03320	Human AMP
6	1551	100.0	2115	12	ADP43247	Human AMP
7	1551	100.0	2781	8	AAD49456	Human kin
8	1544	99.5	2314	6	ABQ61173	AMP kinase
9	1525	98.3	2290	12	ADP87618	Human NOV
10	1525	98.3	2290	14	AE869127	Human mod
11	1507	97.2	1867	4	AAD03295	Pig AMPK
12	1507	97.2	1873	4	AAD03319	Pig AMPK
13	1507	97.2	1873	6	AAD36458	Pig PRKAG
14	1507	97.2	1873	6	AAD36457	Pig PRKAG
15	1507	97.2	1873	6	AAD36456	Pig wild-
16	1507	97.2	2022	4	AAD03321	Sus scrofa
17	1506	97.1	1873	6	AAD36459	Pig PRKAG
18	1503	96.9	1873	6	AAD36460	Pig PRKAG
19	1479	95.4	1518	10	ADF50311	Murine pr
20	1064	68.6	1167	6	AAL48614	Human ins
21	1064	68.6	1435	2	AA06882	Disease a
22	1064	68.6	1846	14	AD280781	Nucleotid
23	1064	68.6	2062	12	ADP43248	Human AMP
24	1064	68.6	2062	12	ADP21388	Gene PRKA
25	1064	68.6	2062	14	AE869126	Human mod
26	1064	68.6	2223	4	AH14839	Human cDN
27	1064	68.6	2223	6	AAL48615	Human ins
28	1064	68.6	2223	12	ADP87610	Human NOV
29	1064	68.6	2223	12	ADP87693	Human AMP
30	1064	68.6	2223	12	ADP87612	Human NOV
31	1059	68.3	2223	12	ADP87614	Human NOV
32	1009	65.1	1500	13	ADQ85336	Human tum
33	1009	65.1	1578	6	AAL48616	Human ins
34	1009	65.1	1578	6	ABK84324	Human cDN
35	1009	65.1	1578	10	ACA56515	Human sig
36	1009	65.1	1578	10	ADK61237	Ovarian c
37	1009	65.1	1578	12	ADI56311	Human pol
38	1009	65.1	1578	12	ADP43250	Human AMP
39	1009	65.1	1578	12	ADP87691	Human AMP
40	1009	65.1	1578	12	ADP87606	Human NOV
41	1009	65.1	1578	13	ACN39423	Tumour-as
42	1009	65.1	1578	14	AE869125	Human mod
43	1009	65.1	1691	3	AAC98774	Human pan
44	1009	65.1	2024	13	ACN42072	Human dia
45	1007	64.9	1328	13	ADV40979	Rat cardi

#### ALIGNMENTS

RESULT 1  
ADF50309  
ID ADF50309 standard; cDNA; 1470 BP.  
XX  
AC ADF50309;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human prkag3 cDNA encoding the AMPK-gamma3 subunit.  
XX  
KW human; gene; ss; transgenic;  
KW AMP-activated protein kinase gamma 3 subunit; Prkag3; AMPK;  
KW energy metabolism; obesity; dyslipidaemia; insulin resistance syndrome;  
KW type 2 diabetes; antidiabetic; anorectic; antilipaemic.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 1..1470  
FT /tag= a  
FT /product= "AMPK-gamma 3 protein"  
XX  
PN WO2003063586-A1.  
XX  
PD 07-AUG-2003.  
XX  
PF 31-JAN-2003; 2003WO-IB000912.  
XX



PR	07-APR-2000; 2000US-0195665P.	Qy	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	180
XX	(AREX-) AREXIS AB.	Db	1052	TACGCACTATCCAAAGATTGGGCGATCGGCACATTCGAGACTTGGCTGTGTGGAG	1111
XX	Andersson L, Luthman H, Marklund S;	Qy	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro	200
XX	WPI; 2001-657170/75.	Db	1112	ACAGACCCATCTGACTGCATCTGGACATCTTTGTGACCGCGTGTCTGCACTGCCT	1171
XX	P-PSDB; Q0847679.	Qy	201	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	220
PT	New variants of human AMP-activated protein kinase gamma3 subunit	Db	1172	GTGCTCAACGAATGTGTGAGTCTGAGTCTCTATTCCCGCTTTGATGTGATTCACCTG	1231
PT	associated with a metabolic disease e.g. diabetes or obesity and method	Qy	221	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	240
PT	for determining a risk estimate of diseases in subject by detecting the	Db	1232	GCTGCCAGCAAACTACAACCACTGCATGATGTGGGAGAAGCCCTGAGGCAGAGG	1291
XX	variant.	Qy	241	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle	260
PS	Disclosure; Fig 5; 25pp; English.	Db	1292	ACATATGTCTGGAGGAGTCTTCTTCTGCGAGCCCAACGAGAGCTTGGGGAAAGTGATC	1351
XX	This sequence represents the full length cDNA encoding the human AMP-	Qy	261	AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	280
CC	activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence	Db	1352	GACAGGATTGCTGGGAGCAGGTACACAGGCTGTGTGTAGTGAGAGAGCCAGCATCTC	1411
CC	of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate	Qy	281	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	300
CC	of a metabolic disease, such as diabetes or obesity, in a subject. The	Db	1412	TTGGCGTGTCTCTCCCTCTCCGACATCTTTCAGGCACTGTGTCTCAGCCCTGCTGGCATC	1471
CC	variation may occur in exons 3, 4 or 10. In exon 3 variation may be a	Qy	301	AspAlaLeuGlyAla	305
CC	substitution of a G for a C at nucleotide 320, resulting in the amino	Db	1472	GATGCCCTCGGGGCC	1486
CC	acid substitution P71A; in exon 4 variation may be a substitution	RESULT 3			
CC	for a C at nucleotide 550; and in exon 10 variation may be a substitution	ID	ADP87616	standard; DNA; 1647 BP.	
CC	of a T for a C at nucleotide 1037, resulting in the amino acid	XX	ADP87616;		
CC	substitution R340W. There may also be nucleotide variation in intron 6.	AC	ADP87616;		
CC	The numbering of these variations is based on the full length cDNA as	XX	23-SEP-2004 (first entry)		
CC	given, rather than on position 1 of the open reading frame	DT	Human NOVX polypeptide encoding DNA, NOV10a.		
SQ	Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 U; 0 Other;	DE	anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;		
		XX	insulin resistance; hybridization probe; chromosome mapping;		
		KW	tissue typing; preventive medicine; pharmacogenomics; NOVX; human; gene;		
		KW	ds.		
		XX	Homo sapiens.		
		OS	WO2004056961-A2.		
		PN	08-JUL-2004.		
		PD	27-OCT-2003; 2003WO-US034114.		
		XX	25-OCT-2002; 2002US-0421239P.		
		PF	28-OCT-2002; 2002US-0421700P.		
		XX	31-OCT-2002; 2002US-0422776P.		
		PR	13-NOV-2002; 2002US-0426197P.		
		PR	20-DEC-2002; 2002US-0435498P.		
		PR	20-DEC-2002; 2002US-0435510P.		
		PR	20-DEC-2002; 2002US-0435568P.		
		PR	21-MAR-2003; 2003US-0456812P.		
		XX	(CURA-) CURAGEN CORP.		
		PA	Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;		
		XX	WPI; 2004-500293/47.		
		PI	P-PSDB; ADP87617.		
		XX	New NOVX nucleic acid molecules and polypeptides useful for preventing or		
		DR	treating NOVX-associated disorders, e.g. diabetes, insulin resistance or		
		XX			
		PT			

PR	07-APR-2000; 2000US-0195665P.	Qy	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	180
XX	(AREX-) AREXIS AB.	Db	1052	TACGCACTATCCAAAGATTGGGCGATCGGCACATTCGAGACTTGGCTGTGTGGAG	1111
XX	Andersson L, Luthman H, Marklund S;	Qy	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro	200
XX	WPI; 2001-657170/75.	Db	1112	ACAGACCCATCTGACTGCATCTGGACATCTTTGTGACCGCGTGTCTGCACTGCCT	1171
XX	P-PSDB; Q0847679.	Qy	201	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	220
PT	New variants of human AMP-activated protein kinase gamma3 subunit	Db	1172	GTGCTCAACGAATGTGTGAGTCTGAGTCTCTATTCCCGCTTTGATGTGATTCACCTG	1231
PT	associated with a metabolic disease e.g. diabetes or obesity and method	Qy	221	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	240
PT	for determining a risk estimate of diseases in subject by detecting the	Db	1232	GCTGCCAGCAAACTACAACCACTGCATGATGTGGGAGAAGCCCTGAGGCAGAGG	1291
XX	variant.	Qy	241	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle	260
PS	Disclosure; Fig 5; 25pp; English.	Db	1292	ACATATGTCTGGAGGAGTCTTCTTCTGCGAGCCCAACGAGAGCTTGGGGAAAGTGATC	1351
XX	This sequence represents the full length cDNA encoding the human AMP-	Qy	261	AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	280
CC	activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence	Db	1352	GACAGGATTGCTGGGAGCAGGTACACAGGCTGTGTGTAGTGAGAGAGCCAGCATCTC	1411
CC	of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate	Qy	281	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	300
CC	of a metabolic disease, such as diabetes or obesity, in a subject. The	Db	1412	TTGGCGTGTCTCTCCCTCTCCGACATCTTTCAGGCACTGTGTCTCAGCCCTGCTGGCATC	1471
CC	variation may occur in exons 3, 4 or 10. In exon 3 variation may be a	Qy	301	AspAlaLeuGlyAla	305
CC	substitution of a G for a C at nucleotide 320, resulting in the amino	Db	1472	GATGCCCTCGGGGCC	1486
CC	acid substitution P71A; in exon 4 variation may be a substitution	RESULT 3			
CC	for a C at nucleotide 550; and in exon 10 variation may be a substitution	ID	ADP87616	standard; DNA; 1647 BP.	
CC	of a T for a C at nucleotide 1037, resulting in the amino acid	XX	ADP87616;		
CC	substitution R340W. There may also be nucleotide variation in intron 6.	AC	ADP87616;		
CC	The numbering of these variations is based on the full length cDNA as	XX	23-SEP-2004 (first entry)		
CC	given, rather than on position 1 of the open reading frame	DT	Human NOVX polypeptide encoding DNA, NOV10a.		
SQ	Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 U; 0 Other;	DE	anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;		
		XX	insulin resistance; hybridization probe; chromosome mapping;		
		KW	tissue typing; preventive medicine; pharmacogenomics; NOVX; human; gene;		
		KW	ds.		
		XX	Homo sapiens.		
		OS	WO2004056961-A2.		
		PN	08-JUL-2004.		
		PD	27-OCT-2003; 2003WO-US034114.		
		XX	25-OCT-2002; 2002US-0421239P.		
		PF	28-OCT-2002; 2002US-0421700P.		
		XX	31-OCT-2002; 2002US-0422776P.		
		PR	13-NOV-2002; 2002US-0426197P.		
		PR	20-DEC-2002; 2002US-0435498P.		
		PR	20-DEC-2002; 2002US-0435510P.		
		PR	20-DEC-2002; 2002US-0435568P.		
		PR	21-MAR-2003; 2003US-0456812P.		
		XX	(CURA-) CURAGEN CORP.		
		PA	Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;		
		XX	WPI; 2004-500293/47.		
		PI	P-PSDB; ADP87617.		
		XX	New NOVX nucleic acid molecules and polypeptides useful for preventing or		
		DR	treating NOVX-associated disorders, e.g. diabetes, insulin resistance or		
		XX			
		PT			

Alignment Scores:					
Pred. NO.:	4.15e-171	Length:	1647		
Score:	1551.00	Matches:	305		
Percent Similarity:	100.00%	Conservative:	0		
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DB:	5	Gaps:	0		

US-10-070-794A-4 (1-305) x AAH43685 (1-1647)					
Qy	1	MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal	20		
Db	572	ATGCGCTTCATGCAAGAGCACCTGCTACATGCCATGCCAAGTACCTCAAGTATGTC	631		
Qy	21	IlePheAspThrMetLeuGluIleLysAlaPhePheAlaLeuValAlaAsnGlyVal	40		
Db	632	ATCTTCACACCATGCTGGAGATCAAGAGCCCTTCTTGTCTGTGTGGCAAGCGTGTG	691		
Qy	41	ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	60		
Db	692	CGGCGAGCCCTCTATGGACAGCAAGCAGAGCTTTGTGGGATGCTGACCATCACT	751		
Qy	61	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	80		
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Db	812	GAACAAATAGATTGAGCTTGAGGGAGATCTACTCTGAGGCTGCTTCAAGCCTCTG	871		
Qy	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120		
Db	872	GTCCTCCATCTCTCCTAATATAGCTGTTTGAAGCTGTCTACACCTCATCAAGACCGG	931		
Qy	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	140		
Db	932	ATCCATCGCTGCTGCTGCTTGTAGCCCGTGTGAGCAACGTAATCCACATCCCTCACAC	991		
Qy	141	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160		
Db	992	AAAGCCTGTCAAGTTCCTGACATCTTTGGTTCCTGTGCCCCCGGCTCTCTCTCTC	1051		

obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1: SEO ID NO 73; 570pp; English.

The invention relates to a novel isolated nucleic acid molecule comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base pairs) fully defined in the specification; or encodes any of the amino acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the specification. The invention further comprises: an isolated polypeptide comprising any of the amino acid sequences cited above; a method for identifying compounds that modulate target polypeptide activity; an antibody that immunospecifically binds to the target polypeptide; where the target polypeptide comprises any of the above-mentioned amino acid sequences, an amino acid sequence that is at least 95% identical to the above amino acid sequences, an amino acid sequence of at least one domain of the above-mentioned amino acid sequences, or an amino acid sequence that is at least 95% identical to the domain of the above amino acid sequences; a method for identifying a potential therapeutic agent for use in treatment of a pathology, where the pathology is related to aberrant expression or aberrant physiological interactions of a target polypeptide; and a method of screening for a modulator of activity of or of latency or predisposition to a pathology associated with a target polypeptide. The modulating compounds have anorectic and antidiabetic activities. The nucleic acid sequences of the invention may be used in gene therapy to treat disorders. The proteins of the invention may be used in creating a vaccine. The composition and methods are useful for identifying compounds that modulate protein activity or for diagnosing, preventing or treating diverse pathological conditions, such as obesity, diabetes or insulin resistance. The nucleic acids are also used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. This polynucleotide sequence represents the DNA encoding a NOVX polypeptide of the invention.

Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 U; 0 Other;

**Alignment Scores:**

Pred. No.:	4.15e-171	Length:	1647
Fragmented Score:	Score: 1551.00	Matches:	305
	Percent Similarity: 100.00%	Conservative:	0
	Best Local Similarity: 100.00%	Mismatches:	0
	Query Match: 100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-070-794A-4 (1-305) x ADP87616 (1-1647)

Qy	1	MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerIysLeuVal	20
Db	572	ATGCGCTTCATGCAGGACACACCTGCTACCATGCCATGCGCACTAGCTCCAAAGCTAGTC	631
Qy	21	IlePheAspThrMetLeuGluIleIysIysAlaPhePheAlaLeuValAlaAenGlyVal	40
Db	632	ATCTTCGACACCATGCTGGAGATCAAGAAAGGCCCTTCCTTGCTGTGGTGGCCAAACGGTGTG	691
Qy	41	ArgAlaAlaProLeuTriPAspSerIysIysGlnSerPheValGlyMetLeuThrIleThr	60
Db	692	CGGGCAGCCCTCTATGGACAGCAAGACAGAGCTTTGTGGGATGCTGACCATCACT	751
Qy	61	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	80
Db	752	GACTTCATCCTGGTGCATCGCTACTACAGGTCCGCCCTGGTCCAGATCTATGAGATT	811
Qy	81	GluGlnHisIysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	812	GAACAACATPAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTCTTCAAGCCCTCTG	871
Qy	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120
Db	872	GTCTCCATCTCTCCTAATGATAGCCTGTTGAGCTGTCTACACCTCATCAGAACC	931
Qy	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	140
Db	932	ATCCATCGCGCTGCTGTGTTCTTGACCGGTGTGAGCAACGTACTCCACATCTCTCACAC	991



PA (KALM/) KALM E.  
XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;  
PI Iannucci N, Gellin J, Le Roy P, Chardon P;  
XX  
XX  
XX WPI: 2001-244810/25.  
XX P-PSDB; AAE00223.  
XX  
XX New variants of the gamma subunit of vertebrate adenosine monophosphate-  
PT activated kinase for diagnosis or treatment of disorders associated with  
PT energy metabolism such as diabetes, obesity, and myopathy.  
XX  
XX Claim 12; Page 65-68; 71pp; English.  
XX  
XX The present sequence is a cDNA encoding human adenosine monophosphate  
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,  
CC complete PRKAG3. Mutation in Prkag3 results in an altered regulation of  
CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is  
CC useful as therapeutic for treating carbohydrate metabolism disorders such  
CC as diabetes, obesity, and disorders associated with muscle metabolism  
CC such as myopathy and cardiovascular diseases, to modulate AMPK activity,  
CC and for restoring a normal AMPK function. PRKAG3 sequence and its  
CC functionally altered mutants are useful for the diagnostic evaluation,  
CC genetic testing and prognosis of a metabolic disorder, preferably a  
CC carbohydrate metabolism disorder. Primers that can detect a genetic  
CC polymorphic marker linked to a sequence encoding PRKAG3, are useful for  
CC detecting a dysfunction of carbohydrate metabolism resulting from the  
CC expression of a functionally altered allele of PRKAG3. Transgenic animal  
CC and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting  
CC of PRKAG3 or its mutant, are useful for screening compounds able to  
CC modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for  
CC detecting mutations in a Prkag3 gene, or in a sequence encoding the first  
CC cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene  
XX therapy  
XX  
SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.05e-171 Length: 2115  
Score: 1551.00 Matches: 305  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
  
US-10-070-794A-4 (1-305) x AAD03320 (1-2115)  
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20  
Db 478 ATGCCCTTCATGCGAGGAGACACCTGCTACGATGCGATGGCACTAGCTCCAGCTAGTC 537  
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
Db 538 ATCTTCGACACCATGCTGAGATCAAGAAGGCTCTTTTGTCTGCTGGTGGCAACGCTGTG 597  
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
Db 598 CGGGGCGGCCCTCTATGGACACGACGACGAGCTTTGTGGGATGCTGACCATCACT 657  
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
Db 658 GACTTCATCCTGGTGGTGCATCGCTACTACAGTCCCCCTGGTCCAGATCTATGAGATT 717  
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db 718 GAACAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCTCTG 777  
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrIleLysAsnArg 120  
Db 778 GTCTCCATCTCTCTAATGATAGCTGTGTGAAGCTGTCTACACCTCATCAAGAACCGG 837  
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db  
838 ATCCATCGCTGCTGTTCTTGACCGGTGTGACGCAACGTAATCTCCACATCTCCACAC 897  
141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
898 AAACGGCTGCTCAAGTTCTTGCACATCTTTGGTTCCTGTGCTGCCCCGGCTCTTCTC 957  
161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180  
958 TACCGCACTATCCAGATTGCGCATCGGCACATTCGAGACTTGGCTGTGGTCTGGAG 1017  
181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
1018 ACAGCACCATCTCTGACTGCACTGGACATCTTTGTGGACCGGCTGTGTCTGCACCTG 1077  
201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
1078 GTGGTCAACGAATGTGGTCAAGTCTGAGGCTCTTATTTCCGCTTTGATGATTCACCTG 1137  
221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
1138 GTGCCCCAGCAACCTACACCATGCAATGAGTGTGGAGAGAGCCCTGAGGCAGAG 1197  
241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260  
1198 ACATATGTCTGGAGGAGTCTTTCTCTGCGAGCCCAACGAGAGCTTTGGGGAAAGTATC 1257  
261 AspArgIleAlaArgGluGlnValHisArgLeuValValLeuValAspGluThrGlnHisLeu 280  
1258 GACAGGATTCCTGGGAGCAGGTACACAGGCTGGTGTGTAGTGGACGAGACCCACATCTC 1317  
281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
1318 TTGGGCGTGGTCTCCCTCTCCGACATCTTCAGGCACTGGTGTCTCAGCCCTGCTGTCATC 1377  
301 AspAlaLeuGlyAla 305  
1378 GATGCCCTCGGGGC 1392  
  
RESULT 6  
ADP43247  
ID ADP43247 standard; DNA; 2115 BP.  
XX  
XX ADP43247;  
AC  
XX  
XX  
DT 09-SEP-2004 (first entry)  
XX  
XX Human AMP-activated protein kinase gamma subunit coding sequence.  
DE  
XX  
XX cardiovascular; neuroprotective; dermatological; cytostatic;  
KW AMPK modulator; AMPK agonist; gene therapy;  
KW adenosine monophosphate-activated protein kinase; AMPK;  
KW cardiovascular disorder; neurological disorder; metabolic disorder;  
KW dermatological disorder; neoplastic disorder; age-associated disorder;  
KW geriatric disorder; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004050898-A2.  
FN  
XX  
XX 17-JUN-2004.  
PD  
XX  
XX 04-DEC-2003; 2003WO-US038628.  
PF  
XX  
XX 04-DEC-2002; 2002US-0430804P.  
PR  
XX  
XX 18-JUL-2003; 2003US-0488261P.  
PR  
XX  
XX (ELIX-) ELIXIR PHARM INC.  
PA  
XX  
XX Apfeld J, O'Connor G;  
PI  
XX  
XX WPI: 2004-450740/42.  
DR  
XX  
XX Evaluating a compound, useful for treating e.g., age-related disorder,  
PT

comprises contacting a polypeptide at least 85% identical to e.g., alpha adenosine monophosphate-activated protein kinase (AMPK) subunit with a test compound.

Disclosure; SEQ ID NO 50; 160pp; English.

The invention relates to a method of evaluating a compound by contacting a polypeptide comprising a sequence at least 8% identical to alpha, beta or gamma adenosine monophosphate-activated protein kinase (AMPK) subunit or a functional domain in vitro with a test compound, evaluating interaction between compound and polypeptide, contacting a cell or organism that produces the polypeptide with test compound, and evaluating a rate of aging of the cell or organism. A method comprising providing a modulator of the AMPK pathway to the subject is useful for treating or preventing a disease or disorder in a subject, preferably a cardiovascular disorder, a neurological disorder, a metabolic disorder, a dermatological disorder, a neoplastic disorder, an age-associated disorder, or a geriatric disorder. A compound that alters the expression or activity of an AMPK pathway component is useful for altering lifespan regulation in a cell or organism. This sequence represents the DNA sequence encoding one of the AMPK protein subunits.

Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 U; 0 Other;

**Alignment Scores:**

Pred. No.:	6.05e-171	Length:	2115
Score:	1551.00	Matches:	305
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-070-794A-4 (1-305) x ADP43247 (1-2115)

Qy	1	MetArgPheMetGlnGluHisThrCysTyrAspAlaMetalaThrSerSerLysLeuVal	20
Db	478	ATCGCGTTTCATGAGGAGCACACCTGCTAGCATGCCATGGCAACTAGCTCCAGCTAGTC	537
Qy	21	IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal	40
Db	538	ATCTTCGACACCATGCTGGAGATCAAGAGAGCCCTTCCTTGCTCTGGTGGCCAAACGGGTGTG	597
Qy	41	ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	60
Db	598	CGGGCAGCCCTCTATGGGACAGCAAGACGAGCTTTGTGGGGATGCTGGACCATCACT	657
Qy	61	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	80
Db	658	GACTTTCATCTGGTGTGCATCGCTACTACAGGTCCCGCTGGTCCAGATCTATGAGATT	717
Qy	81	GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	718	GAAACAATGAAGATTGAGACTCGAGGGAGATCTACCTGCAAGGCTGCTTCAGAGCCCTCTG	777
Qy	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120
Db	778	GTCTCCATCTCTCTAATGATAGCCTGTTTGAAGCTGCTACACCTTCATCAGAACCGG	837
Qy	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	140
Db	838	ATCCATCGCCTGCCTGTGTCTTGACCCCGGTGTGAGGCAACGTACTCCACATCTCTCACAC	897
Qy	141	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160
Db	898	AAACGCTGCTCAAGTTCTCGCATCTTTGGTTTCCCTGCTGCCCCCGGCCCTCTCTCCCT	957
Qy	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	180
Db	958	TACCGCACTATCCAAGATTTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGTGGAG	1017
Qy	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	200
Db	1018	ACAGCAACCATCTGACTGCACTGGACATCTTTGTGACCGGGTGTGTGCACTGCCT	1077

Qy	201	valvalasndglucysgylglnvalvalgylleutyrserrargpheaspvalliehisleu	220
Db	1078	GTGGTCAACGAATGTGGTTCAGGTCGTGGGCTCTATTCCGCGCTTGTATGTGATTCACCTG	1137
Qy	221	AlaAlaglnGlnThrTyrrasnHisLeuAspMetSerValgylglualaleuargGlnArg	240
Db	1138	GCTGCCCAGCAACCTACAAACCACCTGGACATCAGTGTGGGAGAAGCCCTTGAGGCGAGAGG	1197
Qy	241	ThrleucysleugluGlyValleuSerCysglnProHisclussrleuGlyGluValIle	260
Db	1198	ACACTATGTCGTGAGGAGTCCCTTCTCCGACCCACGAGAGCTTGGGGGAAGTGATC	1257
Qy	261	AspArgilealaargGluGlnValHisArgLeuValleuValaspGluThrGlnHisLeu	280
Db	1258	GACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGTCTAGTGGACGAGACCCAGCATCTC	1317
Qy	281	LeucllyValValserleuSeraspIleLeuGlnAlaleuValleuSerProAlaGlyIle	300
Db	1318	TTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGTCTCAGCCCTGCTGGCATC	1377
Qy	301	AspAlaLeuGlyAla	305
Db	1378	GATGCCCTCGGGGCC	1392

## RESULT 7

AAD49456

ID AAD49456 standard; cDNA; 2781 BP.

XX

AC AAD49456;

XX

DT 24-MAR-2003 (first entry)

**XXI**

Human kinase and phosphatase (KPP)-15 cDNA.

DE  
XX  
KW Human; kinase and phosphatase; KPP; cardiovascular; hypertension;  
KW myocardial infarction; angina pectoris; Alzheimer's disease; epilepsy;  
KW acquired immune deficiency syndrome; AIDS; Grave's disease; diabetes;  
KW neurological; Parkinson's disease; cirrhosis; psoriasis; gene therapy;  
KW hypercholesterolaemia; anticonvulsant; hepatotropic; lipid myopathy;  
KW cell proliferative disorder; cancer; cardiant; neuroprotective; enzyme  
KW neuroptic; ophthalmological; anorectic; cytostatic; cataract; obesity;  
KW gene; ss.

OS Homo sapiens.

XX	Key	Location/Qualifiers
FH		

ET	CDS	21
ET	CDS	21

LE  
FT

```
FT
/product= "Human KPP protein"
```

PN WO200283709-A2.

PD 24-OCT-2002.

05-APR-2002: 2002WO-US010818.

[illegible]

PR 06-APR-2001: 2001US-0282119P.

PR 13-APR-2001; 2001US-0283588P.

PR 13-APR-2001; 2001US-0283759P.

PR 20-APR-2001; 2001US-0285589P.

PR 27-APR-2001; 2001US-0287036P.

PR 27-APR-2001; 2001US-0287037P.

PR 04-MAY-2001; 2001US-0288608P.

PR 04-MAY-2001; 2001US-0288712P.

PR 09-MAY-2001; 2001US-0289909P.

PR 17-MAY-2001; 2001US-0292246P

XX

PA (INCY-) INCYTE GENOMICS INC.

[illegible]

PI Recipon SA, Burrill JD, Marcus GA, Zingler KA, Tang YT;





PT XX

PS Claim 1; SEQ ID # 386; 357pp + Sequence Listing; English.

XX The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, vulnary, neuroprotective, immunomodulator, cytostatic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABQ60788-CC ABQ61233 represent polynucleotides of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 2314 BP; 513 A; 677 C; 618 G; 506 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	4.58e-170	Length:	2314
Score:	1544.00	Matches:	303
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	99.34%	Mismatches:	0
Query Match:	99.55%	Indels:	0
DB:	6	Gaps:	0

US-10-070-794A-4 (1-305) x ABQ61173 (1-2314)

Qy	1	MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal	20
Db	574	ATGGCGTTCATCGAGGAGCACACCTGTAGCATGCCATGCCATAGCTCCAAAGCTAGTC	633
Qy	21	IlePheAspThrMetLeuGluIleLysIleAlaPheAlaLeuValAlaAenGlyVal	40
Db	634	ATCTTCGACACCATCGCTGGAGATCAAGAGCCCTCTTGTCTGGTGGCCAAACGGGTG	693
Qy	41	ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr	60
Db	694	CGGCGACCCCTCTATGGGACAGCAGACAGACAGCTTTGTGGGATGCTGACCATCACT	753
Qy	61	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluile	80
Db	754	GACTTCATCTGTGTGTCATCGTACTACAGGTCCCTGGTCCAGATCTATGAGATT	813
Qy	81	GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	814	GAACAACATAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTG	873
Qy	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120
Db	874	GTCTCCATCTCTCTTANTATGAGCTGTTTGAAGCTGTCTACACCTCATCAAGACCGG	933
Qy	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	140
Db	934	ATCCATCGCTGCTGCTGCTTGTACCCCGTGTTCAGGCAACGTACTCCACATCTCTCACAC	993
Qy	141	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160
Db	994	AAAGCGCTGCTCAAGTTCCTGCAATCTTTGGTTCCTGCTGCCCGCCCTCTCTCTC	1053
Qy	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	180
Db	1054	TACCGCATATCCAGATTGGGCATCCGACATTCGAGACTGGCTGTGGTGGAG	1113
Qy	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	200
Db	1114	ACAGACCCATCTCTGACTGACATGGACATCTTTGTGGACCGGCTGTCTGCACTGCCT	1173
Qy	201	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	220

Db	1174	GTGGTCAACGAATGTGTGTGGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTG	1233
Qy	221	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	240
Db	1234	GCTGCCCAGCAAACTTACACCACTGGACATGAGTGTGGGAGAAGCCCTGAGGACAGG	1293
Qy	241	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValle	260
Db	1294	ACACTATGTCTGGAGGAGTCTTCTCTGTCAGCCACGAGAGCTTTGGGGGAAGTATC	1353
Qy	261	AspArgIleAlaArgGluGlnValHisArgLeuValLeuValLeuValLeuValLeu	280
Db	1354	GACAGATTCTCGGAGCAGGTACACAGGCTGTGTGTGGACGAGACCCCATCTC	1413
Qy	281	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyle	300
Db	1414	TTGGGCGTGTCTCTCTCTCGACATCTTTCAGGCACTGTGTCTCAGCCCTGTGTGGCATC	1473
Qy	301	AspAlaLeuGlyAla	305
Db	1474	GATGCCCTCGGGCC	1488
RESULT 9			
ADP87618			
ID	ADP87618	standard; DNA; 2290 BP.	
XX	AC	ADP87618;	
XX	XX	23-SEP-2004 (first entry)	
DT	XX	Human NOVX polypeptide encoding DNA, NOV10b.	
DE	XX	anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;	
XX	KW	insulin resistance; hybridization probe; chromosome mapping;	
KW	KW	tissue typing; preventive medicine; pharmacogenomics; NOVX; human; gene;	
KW	ds.		
XX	OS	Homo sapiens.	
XX	XX	WO2004056961-A2.	
XX	XX	08-JUL-2004.	
XX	XX	27-OCT-2003; 2003WO-US034114.	
XX	XX	25-OCT-2002; 2002US-0421239P.	
PR	PR	28-OCT-2002; 2002US-0421700P.	
PR	PR	31-OCT-2002; 2002US-0422776P.	
PR	PR	13-NOV-2002; 2002US-0426197P.	
PR	PR	20-DEC-2002; 2002US-0435498P.	
PR	PR	20-DEC-2002; 2002US-0435510P.	
PR	PR	20-DEC-2002; 2002US-0435568P.	
PR	PR	21-MAR-2003; 2003US-0456812P.	
XX	XX	(CURA-) CURAGEN CORP.	
PA	XX	Berghs C, Catterton B, Ellerman K, Ort T, Rieger D, Chaudhuri A;	
PI	XX	WPI; 2004-500293/47.	
XX	XX	P-PSDB; ADP87619.	
DR	DR	New NOVX nucleic acid molecules and polypeptides useful for preventing or	
PT	PT	treating NOVX-associated disorders, e.g. diabetes, insulin resistance or	
PT	PT	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.	
XX	XX	Claim 1; SEQ ID NO 75; 570pp; English.	
XX	XX	The invention relates to a novel isolated nucleic acid molecule	
CC	CC	comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base	
CC	CC	pairs) fully defined in the specification; or encodes any of the amino	
CC	CC	acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the	
CC	CC	specification. The invention further comprises: an isolated polypeptide	
CC	CC	comprising any of the amino acid sequences cited above; a method for	



CC agent, the system provides a reference activity and detecting a test  
 CC agent-biased activity of the assay system, where a difference between the  
 CC test agent-biased activity and the reference activity identifies the test  
 CC agent as a candidate IGFR pathway modulating agent. The invention also  
 CC relates to methods for modulating an IGFR pathway of a cell or in a  
 CC mammalian cell and a method for diagnosing a disease in a patient. The  
 CC methods are useful for diagnosing or treating cancer or for identifying  
 CC modulators of an IGFR pathway, which may be utilized as therapeutic  
 CC targets for disorders associated with defective IGFR function, such as  
 CC cancer. This sequence represents a human modulator of IGFR pathway  
 CC polynucleotide of the invention.

SQ Sequence 2290 BP; 501 A; 674 C; 617 G; 498 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 7.62e-168 Length: 2290  
 Score: 1525.00 Matches: 299  
 Percent Similarity: 99.34% Conservative: 3  
 Best Local Similarity: 98.36% Mismatches: 2  
 Query Match: 98.32% Indels: 0  
 DB: 14 Gaps: 0

US-10-070-794A-4 (1-305) x AEB69127 (1-2290)

Qy 1 MetArgPheMetGlnGluHisThrCysTyAspAlaMetAlaThrSerSerLysLeuVal 20  
 Db 574 ATGGCTTTCATCGAGGAGCACACCTGTACGATGCCATGCGCACTAGCTCCAAAGTAGTC 633  
 Qy 21 IlePheAspThrMetLeuGluIleLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
 Db 634 ATCTTCGACACCATGCTGGAGATCAAGAGCGCTTCTTGTCTGTGGGCCAACGGGTG 693  
 Qy 41 ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60  
 Db 694 CGGCGACCCCTCTATCGGACGACAGACAGACAGCTTGTGGGATGCTGACCATCACT 793  
 Qy 61 AspPheIleLeuValLeuHisArgTyTyArgSerProLeuValGlnIleTyrgluile 80  
 Db 754 GACTTCATCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813  
 Qy 81 GluGlnHisLysValIleGluThrTrpArgGluIleTyrgluileGlyCysPheLysProLeu 100  
 Db 814 GAACAACATGAAGATTGAGACTGGAGGAGATCTACCTGCAAGCGCTCTTCAAGCCCTG 873  
 Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyThrLeuIleLysAsnArg 120  
 Db 874 GTCTCCATCTCTCTATGATGAGCTCTTGAAGCTGTCTACACCTCATCAAGACCGG 933  
 Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
 Db 934 ATCCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 993  
 Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
 Db 994 AAAGCGCTGCTCAAGTTCCTGTCACATCTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTG 1053  
 Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180  
 Db 1054 TACCGCACTATCCAGATTGGGCTGCGGACATTCGACACTTGGCTGTGTGTGGAG 1113  
 Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
 Db 1114 ACAGCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1173  
 Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTySerArgPheAspValIleHisLeu 220  
 Db 1174 GTGGTCAACGAATGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 1233  
 Qy 221 AlaAlaGlnGlnThrTyAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
 Db 1234 GCTGCCCGGCAACCTTACACACCTGAGTATGATGTGGAGAGCCCTCGAGAGAGG 1293  
 Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260

Db 1294 ACATATGTCTGGAGGAGTCTTCTTCTGCGAGCCCGAGAGCTTGGGGAGAGTAGTC 1353  
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValLeuValLeuValLeuValLeu 280  
 Db 1354 GACAGGATTCCTCGGAGCAGGTACACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1413  
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
 Db 1414 TTGGGGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1473  
 Qy 301 AspAlaLeuGly 304  
 Db 1474 GATCCCTCGGGG 1485  
 RESULT 11  
 AAD03295  
 ID AAD03295 standard; cDNA; 1867 BP.  
 XX  
 AC AAD03295;  
 XX  
 DT 13-JUN-2001 (first entry)  
 XX  
 DE Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.  
 XX  
 KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;  
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;  
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;  
 KW cystathione beta synthase; CBS; cardiac; gene therapy; RN locus;  
 KW chromosome 15; ss.  
 XX  
 OS Sus scrofa.  
 XX  
 FH Key Location/Qualifiers  
 FT 5'UTR 1..471  
 FT CDS /tag= a  
 FT 472..1389  
 FT /tag= b  
 FT /product= "Sus scrofa PRKAG3 protein"  
 FT 3'UTR 1390..1867  
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 PN WO200120003-A2.  
 XX  
 PD 22-MAR-2001.  
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 PF 11-SEP-2000; 2000WO-EP009896.  
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 PR 10-SEP-1999; 99EP-00402236.  
 PR 18-MAY-2000; 2000EP-00401388.  
 XX  
 PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 PA (ANDE/) ANDERSSON L.  
 PA (LOOF/) LOOFT C.  
 PA (KALM/) KALM E.  
 XX  
 PI Andersson L, Loof C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;  
 PI Tannuccelli N, Gellin J, Le Roy P, Chardon P;  
 XX  
 DR WPI; 2001-244810/25.  
 DR P-PSDB; AAE00220.  
 XX  
 PT New variants of the gamma subunit of vertebrate adenosine monophosphate-  
 PT activated kinase for diagnosis or treatment of disorders associated with  
 PT energy metabolism such as diabetes, obesity, and myopathy.  
 XX  
 PS Claim 12; Fig 2; 71pp; English.  
 XX  
 CC The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)  
 CC -activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3.  
 CC Prkag3 gene is located in the RN locus of chromosome 15. Mutation in  
 CC Prkag3 results in an altered regulation of carbohydrate metabolism,  
 CC particularly in skeletal muscle. PRKAG3 is useful as therapeutic for

CC treating carbohydrate metabolism disorders such as diabetes, obesity, and  
 CC disorders associated with muscle metabolism such as myopathy and  
 CC cardiovascular diseases, to modulate AMPK activity, and for restoring a  
 CC normal AMPK function. PRKAG3 sequence and its functionally altered  
 CC mutants are useful for the diagnostic evaluation, genetic testing and  
 CC prognosis of a metabolic disorder, preferably a carbohydrate metabolism  
 CC disorder. Primers that can detect a genetic polymorphic marker linked to  
 CC a sequence encoding PRKAG3, are useful for detecting a dysfunction of  
 CC carbohydrate metabolism resulting from the expression of a functionally  
 CC altered allele of PRKAG3. Transgenic animal and host cell transformed  
 CC with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant,  
 CC are useful for screening compounds able to modulate AMPK activity.  
 CC Nucleic acid encoding PRKAG3 is useful for detecting mutations in a  
 CC Prkag3 gene, or in a sequence encoding the first cystathione beta  
 CC synthase (CBS) domain of PRKAG3 and is useful in gene therapy  
 XX  
 SQ Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 7,21e-166 Length: 1867  
 Score: 1507.00 Matches: 296  
 Percent Similarity: 98.36% Conservative: 4  
 Best Local Similarity: 97.05% Mismatches: 5  
 Query Match: 97.16% Indels: 0  
 DB: 4 Gaps: 0

US-10-070-794A-4 (1-305) x AAD03295 (1-1867)

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 DB 532 ATCTTCGACACCATGCTGCAGATCAAGAAGGCTCTTTTGGCCCTGGTGGCCCAAGCGGCTC 591  
 QY 41 ArgAlaAlaProLeuThrAspSerIleLysGlnSerPheValGlyMetLeuThrIleThr 60  
 DB 592 CGAGCGGCACCTTTGTGGGACGACGAAGACAGAGCTTCGTGGGATGCTGACCATACACA 651  
 QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
 DB 652 GACTTCATCTGTTGCTGCACCGCTATTACAGGTCCCTGCTCCAGATCTACGAGATT 711  
 QY 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheIleAsnArg 100  
 DB 712 GAAGAACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 771  
 QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
 DB 772 GTCTCCATCTCTCCCAATGACAGCCTGTTCGAAGCTGTCTAGCCCTCATCAAGAACCGG 831  
 QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
 DB 832 ATCCACCGCTCCCGCTGCTGACACCTGCTCCGGGGCTGTCTCCACATCTCCACAT 891  
 QY 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
 DB 892 AAGCGGCTTCTCAAGTTCCTGCACATCTTTGGCACCTGTCTGCGCCGCTCTCTCTC 951  
 QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180  
 DB 952 TACCGCACCATCCAGATTGGGCATCGGCACATTCGAGAGCTTGGCGGTGGTGTGGAA 1011  
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 DB 1012 ACGGGCCCATCTCCGCCACTGACATCTTCGTGGACCGGCGGTGTCTGCGCTGCT 1071  
 QY 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
 DB 1072 GTGGTCAACGAACCTGGACAGGTAGTGGGCTCTACTCTCGCTTTGTGTATCCACCTG 1131  
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DB 1132 GCTGCCCAACAACATACACCACTGGACATGAATGTGGGAGAAGCCCTGAGCGCGG 1191  
 QY 241 ThrIeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValle 260  
 DB 1192 ACATCTGTCTGGAAGCGCTCTTCTGTCAGCCCCACAGACCTTTGGGGGAAGTCAAT 1251  
 QY 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
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 QY 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
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 ID AAD03319 standard; cDNA; 1873 BP.  
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 AC AAD03319;  
 XX  
 DT 13-JUN-2001 (first entry)  
 XX  
 DE Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.  
 XX  
 KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;  
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;  
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;  
 KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;  
 KW chromosome 15; ss.  
 XX  
 OS Sus scrofa.  
 XX  
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 FT 1..1395  
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 FT /product= "Sus scrofa complete Prkag3 protein"  
 XX  
 PN WO200120003-A2.  
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 PD 22-MAR-2001.  
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 PF 11-SEP-2000; 2000WO-EP009896.  
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 PR 10-SEP-1999; 99EP-00402236.  
 PR 18-MAY-2000; 2000EP-00401388.  
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 PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 PA (ANDE/) ANDERSSON L.  
 PA (LOOF/) LOOFT C.  
 PA (KALM/) KALM E.  
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 PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;  
 PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;  
 XX  
 DR WPI; 2001-244810/25.  
 DR P-PSDB; AAE00222.  
 XX  
 PT New variants of the gamma subunit of vertebrate adenosine monophosphate-  
 PT activated kinase for diagnosis or treatment of disorders associated with  
 PT energy metabolism such as diabetes, obesity, and myopathy.  
 XX  
 PS Claim 12; Page 62-64; 71pp; English.  
 XX  
 CC The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)  
 CC -activated kinase (AMPK) gamma subunit muscle-specific isoform, complete  
 CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation  
 CC in Prkag3 results in an altered regulation of carbohydrate metabolism,  
 CC particularly in skeletal muscle. PRKAG3 is useful as therapeutic for

CC treating carbohydrate metabolism disorders such as diabetes, obesity, and  
 CC disorders associated with muscle metabolism such as myopathy and  
 CC cardiovascular diseases, to modulate AMPK activity, and for restoring a  
 CC normal AMPK function. PRKAG3 sequence and its functionally altered  
 CC mutants are useful for the diagnostic evaluation, genetic testing and  
 CC prognosis of a metabolic disorder, preferably a carbohydrate metabolism  
 CC disorder. Primers that can detect a genetic polymorphic marker linked to  
 CC a sequence encoding PRKAG3, are useful for detecting a dysfunction of  
 CC carbohydrate metabolism resulting from the expression of a functionally  
 CC altered allele of PRKAG3. Transgenic animal and host cell transformed  
 CC with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant,  
 CC are useful for screening compounds able to modulate AMPK activity.  
 CC Nucleic acid encoding PRKAG3 is useful for detecting mutations in a  
 CC PRKAG3 gene, or in a sequence encoding the first cystathione beta  
 CC synthase (CBS) domain of PRKAG3 and is useful in gene therapy  
 XX  
 SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.24e-166 Length: 1873  
 Score: 1507.00 Matches: 296  
 Percent Similarity: 98.36% Conservative: 4  
 Best Local Similarity: 97.05% Mismatches: 5  
 Query Match: 97.16% Indels: 0  
 DB: 4 Gaps: 0

US-10-070-794A-4 (1-305) x AAD03319 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20  
 Db 478 ATGCACCTTCATGAGGAGCAGACCTCTACATGCCATGGGACCACTCCAAACTGGTC 537  
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 Db 538 ATCTTCGACACCATGCTGGAGATCAAGAGAGGCTTCTTGGCCCTGGTGGCAACGGGCTC 597  
 Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
 Db 598 CGAGCGGACCTTTGTGGGACAGCAAGAGCAGAGCTTCGTGGGGATGCTGACCATCACA 657  
 Qy 61 AspPheIleLeuValLeuHisAspTyrTyrArgSerProLeuValGlnIleTyrGluile 80  
 Db 658 GACTTCATCTTGGTGTGACCGCTATTACAGGTCCCTGGTCCAGATCTACGAGATT 717  
 Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
 Db 718 GAAGAACAATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777  
 Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
 Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837  
 Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
 Db 838 ATCCACCGCTTCCCGGCTTGGACCTGTCTCCGGGGCTGTGCTCCACATCCTCACAAT 897  
 Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
 Db 898 AAGCGGCTTCTCAAGTCTTCGCACATCTTTGGCACCTGTGCTCCCGGCTCTCTCTCTC 957  
 Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180  
 Db 958 TACGCGACCATCCAAAGATTGGGATCGGCATCCGACATTCGAGACTTGGCGGTGGTGGAA 1017  
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 Db 1018 ACGCGGCCATCTTCAGCCGACCTGGACATCTTCTGGACCGGCTGTGCTGGGCTGCCT 1077  
 Qy 201 ValValAsnGluCysGlyGlnValValIcLysLeuTyrSerArgPheAspValIleHisLeu 220  
 Db 1078 GTGGTCAACGAACCTGACAGGATAGTGGGCTTACTCTCTGCTTTGATGTGATCCACCTG 1137  
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Db 1138 GCTGCCCAACAAACATACACACCTGGACATGAATGTGGAGAAAGCCCTGAGCAGCGG 1197  
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 Db 1198 ACATGTGTCTGGAGGCGTCTTCTCTGCAGGCCACGAGACTTGGGGGAAGTCAATT 1257  
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
 Db 1258 GACCGGATTCTCCGGGAACAGGTGCACCGCTGGTGTCTCGTGGATGAGACCCAGCACCTT 1317  
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
 Db 1318 CTGGCGCTGTGTCCCTCTCTGACATCTTCAGGCTCTGTGCTGCTGCTGCTGCTGCTG 1377  
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 RESULT 13  
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 ID AAD36458 standard; DNA; 1873 BP.  
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 AC AAD36458;  
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 DT 09-AUG-2002 (first entry)  
 XX  
 DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).  
 XX  
 KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;  
 KW screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;  
 KW variant; ds.  
 XX  
 OS Sus scrofa.  
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 FT variation replace(154, A)  
 FT /tag= b  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
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 PN WO200220850-A2.  
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 PD 14-MAR-2002.  
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 PF 10-SEP-2001; 2001WO-US028283.  
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 PR 08-SEP-2000; 2000US-0231045P.  
 PR 08-JAN-2001; 2001US-0260239P.  
 PR 18-JUN-2001; 2001US-0299111P.  
 XX  
 PA (IOWA ) UNIV IOWA STATE RES FOUND INC.  
 XX  
 PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;  
 XX  
 DR WPI; 2002-393850/42.  
 DR P-PSDB; AAE22986.  
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 PT Screening animals to determine those likely to produce larger litters and  
 PT improved meat quality traits involves assaying for the presence of  
 PT polymorphisms in the AMP activated protein kinase regulatory gamma  
 PT subunit gene.  
 XX  
 PS Claim 34; Page 93-95; 109pp; English.  
 XX  
 CC The invention relates to a method for screening animals to determine  
 CC those more likely to produce large litters and improved meat quality  
 CC traits. The method involves assaying for the presence of a genotype in  
 CC the sample of genetic material obtained from animal. The genotype is  
 CC characterised by polymorphism(s) in the AMP activated protein kinase  
 CC regulatory gamma subunit (PRKAG3) gene. The method is used for screening

CC animals e.g., pigs to determine those most likely to exhibit improved  
 CC meat quality traits and to produce larger litters. The present sequence  
 CC is pig PRKAG3 polymorphic variant DNA (PRKAG3-52)  
 XX  
 SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 7.24e-166 Length: 1873  
 Score: 1507.00 Matches: 296  
 Percent Similarity: 98.36% Conservative: 4  
 Best Local Similarity: 97.05% Mismatches: 5  
 Query Match: 97.16% Indels: 0  
 DB: 6 Gaps:

US-10-070-794A-4 (1-305) x AAD36458 (1-1873)

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 Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
 Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTCTTTGGCCCTGGTGGCCAAACGGGTC 597  
 Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
 Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGAGAGCTTCGTGGGGATGCTGACCATCACA 657  
 Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
 Db 658 GACTTCATCTTGGTGTGTCACCGCTATTACAGTCCCTCCCTGGTCCAGATCTACGAGATT 717  
 Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
 Db 718 GAAGAACATAAGATTGAGACCTGGAGGAGATCTACCTTTCAAGGCTGCTTCAAGCCTCTG 777  
 Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
 Db 778 GTCTCCATCTCTCCCAATGACAGCCTGTTCGAAAGCTGTCTACGCGCTCTATCAAGAACCGG 837  
 Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
 Db 838 ATCCACCCCTGCGGCTCTGGACCTGTCTCCGGGGCTGTCTCCACATCTCACACAT 897  
 Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
 Db 898 AAGGGCTTCTCAAGTTCTGCACATCTTTGGCACCTGTCTGCCCGGCCCTCTCTTCCTC 957  
 Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180  
 Db 958 TACCGCACCATCCAAAGATTGGGCATCGGCACATTCGAGACCTTGGCCGTGTGTCTGGAA 1017  
 Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200  
 Db 1018 ACGGCGCCCATCTGACCGCCTGACATCTTCGTGGACCGCGTGTCTCTGGCGTGGCT 1077  
 Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
 Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGTATCCACCTG 1137  
 Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
 Db 1138 GCTGCCCAACAAACATACAAACCATCGGACATGAATGTGGGAGAGCCCTGAGGACGGG 1197  
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 Db 1198 ACACGTGTCTGGAAGGGCTCTTCTTCGACGCCGCCACGACCTTGGGGGAATCAT 1257  
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
 Db 1258 GACCGGATTTGCCGGGACAGGTGACCGCTGTGTCTGTGATGAGACCCAGCACCTT 1317  
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300

Db 1318 CTGGCGTGTGTCTCTCTCTGATCATCTTCAGGCTGTGTCTCAGCCCTGCTGGAATT 1377  
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 DT 09-AUG-2002 (first entry)  
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 DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).  
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 KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;  
 KW screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;  
 KW variant; ds.  
 XX  
 OS Sus scrofa.  
 XX  
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 CDS 1..1395  
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 FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"  
 FT /replace (89, C)  
 FT /\*tag= b  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 XX  
 PN WO200220850-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-US028283.  
 XX  
 PR 08-SEP-2000; 2000US-0231045P.  
 PR 08-JUN-2001; 2001US-0260239P.  
 PR 18-JUN-2001; 2001US-0299111P.  
 XX  
 PA (IOWA ) UNIV IOWA STATE RES FOUND INC.  
 XX  
 PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;  
 XX  
 XX WPI; 2002-393850/42.  
 DR P-PSDB; RAE22985.  
 XX  
 PT Screening animals to determine those likely to produce larger litters and  
 PT improved meat quality traits involves assaying for the presence of  
 PT polymorphisms in the AMP activated protein kinase regulatory gamma  
 PT subunit gene.  
 XX  
 PS Disclosure; Page 89-91; 109pp; English.  
 XX  
 CC The invention relates to a method for screening animals to determine  
 CC those more likely to produce large litters and improved meat quality  
 CC traits. The method involves assaying for the presence of a genotype in  
 CC the sample of genetic material obtained from animal. The genotype is  
 CC characterised by polymorphism(s) in the AMP activated protein kinase  
 CC regulatory gamma subunit (PRKAG3) gene. The method is used for screening  
 CC animals e.g., pigs to determine those most likely to exhibit improved  
 CC meat quality traits and to produce larger litters. The present sequence  
 CC is pig PRKAG3 polymorphic variant DNA (PRKAG3-30)  
 XX  
 SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 7.24e-166 Length: 1873  
 Score: 1507.00 Matches: 296  
 Percent Similarity: 98.36% Conservative: 4  
 Best Local Similarity: 97.05% Mismatches: 5  
 Query Match: 97.16% Indels: 0

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DB: 6 Gaps: 0
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QY 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
DB 478 ATGCACCTTCAGGAGCACACCTCTGATCCATGCCATGGCAGCAGCTCCAACTGGTC 537
QY 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
DB 538 ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTCTTTGGCCCTGGTGGCAACGGCGTC 597
QY 41 ArgAlaAlaProLeuThrProAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
DB 598 CGAGCGGCACCTTTGTGGGACAGCAAGAGAGCTTCGCGGGGATGCTGACCATCACA 657
QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
DB 658 GACTTCATCTTGGTGTGCTGCACCGCTATTACAGGTCCCCCTGGTCCAGATCTACGAGATT 717
QY 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
DB 718 GAAGAACAATAAGATTGAGACCTCGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777
QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
DB 778 GTCTCCATCTCTCCCAATGACAGCCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837
QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
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DB 898 AAGCGGCTCTCAAGTCTCTGCACATCTTTGGCACCTCTGTCGCCCGCCCTCTCTCTC 957
QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
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QY 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
DB 1018 ACGGCGCCATCTGACCGCACCTGGACATCTTGTGACCGCGGTGTCTGGCGTGCCT 1077
QY 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
DB 1078 GTGGTCAACGAAACTGCACAGGTAGTGGCTCTACTCTCGCTTTGATGTATACACCTG 1137
QY 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
DB 1138 GCTGCCCAACAACATACACACCTGGACATGAATGTGGGAGAAGCCCTGAGCGAGCGG 1197
QY 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
DB 1198 AACTGTGTCTGAAGCGGTCTTCTGTCAGCGCCACGAGACCTTGGGGGAAGTCATT 1257
QY 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
DB 1258 GACCGGATTCGCGGACAGGTGACCGCTGGTGTCTGTGATGATGACCCAGCACCTT 1317
QY 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
DB 1318 CTGGCGGTGGTGTCTCTCTGACATCTTTCAGGCTCTGGTGTCTGACCCCTGTGGAATT 1377
QY 301 AspAlaLeuGlyAla 305
DB 1378 GATGCCCTCGGGGCC 1392
RESULT 15
ID AAD36456 standard; DNA; 1873 BP.
XX
AC AAD36456;
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XX 09-AUG-2002 (first entry)
DT Pig wild-type PRKAG3 gene.
XX
DB AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;
KW ds.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
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FT /*tag= a
FT /product= "pig PRKAG3 wild-type protein"
FT variation /*tag= b
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XX WO200220850-A2.
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028283.
XX PF
XX 08-SEP-2000; 2000US-0231045P.
XX PR
XX 08-JAN-2001; 2001US-0260239P.
XX PR
XX 18-JUN-2001; 2001US-0299111P.
XX
XX (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
XX WPI; 2002-393850/42.
XX P-PSDB; AAE22984.
XX
XX Screening animals to determine those likely to produce larger litters and
XX improved meat quality traits involves assaying for the presence of
XX polymorphisms in the AMP activated protein kinase regulatory gamma
XX subunit gene.
XX
XX Claim 17; Fig 1; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
XX those more likely to produce large litters and improved meat quality
XX traits. The method involves assaying for the presence of a genotype in
XX the sample of genetic material obtained from animal. The genotype is
XX characterised by polymorphism(s) in the AMP activated protein kinase
XX regulatory gamma subunit (PRKAG3) gene. The method is used for screening
XX animals e.g., pigs to determine those most likely to exhibit improved
XX meat quality traits and to produce larger litters. The present sequence
XX is pig wild-type PRKAG3 gene
XX
XX Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 U; 0 Other;
SQ
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Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservative: 4
Best Local Similarity: 97.05% Mismatches: 5
Query Match: 97.16% Indels: 0
DB: 6 Gaps: 0
US-10-070-794A-4 (1-305) x AAD36456 (1-1873)
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Db |||||  
478 ATGCACCTTCATGTCAGGAGCACACCTGTCTACGATGCCATGGCAGCCAGCTCCAAACTGGTC 537  
QY 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
Db |||||  
538 ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTCTTTGCCCTGGTGGCCAAACGGCGTC 597  
QY 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
Db |||||  
598 CGAGCGGCACCTTTGTGGGACAGACAGACAGAGCTTCGTGGGATGCTGACCATCACA 657  
QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
Db |||||  
658 GACTTCATCTTGGTGTGTCACCGCTATTACAGGTCCCCCTGGTCCAGATCTACGAGATT 717  
QY 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db |||||  
718 GAAGAACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCCTCTG 777  
QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
Db |||||  
778 GTCTCCATCTCTCCATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837  
QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db |||||  
838 ATCCACCGCCTGCCGCTCTGACCCCTGTCTCCGGGGCTGTGCTCCACATCTCCACACAT 897  
QY 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db |||||  
898 AAGCGGCTTCTCAAGTTCTCTGCACATCTTTGGCACCTGTGGCCCTGCTCCCGGCCCTCCTTCCCTC 957  
QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180  
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958 TACCGCACCATCCAGATTGGGCATCCGCACATTCGAGACTTGGCCGTGGTGTGGAA 1017  
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Db |||||  
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Db |||||  
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1318 CTGGGCGTGGTGTCTCTCTGACATCTCTTCAAGGCTCTGGTGTCTCAGCCCTGCTGGAATT 1377  
QY 301 AspAlaLeuGlyAla 305  
Db |||||  
1378 GATGCCCTCGGGGCC 1392



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 25, 2006, 21:45:36 ; Search time 3036.51 Seconds  
(without alignments)  
4699.486 Million cell updates/sec

Title: US-10-070-794A-4

Perfect score: 1551

Sequence: 1 MRFQBHTCYDAMATSSKLV.....LSDIQLVLSPPAGIDALGA 305

Scoring table:

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Ygapop 10.0 , Ygapext	0.5		
Ygapop 6.0 , Xgapext	7.0		
Delop 6.0 , Delext	7.0		

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgm2 1/USPTO.spool\_p/US10070794/runat 24012006.164415.8798/app.query.fasta\_1.1102  
-DB=EST -OPWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0  
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Database :

EST:\*  
1: gb\_est1.\*  
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6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*  
10: gb\_est10.\*  
11: gb\_est11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
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2	1434	92.5	1470 11	DQ030935 Homo sapi
3	1426	91.9	1470 11	DQ030936 Pan trogl
4	1068	68.9	2058 4	BC079017 Rattus no
5	1067	68.8	2839 4	AK032238 Mus muscu
6	1055	68.0	796 6	CD628192 56028554H
7	1054	68.0	1990 4	CR861174 Pongo pyg

c	8	1048	67.6	754	6	CD628194
9	1027	66.2	824	8	8	56028552H
10	1009	65.1	1136	5	5	JGI XZT90
11	1009	65.1	1144	5	5	BX403964 BX403964
12	1009	65.1	1561	4	4	CR604823 full-leng
13	1009	65.1	1577	4	4	CR608916 full-leng
14	1009	65.1	1584	4	4	CR613967 full-leng
15	1009	65.1	1600	4	4	CR596899 full-leng
16	1009	65.1	1610	4	4	CR612109 full-leng
17	1009	65.1	1648	4	4	CR620523 full-leng
18	1006	64.9	1015	3	3	BM907915 AGENCOURT
19	1004	64.7	900	10	10	AY420782 Mus muscu
20	1003	64.7	900	10	10	AY420780 Homo sapi
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22	996	64.2	978	1	1	AL533446 AL533446
23	981	63.2	1623	4	4	CR611774 full-leng
24	976	62.9	1912	4	4	CNSOGLSJ Tetraodon
25	974	62.8	1081	1	1	AL554278 AL554278
26	969	62.5	1096	5	5	BX424876 BX424876
27	964.5	62.2	1023	1	1	AL555228 AL555228
28	952	61.4	929	1	1	AL548987 AL548987
29	947	61.1	1085	3	3	BM548053 AGENCOURT
30	946	61.0	857	8	8	DR866220 JGI CARG8
31	945	61.0	1082	1	1	AL524822 AL524822
32	933	60.2	944	5	5	BQ954908 AGENCOURT
33	920	59.3	1033	5	5	BQ382758 BX382758
34	915.5	59.0	1070	3	3	BQ224866 AGENCOURT
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#### ALIGNMENTS

RESULT 1

AK036585

LOCUS

DEFINITION

AK036585 2256 bp mRNA linear HTC 03-APR-2004  
Mus musculus adult male bone cDNA, RIKEN full-length enriched  
library, clone:9830138C07 product:5'-AMP-ACTIVATED PROTEIN KINASE,  
GAMMA-3 SUBUNIT (AMPK GAMMA-3 CHAIN) (AMPK GAMMA3) homolog [Homo  
sapiens], full insert sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

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Qy 281 LeuGlyValSerLeuSerAspIleuGlnAlaLeuValLeuSerProAlaGlyLe 300
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LOCUS DQ030935 1470 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens PRKAG3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ030935
VERSION DQ030935.1 GI:66882139
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1470)
AUTHORS Nielsen.R., Bustamante.C., Clark.A.G., Glanowski.S., Sackton.T.B.,
Hubisz.M.J., Fiedel-Alon.A., Tanenbaum.D.M., Civello.D.,
White.T.J., Sninsky.J.J., Adams.M.D. and Cargill.M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1470)
AUTHORS Nielsen.R., Bustamante.C., Clark.A.G., Glanowski.S., Sackton.T.B.,
Hubisz.M.J., Fiedel-Alon.A., Tanenbaum.D.M., Civello.D.,
White.T.J., Sninsky.J.J., Adams.M.D. and Cargill.M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
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Query Match: 92.46% Indels: 0
DB: 11 Gaps: 0

US-10-070-794a-4 (1-305) x DQ030935 (1-1470)

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Qy 21 IlePheAspThrMetLeuGluIleLysValAlaPheAlaLeuValAlaAsnGlyVal 40
Db 613 ATCTTCACACCACTCTGGAGATCAAGAGCCCTCTTTGCTCTGGTGGCCACAGGCTG 672
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 673 CGGCGACCCCTCTATGGGACAGCAGAGAGCTTTGTGGGATGCTGACCATCACT 732
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80

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Qy 301 AspAlaLeuGlyAla 305
Db 1453 GATGCCCTCAGCGCC 1467

DQ030936 1470 bp DNA linear GSS 02-JUN-2005
LOCUS DQ030936
DEFINITION Pan troglodytes PRKAG3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ030936
VERSION DQ030936.1 GI:66882140
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE 1 (bases 1 to 1470)
AUTHORS Nielsen.R., Bustamante.C., Clark.A.G., Glanowski.S., Sackton.T.B.,
Hubisz.M.J., Fiedel-Alon.A., Tanenbaum.D.M., Civello.D.,
White.T.J., Sninsky.J.J., Adams.M.D. and Cargill.M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1470)

```

**AUTHORS** Nielsen, R., Bustamante, C., Clark, A.G., Gnanowsk, S., Sachton, T.B., Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civallo, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

**COMMENT** This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

**FEATURES**

source	Location/Qualifiers	
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**ORIGIN**

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Query Match:	91.94%	Indels:	0
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US-10-070-794A-4 (1-305) x DQ030936 (1-1470)

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Qy	81	GluGlnHisLysIleGluIleThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	793	GAACAAATAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	852
Qy	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120
Db	853	GTCTCCCATCTCTCTAATGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	912
Qy	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	140
Db	913	ATCCATCGCGCTGCTGTTCTGGACCCGGTGTCCAGCNACGCTACTCCACATCTCCACAC	972
Qy	141	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160
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Qy	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu	180
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Qy	201	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	220
Db	1153	GTGGTCAACGAATGTGTGAGTGTGGGCTCTATTCCCGCTTTGATTGATTCACCTG	1212

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, J., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAP Plate: 182 Row: m Column: 20  
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein  
 This clone has the following problem: frame shifted.

## FEATURES

Location/Qualifiers  
 1..2058  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="IMAGE:7113709"  
 /tissue type="Testis, rat (Brown Norway)"  
 /clone\_lib="NIH\_MGC\_237"  
 /lab\_host="DH10B"  
 /note="vector: pExpress1"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1..59e-111 Length: 2058  
 Score: 1068.00 Matches: 195  
 Percent Similarity: 86.29% Conservative: 63  
 Best Local Similarity: 65.22% Mismatches: 41  
 Query Match: 68.86% Indels: 0  
 DB: 4 Gaps: 0

US-10-070-794A-4 (1-305) x BC079017 (1-2058)

Qy 1 MetArgPheMetGlnGluHisThrCytTyAspAlaMetAlaThrSerSerLysLeuVal 20  
 Db 838 ATGGATTTCATGAGTGCACCAAGTGTATGACATCGTTCACACCACTCAAGCTTGT 897  
 Qy 21 IlePheAspThrMetLeuGluIleLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
 Db 898 GTCTTCGACACTACGTTGCAAGTAAAGAGCCCTCTTGTGTTGGTAGCAACGGAGTC 957  
 Qy 41 ArgAlaAlaProLeuTrpAspSerLysValGlnSerPheValGlyMetLeuThrIleThr 60  
 Db 958 CGTGCAGCGCGCTGTGGAAAGTAAAGCAGAGCTTCGTAGGATGCTCACAAATTACA 1017  
 Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
 Db 1018 GATTTTCATAACATCTACACAGATCTATAAATCCCATGCTGTACAGATTATGATTTG 1077  
 Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
 Db 1078 GAGGAACATGAAGTTGAACGTGGAGGGAACGTGACTTCAAGAAACCTTCAAGCCCTTG 1137  
 Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
 Db 1138 GTGAATATCTTCAGATGCGAGCTTCGATGCTGTATCTGTTGATGATCAAAATAAA 1197  
 Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
 Db 1198 ATCCACAGATGCGCATTTATGACCTATCAGTGGGAATGCATTTATATACTTACCAC 1257  
 Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
 Db 1258 AAAAGATCTCTCAAGTCTCTCCAGCTTTTATGCTGACATGCCAAAGCCGCTTCATG 1317  
 Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180  
 Db 1318 AAGCAGAACTCGATGAGCTCGGAATAGGAACATATCACAAATATGCTTCATTCACCCG 1377  
 Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
 Db 1378 AATACCCCATCATCAAGCTTGAACATCTTTGTGGAGAGCGGATATCTGGCGCTCT 1437  
 Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220

Db 1438 GTGGTGTAGTGCAGGAAAGTTGTAGATATTACTCCAGTTTGTATGTAATTAATCTT 1497  
 Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
 Db 1498 CTGCTGAGAAACGTAACATACCTAGACATACGGTGACCCAGGCGCTTCACACCGC 1557  
 Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyValIle 260  
 Db 1558 TCACAGTATTTTGGAGGTGTGGTCAAGTGCAGTAAGCTGGAACACCTGGAGACCATGTG 1617  
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
 Db 1618 GACAGAATAGTAGAGCGGAGGTCCATCGGTGGTGTGATGATGAAGCAGCAGATGATT 1677  
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299  
 Db 1678 GTGGTATATATCTCCCTGTGACATCTCGAGCCCTGATCTTCACACCGAGGT 1734

RESULT 5  
 AK032238

## LOCUS

## DEFINITION

AK032238 2839 bp mRNA linear HTC 03-APR-2004  
 Mus musculus adult male olfactory brain cDNA, RIKEN full-length  
 enriched library, clone:8430509K05 product:similar to AMP ACTIVATED  
 PROTEIN KINASE GAMMA 1 (FRAGMENT) [Mus musculus], full insert  
 sequence.

## ACCESSION

AK032238

## VERSION

AK032238.1 GI:26328068

## KEYWORDS

HTC; CAP trapper.

## SOURCE

Mus musculus

## ORGANISM

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)

## REFERENCE

2

## AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

## TITLE

Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes

## JOURNAL

Genome Res. 10 (10), 1617-1630 (2000)

## PUBMED

11042159

## REFERENCE

3

## AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

## TITLE

RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer

## JOURNAL

Genome Res. 10 (11), 1757-1771 (2000)

## PUBMED

11076861

## REFERENCE

4

## AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.

## TITLE

Functional annotation of a full-length mouse cDNA collection

## JOURNAL

Nature 409, 685-690 (2001)

## REFERENCE

5

## AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.

## TITLE

Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs

## JOURNAL

Nature 420, 563-573 (2002)

## REFERENCE

6 (bases 1 to 2839)

## AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katon, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, FAX: 81-45-503-9216)

CNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

# FEATURES

source

Location/Qualifiers  
1. 2839  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
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/db\_xref="taxon:10090"  
/clone="6430509K05"  
/sex="male"  
/tissue\_type="olfactory brain"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="adult"  
400. 1731

## CDS

/note="unnamed protein product; putative similar to AMP ACTIVATED PROTEIN KINASE GAMMA 1 (FRAGMENT) [Mus musculus] (SPTK[Q925V0, evidence: FASTV, 77%ID, 96.8%length, match=182)"  
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polyA\_signal

/note="putative"

polyA\_site

/note="putative"

## ORIGIN

Alignment Scores:  
Pred. No.: 3,35e-111 Length: 2839  
Score: 1067.00 Matches: 195  
Percent Similarity: 86.29% Conservative: 63  
Best Local Similarity: 65.22% Mismatches: 41  
Query Match: 68.79% Indels: 0  
DB: 4 Gaps: 0

US-10-070-794A-4 (1-305) x AK032238 (1-2839)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20  
Db 805 ATGCAGTTCATGAGGTCACACAGAGTGTATGACATCGTTCCCAACAGTCGTTGTT 864

Qy 21 IlePheAspThrMetLeuGluIleValLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
Db 865 GTCTTCGACACTACGTTGCAAGTCAAAAGGCTCTTTTCCTTGGTAGCAACGGAGTC 924  
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
Db 925 CGTGCAGCGCGCTGTGGGAAAGTAAAGACAGAGCTTTGTAGGAATGCTCAGCATACA 984  
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
Db 985 GATTTCATAAATATCCTACACAGATCTATATAATACCCCATGGTACAGATTTATGAANTG 1044  
Qy 81 GluGlnHisLysIleGluThrTrpAspGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db 1045 GAGAACATGAAGATTGAACCTGGAGGAGTGTACTTACAGAAACCTTCAGACCTTTG 1104  
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
Db 1105 GTGAACATCTCTCCAGATGCGAGCTCTTCGATGCTGTATCTCGTTGATCAAAATAA 1164  
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db 1165 ATCCACAGATTGCGAGTTATTGACCTTACCTCAGTGGGAAACGACTTATATATCTAC 1224  
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db 1225 AAAAGAACTCTCAAGTCTCTCCAGCTTTTATGCTGACATGCCAACAATATTGCTTC 1284  
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180  
Db 1285 AAGCAGAACCTCGATGAGCTTGGAAATCGGAACGTCACACAATATTGCTTCATCCAC 1344  
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
Db 1345 GACACTCCCATCATCAAGGCTTGAACATCTCTCGGAGAGACGATATCGCATTCGCT 1404  
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
Db 1405 GTGTGTGATGAGTCAGGAAAGTTGTAGATATTTATTCGAATTTGATGATTAATCTT 1464  
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
Db 1465 GCTGCTGAGAAACGTAACAATAACTTGGACATCAGTGCACCCAGCGGCTCGACACCGC 1524  
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260  
Db 1525 TCGCAGTATTTTGGGCTGTGGTGAAGCTAGCTGAAGCACTGGAGACCATCGTG 1584  
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
Db 1585 GACAGGATAGTGAGCGGAGTCCATCGGCTGGTGTGTAGTATGATGAGCAGATAGCAT 1644  
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299  
Db 1645 GTGGGTATTTATCTCCCTGTCAGACATCTCGCAAGCCCTGATCTTCACACAGCAGGT 1701

RESULT 6  
CD628192/c 796 bp mRNA linear EST 12-JAN-2004  
LOCUS 56028554H1 FLP Homo sapiens cDNA, mRNA sequence.  
DEFINITION CD628192  
ACCESSION CD628192  
VERSION CD628192.1 GI:40276458  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo  
1 (bases 1 to 796)  
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

QY 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20



Db 898 ATGGATTTCATGAGTTCACACAAAGTGTATGACATCGTTCACACAGCTTCAAAGCTTGTT 957

Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyVal 40

Db 958 GTCTTTGATACATACAAAGTTAAAGAGCCCTCTCTGCTTTGGTAGCAACGGGTGC 1017

Qy 41 ArgAlaAlaProLeuThrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60

Db 1018 CGAGCAGCGCGCTGTGGGAGAGTAAAGAAACAAAGTTTGTAGGAATGCTAAACAATACA 1077

Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80

Db 1078 GATTTCTAATAATACATACATAGTACTATAATACACTATGTGTACAGATTTATGATTA 1137

Qy 81 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100

Db 1138 GAGGAACATAAAATTGAACATGAGGAGGCTTTATTATCAAGAAACATTTAAGCCCTTA 1197

Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120

Db 1198 GTGAATATATCTCCAGATGCAAGCTCTCGATGCTGTATACTCTTTGATCAAAATAA 1257

Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140

Db 1258 ATCCACAGATGCCGCTTATGACCTATCAGTGGGAATGCGCTTTATATACCTTACCAC 1317

Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160

Db 1318 AAAAGAATCTCAAGTCTCTCCAGCTTTTATGCTGTATATGCTCAAGAGCTGCTTCATG 1377

Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180

Db 1378 AAGCAGAACCTCGGATGAGCTTGGAAATAGGAACATACCAACATTTGCTTCATACATCCA 1437

Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200

Db 1438 GACACTCCCATCATCAAGCTTGAACATATTTGTGGAAAGCAAGATATCAGCTTCGCT 1497

Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220

Db 1498 GTTGTGGATGATCAGGAAAGATTGTAGATATTATTTATCCAAATTTGATGTAATTAATCTT 1557

Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240

Db 1558 GCTGCTGAGAAACATACATAAATACATAGATATCATGACCGCCGCTTCAGACCGCT 1617

Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260

Db 1618 TCACAGTATTTGAAGGTTGTGAAGTGCATTAAGCTGGAAATACCTGGAGACCATTTGTG 1677

Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280

Db 1678 GACAGATAGTAAGAGCTGAGTCCATCGCTGGTGGTGGCAATGAAGCAGATAGTATT 1737

Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299

Db 1738 GTGGGTATTATTTCCCTGTGACATTTCTGCAAGCCCTGATCCTCACACAGCAGGT 1794

RESULT 8

CD628194/c CD628194 754 bp mRNA linear EST 12-JAN-2004

LOCUS 56028562H1 FLP Homo sapiens cDNA, mRNA sequence.

DEFINITION CD628194

ACCESSION CD628194

VERSION CD628194.1 GI:40276460

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 754)

AUTHORS Fu, G.K., Wang, J.T., Yang, J., Xu-Young, J. and Stuve, L.L.

TITLE Circular rapid amplification of cDNA ends for high-throughput

extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)

15203218

Contact: Fu GK

Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102

Email: gfu@incyte.com.

Location/Qualifiers

source

1. .754

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone\_lib="FLP"

/note="Vector: pDrive Cloning Vector"

ORIGIN

Alignment Scores:

Pred. No.: 7,28e-110 Length: 754

Score: 1048.00 Matches: 207

Percent Similarity: 99.04% Conservative: 0

Best Local Similarity: 99.04% Mismatches: 1

Query Match: 67.57% Indels: 1

DB: 6 Gaps: 0

US-10-070-794a-4 (1-305) x CD628194 (1-754)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThr-SerSerLysLeuVa 20

Db 626 ATGGCTTTCATGCGAGGAGCACCTGCTACGATGCCATGGCACTTAGCTTCAAGCTAGT 567

Qy 20 lIlePheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyVa 40

Db 566 CATCTTCGATACCATGCTGGAGATCAAGAGCCCTTCTTGTCTGTGGCCACGCTGT 507

Qy 40 lArgAlaAlaProLeuThrAspSerLysLysGlnSerPheValGlyMetLeuThrIleTh 60

Db 506 GCGGCGACGCCCTCTATGGGACAGCAAGAGAGCTTTGTGGGATGCTGCACATCAC 447

Qy 60 rAspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluI 80

Db 446 TGACTTTCATCTGCTGCTGCTACTACGATCCCTCCCTGCTGCTCAGATCTATGAGT 387

Qy 80 eGluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLe 100

Db 386 TGAACACATAAAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTCAAGCTCT 327

Qy 100 uValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnAr 120

Db 326 GGTCTCCATCTCTCTAATGATAGCTTTTGAAGCTGTCTACACCTCATCAAGAACCG 267

Qy 120 gIleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHi 140

Db 266 GATCCACCGCTGCGAGTCTTGACCCCGGTGTACGCAACGCTACTTCCATCTCTCACACA 207

Qy 140 sLysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLe 160

Db 206 CAAAGCGCTGCTCAAGTTCCTGCAATCTTTGGTTCCCTGCTGCTCCCGGCTCTCTCTCT 147

Qy 160 uTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGl 180

Db 146 CTACCGCACTATCCAAGATTTGGGCATCGGCACATTCGAGACTTGGCTGTGGTCTGGG 87

Qy 180 uThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPr 200

Db 86 GACAGACCCATCTGACTGCACTGCACTCTTTGTGGACCGGCGTGTGTCTGCATGCC 27

Qy 200 oValValAsnGluCysGlyGlnVal 208

Db 26 TGTGTGTCAACGAATGTGTGCTCAGGTC 2

RESULT 9

CK313244





end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 6712.f

For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?s=CL0BB0072F11RP1&c=6712.f>.

FEATURES  
source  
1. .1136  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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/clone\_lib="Homo sapiens NEUROBLASTOMA"  
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.2e-105 Length: 1136  
Score: 1009.00 Matches: 192  
Percent Similarity: 82.99% Conservative: 52  
Best Local Similarity: 65.31% Mismatches: 50  
Query Match: 65.05% Indels: 0  
DB: 5 Gaps: 0

US-10-070-794A-4 (1-305) x BX403964 (1-1136)

QY 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22  
DB 85 TTCTGAAGTCTATCGTCTGATGACCTGATCCACAGCTCCAAATGGTTGTTATT 144  
QY 23 AspThrMetLeuGluIleLysLeuAlaPhePheAlaLeuValAlaAenGlyValArgAla 42  
DB 145 GATACGTCCTCGAGGTGAGAAAGCTTTTCTTGTGTGACTAAACGGGTGTACGAGCT 204  
QY 43 AlaProLeuTrpAspSerLysLeuGlnSerPheValGlyMetLeuThrIleThrAspPhe 62  
DB 205 GCCCCTTATGGGATAGTAAGAGCAAGTTTGTGGCATGCTGACCATCAGATTTC 264  
QY 63 IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGln 82  
DB 265 ATCAATATCTCGACCGCTACTATAAATCAGCCTTGGTACAGATCTATGAGCTAGAGAA 324  
QY 83 HisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSer 102  
DB 325 CACAAGATAGAAACTTGGAGAGGTGTATCTCCAGGACTCCTTTAAACCGCTTGTCTGC 384  
QY 103 IleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHis 122  
DB 385 ATTTCTCTTAATGCCAGCTGTGTGATGCTGTCTCTTCAATTAATTCGGAACAGATCCAC 444  
QY 123 ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArg 142  
DB 445 AGGTCGCCAGATTATGGACCCAGATCAGGCAATATCTTTGTACATCTCCACCACAAGCGC 504  
QY 143 LeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg 162  
DB 505 ATTCGTAAGTTCCTCAAAATGTTTATCACTGAGTTCGCCCAAGCCAGAGTTTCATGTCGAAG 564  
QY 163 ThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThrAla 182  
DB 565 TTCTGGGAAGACTACAGATTCGGACCTATGCCAATATGCTATGTTGCGCACTACACC 624  
QY 183 ProfileLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProValVal 202  
DB 625 CCCGCTATGTGCTCTGGGATTTTGTACAGCATCGAGTCTCAGCCCTGCGCAGTGTG 684  
QY 203 AsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAlaala 222

DB 685 GATGAGAGGGCGTGTGGTGCATCTACTCCAGTTTGATGTTTATCAATCTGGCAGCA 744  
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DB 745 GAAAGACCTACAAACACCTAGATGTATCTGTGACTAAAGCCTTGCAACATCGATCAT 804  
QY 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 262  
DB 805 TACTTTGAGGGTGTCTCAAGTGTCTACCTGCATGAGACTCTGGAGACCATCATCAACAG 864  
QY 263 IleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuGly 282  
DB 865 CTATGGAGACGAGGTTACCGACTGTGTAGTGTGATGAAATGATGTGGTCAAGGGA 924  
QY 283 ValValSerLeuSerAspLeuGlnAlaLeuValLeuSer 296  
DB 925 ATTGTATCACTGTCTGACATCTCTGCAGGCCCTGGTGTCTACA 966

RESULT 11  
BX421925 1144 bp mRNA linear EST 01-MAY-2004  
LOCUS  
DEFINITION  
BX421925 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA  
clone CSODH005YN22 5-PRIME, mRNA sequence.

ACCESSION  
BX421925  
VERSION  
BX421925.2 GI:46925182  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE  
1. (bases 1 to 1144)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
COMMENT  
On May 13, 2003 this sequence version replaced gi:30638442.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
This sequence belongs to sequence cluster 6712.f  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?s=CSODH005DG11QP1&c=6712.f>.

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/cell\_line="JURKAT CELL LINE"  
/clone\_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"  
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.24e-105 Length: 1144  
Score: 1009.00 Matches: 192  
Percent Similarity: 82.99% Conservative: 52  
Best Local Similarity: 65.31% Mismatches: 50  
Query Match: 65.05% Indels: 0  
DB: 5 Gaps: 0

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US-10-070-794A-4 (1-305) x BX421925 (1-1144)

Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
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Qy 23 AspThrMetLeuGluIleLysLeuAlaPhePheAlaLeuValAlaAsnGlyValArgAla 42
Db 145 GATACGTCCTCGAGGTGAAGAAAGCTTTTTCCTTGGTGACTAAACGGTGTACGAGCT 204

Qy 43 AlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 205 GCCCTTTATGGGATAGTAGAAGCAAAAGTTTGTGGCATGCTGACCATCCTGATTTTC 264

Qy 63 IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGln 82
Db 265 ATCAATATCTTCGACCGCTACTATAAATCAGCCTTGGTACAGATCTATGAGCTAGAAGAA 324

Qy 83 HisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSer 102
Db 325 CACAAGATAGAAACTTGGAGAGAGGTGTATCTCCAGAGCTCTTTAAACCGCTTGTCTGC 384

Qy 103 IleSerProLeuAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHis 122
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Qy 123 ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArg 142
Db 445 AGGCTGCCAGTTATTGACCCAGAAATCAGCAATACTTTGTATCTCTCACCACCAAGCGC 504

Qy 143 LeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg 162
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Qy 163 ThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThrAla 182
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Qy 183 ProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProValVal 202
Db 625 CCGCTCTATGCTGCTCTGGGATTTTGTGACAGCATCGAGTCTCAGCCCTGCCAGTGGTG 684

Qy 203 AsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAlaAla 222
Db 685 GATGAGAAGGGGGTGGTGGGACATCTACTCCAAGTTTGTATGTTATCAATCTGGCAGCA 744

Qy 223 GlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242
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Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 262
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Qy 263 IleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeuGly 282
Db 865 CTAGTGAAGCAGAGGTTTCCACCACTTGTAGTGTGTGATCAAAATGATGTGGTCAAGGGA 924

Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 925 ATGTATCACTGCTGATCATCTCTGCAGGCCCTGCTGCTCA 966

RESULT 12
LOCUS CR604823 1561 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODK007E02 of HeLa cells Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR604823
VERSION CR604823.1 GI:50485630
KEYWORDS HTC; cNSLT cDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1561)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : feng liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1561)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. .1561
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/clone="CSODK007E02"
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ORIGIN

Alignment Scores:
Pred. No.: 6,72e-105 Length: 1561
Score: 1009.00 Matches: 192
Percent Similarity: 82.99% Conservative: 52
Best Local Similarity: 65.31% Mismatches: 50
Query Match: 65.05% Indels: 0
DB: 4 Gaps: 0

US-10-070-794A-4 (1-305) x CR604823 (1-1561)

Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
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Qy 23 AspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAla 42
Db 146 GATACGTCCTCGAGGTGAAGAAAGCTTTTTCCTTGGTGACTAAACGGTGTACGAGCT 205

Qy 43 AlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 206 GCCCTTTATGGGATAGTAGAAGCAAAAGTTTGTGGCATGCTGACCATCCTGATTTTC 265

Qy 63 IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGln 82
Db 266 ATCAATATCTTCGACCGCTACTATAAATCAGCCTTGGTACAGATCTATGAGCTAGAAGAA 325

Qy 83 HisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSer 102
Db 326 CACAAGATAGAAACTTGGAGAGAGGTGTATCTCCAGAGCTCTCTTAAACCGCTGTCTGC 385

Qy 103 IleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHis 122
Db 386 ATTTCTCTTAATGCACGCTTGTGTTGATGCTGCTCTCTTCAATTAATTCGAACAGATCCAC 445

Qy 123 ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArg 142
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Qy 143 LeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg 162
Db 506 ATTCGTAAGTTCTCTCAAAATGTTTATCACTGAGTTCCCAAGCCAGAGTTTCATGTCCAAG 565

Qy 163 ThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThrAla 182

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SOURCE  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
JOURNAL Homiidae; Homo.  
REMARK 1 (bases 1 to 1584)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paraday Avenue  
2 (bases 1 to 1584)  
Genoscope.  
Direct Submission  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

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source  
1. .1584  
/organism="Homo sapiens"  
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Alignment Scores:  
Pred. No.: 6.87e-105 Length: 1584  
Score: 1009.00 Matches: 1584  
Percent Similarity: 82.99% Conservative: 52  
Best Local Similarity: 65.31% Mismatches: 50  
Query Match: 65.05% Indels: 0  
DB: 4 Gaps: 0

US-10-070-794A-4 (1-305) x CR613967 (1-1584)

QY 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22  
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QY 23 AspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaSerGlyValArgAla 42  
DB 146 GATACGTCCTCGAGGTGAAGAAGCTTTTTCCTTTGGTGACTAACGGTGATCCGAGCT 205

QY 43 AlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62  
DB 206 GCCCTTTATGGATAGTAGAGCAAGTTTGTGGCGATGCTGACCATCATGATTTTC 265

QY 63 IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGln 82  
DB 266 ATCAATATCTCGACCGCTACTATAATACAGCTTGGTACAGATCTATGAGCTAGAAGAA 325

QY 83 HisValIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSer 102  
DB 326 CACAAGATAGAAACTTGGAGAGAGGTGTATCTCCAGGACTCTCTTAACCGCTTGTCTGC 385

QY 103 IleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHis 122  
DB 386 ATTCTCTTAATGCCAGCTGTTTGTATGCTGTCTCTTAATTCGGAACAGATCCAC 445

QY 123 ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArg 142  
DB 446 AGGCTGCCAGTTATGACCCAGAAATCAGGCAATACITTTGTACATCTCCACCCACAGCGC 505

QY 143 LeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg 162  
DB 143 LeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg 162

506 ATTCTGAAGTCTCTCAAAATTTTATCATCTAGTTCCTCCCAAGCCAGAGTTTCATGTCCAAG 565

QY 163 ThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAla 182  
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QY 183 ProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProValVal 202  
DB 626 CCGCTCTATGTGCTCTGGGGATTTTGTACAGCATCGAGTCTCAGCCCTGCCAGTGGTG 685

QY 203 AsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAlaAla 222  
DB 686 GATGAGAAGGGGGCTGTGGTGACATCTACTCAAGTTTGTATTTATCAATCTGGCAGCA 745

QY 223 GlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242  
DB 746 GAAAAGACCTACACCAACCTAGATGTATCTGTGACTTAAGCCTTGCACATCGATCAT 805

QY 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 262  
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QY 263 IleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeuGly 282  
DB 866 CTAGTGAAGCAGAGGTTCCAGCACTTGTAGTGGTGATGAAAATGATGTGGTCAAGGGA 925

QY 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296  
DB 926 ATTGTATCACTGTCTGACATCTCTGAGGCCCTGGTGTCTCACA 967

RESULT 15  
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DEFINITION CR596899  
ACCESSION CR596899.1 GI:50477706  
VERSION HTC; CNSLT\_CDNA.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 1600)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paraday Avenue  
2 (bases 1 to 1600)  
Genoscope.  
Direct Submission  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

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/plasmid="pCMVSPORT\_6"

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Pred. No.: 6.97e-105 Length: 1600



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 25, 2006, 21:59:11 ; Search time 157.061 Seconds  
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3451.881 Million cell updates/sec

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	1506	97.1	1873	3	US-09-950-022A-7
5	1503	96.9	1873	3	US-09-950-022A-9
6	1064	68.6	1435	2	US-08-878-989-14
7	1064	68.6	1435	3	US-09-272-796-14
8	1064	68.6	1506	3	US-09-949-016-2390
9	1009	65.1	1500	3	US-09-949-016-5010

ALIGNMENTS

RESULT 1

US-09-950-022A-1  
; Sequence 1, Application US/09950022A

; Patent No. 6919177  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark.  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950,022A  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
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; TYPE: DNA  
; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1392)  
; OTHER INFORMATION:  
US-09-950-022A-1

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Sequence 63, Appl  
Sequence 16752, A  
Sequence 1659, Ap  
Sequence 4769, Ap  
Sequence 134, App  
Sequence 4899, Ap  
Sequence 432, App  
Sequence 1, Appli  
Sequence 14132, A  
Sequence 673, Appli  
Sequence 1, Appli  
Sequence 82286, A  
Sequence 987, App  
Sequence 2, Appli  
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Sequence 82262, A  
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US-10-070-794A-4 (1-305) x US-09-950-022A-1 (1-1873)

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Db	538	ATCTTCGACACCATGCTGGAGATCAGAGCCCTCTTTGGCCCTGGTGGCCCAACGGCGTC	597
Qy	41	ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr	60
Db	598	CGAGCGGCACCTTTGGGACAGCAAGACAGAGCTTCGTGGGGATGCTGACCATCACA	657
Qy	61	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	80
Db	658	GACTTCATCTTGGTGTGCACCGCTATTACAGGTCCCTGGTCCAGATCTACGAGATT	717
Qy	81	GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	718	GAAGACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGCGTCTTCAAGCCCTCTG	777
Qy	101	ValSerIleSerProAsnAspSerLysGlnSerPheValGlyMetLeuThrIleThr	120
Db	778	GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGACCGG	837
Qy	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	140
Db	838	ATCCACCGCCTGCCGGTCTCTGACATCCTTACAGGCTGTCTACGCCCTCATCAAGACCGG	897
Qy	141	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160
Db	898	AAGCGGCTTCTCAAGTCTCTGCACATCTTTGGCACCCCTGCTGCCCGCCCTCTCTCTC	957
Qy	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu	180
Db	958	TACCGCACCATCCAAAGATTGGGCATCGGCATCTCGAGACTTGGCGGTGGTGTGAA	1017
Qy	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	200
Db	1018	ACGGGCCCCATCCTGACCGCACTGGACATCTTCGTGGACCGCGGTGTCTCGCGCTGCT	1077
Qy	201	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	220
Db	1078	GTGGTCAACGAACCTGGACAGGTAGTGGCCTCTACTCTCGCTTTGATGTATCCACCTG	1137
Qy	221	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	240
Db	1138	GCTGCCCAACAACATAACAACACCTGGACATGAATGTGGGAGAGCCCTCAGGCGCGG	1197
Qy	241	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyValIle	260
Db	1198	ACACTGTGTGGAAAGGGGTCTTCTTCGCCAGCCCAAGAGACTTGGGGGAGTCAATT	1257
Qy	261	AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	280
Db	1258	GACCGGATTGTCCGGGAACAGGTGCACCGCTGGTGTCTCGTGGATGAGACCCAGCACCTT	1317
Qy	281	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	300
Db	1318	CTGGCGGTGGTGTCTCTGACATCCTTACAGGCTCTGGTGTCTCAGCCCTCTGGAATT	1377
Qy	301	AspAlaLeuGlyAla 305	
Db	1378	GATGCCCTCGGGGCC 1392	

RESULT 2  
US-09-950-022A-3  
; Sequence 3, Application US/09950022A  
; Patent No. 6919177  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950, 022A  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260, 239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299, 111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1873  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) ..(1392)  
; OTHER INFORMATION:

Alignment Scores:  
Pred. No.: 4.53e-175 Length: 1873  
Score: 1507.00 Matches: 296  
Percent Similarity: 98.36% Conservative: 4  
Best Local Similarity: 97.05% Mismatches: 5  
Query Match: 97.16% Indels: 0  
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022A-3 (1-1873)

Qy	1	MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal	20
Db	478	ATGCACCTTCATGCAGGACACACCTGCTACGATGCCATGGCGACAGCTCCAAACTGGTC	537
Qy	21	IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal	40
Db	538	ATCTTCGACACCATGCTGGAGATCAGAGCCCTCTTTGGCCCTGGTGGCCCAACGGCGTC	597
Qy	41	ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr	60
Db	598	CGAGCGGCACCTTTGGGACAGCAAGACAGAGCTTCGTGGGGATGCTGACCATCACA	657
Qy	61	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	80
Db	658	GACTTCATCTTGGTGTGCACCGCTATTACAGGTCCCTGGTCCAGATCTACGAGATT	717
Qy	81	GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	718	GAAGACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGTCTTCAAGCTCTG	777
Qy	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120
Db	778	GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGACCGG	837
Qy	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	140
Db	838	ATCCACCGCCTGCCGGTCTCTGACATCCTTCCCGGGCTGTGCTCCATCTCACAT	897
Qy	141	LysArgLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160



Db 998 AAGCGGCTTCAAGATTCCTGCACATCTTTGGCACCTGTGCGCCCGCCCTCTCCTC 957  
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180  
Db 958 TACCGCACCATCCAGATTTGGGATCGGCATCCGACATTCGAGACTTGGCGGTGCTGGAA 1017  
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200  
Db 1018 ACGCGGCCCATCTCGACCGCATCTTCGACCGCGGTGTCTGCGCTGCCT 1077  
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
Db 1078 GTGTCTAACGAACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGTATCCACTG 1137  
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
Db 1138 GCTGCCCAACAACATACACCATCTGGACATGATGTGGAGAGCCCTGAGCAGCGG 1197  
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260  
Db 1198 ACTGTGTCTGGAAGCGCTCTTCTCTCCAGCCCGCCAGACCTTGGGGAAGTCATT 1257  
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
Db 1258 GACCGGATGTCCGGGAACAGGTGCACCGCTGTGTCTGTGGATGAGACCCACACTT 1317  
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
Db 1318 CTGGCGGTGTGTCTCTCTGACATCTCTCAGGCTCTGTGTCTCAGCCCTGTGTGAATT 1377  
Qy 301 AspAlaLeuGlyAla 305  
Db 1378 GATGCCCTCGGGGCC 1392

## RESULT 3

US-09-950-022A-5  
; Sequence 5, Application US/09950022A  
; Patent No. 6919177  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P0468US3  
; CURRENT APPLICATION NUMBER: US/09/950,022A  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 1873  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1392)  
; OTHER INFORMATION:  
US-09-950-022A-5  
Alignment Scores:  
Pred. No.: 4,53e-175 Length: 1873  
Score: 1507.00 Matches: 296  
Percent Similarity: 98.36% Conservativeness: .4  
Best Local Similarity: 97.05% Mismatches: 5

Query Match: 97.16% Indels: 0  
DB: 3 Gaps: 0  
US-10-070-794A-4 (1-305) x US-09-950-022A-5 (1-1873)  
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20  
Db 478 ATGCACCTTCATGCGAGGACACACCTGTACGATGCCATGGCAGCTCCAAACTGGTC 537  
Qy 21 IlePheAspThrMetLeuGluIleLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
Db 538 ATCTTCGACACCATGTCTGGAGATCAAGAGGCCCTTCTTGCCCTGTGTGGCCACGGCGTC 597  
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGATGCTGACCATCACA 657  
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
Db 658 GACTTCATCTTGTGTGTCACCGCTATTACAGGTCCCGCTGTGTGTCAGATCTACGAGATT 717  
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db 718 GAGAACATTAAGATTGAGACTTGGAGGAGATCTACCTTCAGGCTGCTTCAAGCCTCTG 777  
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGTGTCTACGGCCTCATCAAGAACCGG 837  
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db 838 ATCCACCGCCTGCGGTCTCTGGACCTGTCTCGGGGCTGTGTCTCCACATCTCTCACAT 897  
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db 898 AAGCGGCTTCTCAAGTCTCTGCAATCTTTGGACACCTGTGTGCCCCGCCCTCTCTCTC 957  
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180  
Db 958 TACCGCACCATCCAGATTTGGGACATCGGCACATTCGAGACTTGGCGGTGCTGGAA 1017  
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
Db 1018 ACGCGGCCCATCTCTGACCGCATCTTCGTGGACCGCGGTGTGTCTGCGCTGCCT 1077  
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
Db 1078 GTGTCTAACGAAACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGTATCCACTG 1137  
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
Db 1138 GCTGCCCAACAACATACACCATCTGGACATGATGTGGGAGAGCCCTGAGCAGCGG 1197  
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260  
Db 1198 ACATGTGTCTGGAAGCGGTCTTCTTCTGACCGCCCGCCAGACACTTGGGGGAAGTCATT 1257  
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
Db 1258 GACCGGATGTCCGGGAACAGGTGCACCGCTGTGTGTCTGTGATGAGACCCAGCCTT 1317  
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
Db 1318 CTGGCGGTGTGTCTCTCTGACATCTCTCAGGCTCTGTGTGTCTCAGCCCTGTGTGAATT 1377  
Qy 301 AspAlaLeuGlyAla 305  
Db 1378 GATGCCCTCGGGGCC 1392

## RESULT 4

US-09-950-022A-7  
; Sequence 7, Application US/09950022A  
; Patent No. 6919177

```
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-09-950-022A-7

Alignment Scores:
Pred. No.: 6,01e-175 Length: 1873
Score: 1506.00 Matches: 295
Percent Similarity: 98.36% Conservative: 5
Best Local Similarity: 96.72% Mismatches: 5
Query Match: 97.10% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022A-7 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 478 ATGCACCTTCATGCAGGAGCACACCTGCTACGATGCCATGGGACGAGCTCCAAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTCTTTGGCCCTGGTGGCCAAACGGCATC 597
Qy 41 ArgAlaAlaProLeuTrrPheSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGCACCTTTGTGGGACAGCAGCAGCAGCTTCGTGGGATGCTGACCATCA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACITTCATCTTGGTCTGCACCGCTATTACAGGTCCCTCCCTGGTCCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGAACAATAGATTGAGACCTGGAGGAGAGATCTACCTTCAAGGCTGCTCAAGCCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCCTGTTCGAGCTGTCTACGCCCTCATCAAGNACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCCTGCGGTCTCGACCTGTCTCCGGGGCTGTGCTCCACATCTCCACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuProArgProSerPheLeu 160
Db 898 AAGCGCGCTTCTCAAGTCTCTGCACATCTTTGGCACCTGTTCGCCCGCCCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
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Db 958 TACCGCACCATCCAGAGATTTGGGCATCGGCACATCCGAGACTTGGCCGTGCTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1018 ACGGCCCCCATCTGACCGCAGCATCTTCGTGACCGCGGTGTCTGCGCTGCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAAGAACTGGACAGGTAGTGGGCTCTACTCTCGCTTGTATGTGATCCACCTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAAACATACACCACTGGACATCAATATGTGGGAAAGCCCTGAGGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1198 ACACCTGTCTGGAAGCGCTCTTCTGTCACGCCACGACCTTGGGGGAAGTCATT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCGGGAACAGGTGACCGCTGCTGCTGCTGATGAGACCCAGACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGGTGGTGTCCCTCTCTGACATCTTCAGGCTCTGCTGCTCAGCCCTGCTGGAATT 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 5
US-09-950-022A-9
; Sequence 9, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-09-950-022A-9

Alignment Scores:
Pred. No.: 1,41e-174 Length: 1873
Score: 1503.00 Matches: 295
Percent Similarity: 98.36% Conservative: 5
Best Local Similarity: 96.72% Mismatches: 5
Query Match: 96.91% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022A-9 (1-1873)
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Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 478 ATGCATTTTCATGAGGAGCACACCTGCTACCATCCATGGCAGCAGCTCCAAACTGGTC 537

Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAGGCTTCTTGGCCCTGGTGGCCAGCGGCTC 597

Qy 41 ArgAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CAAGCGGCACCTTGTGTGGAGCAGCAGCAAGAGCAGAGCTTCGTGGGCGATGCTGACCATCA 657

Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluLe 80
Db 658 GACTTCATCTTGGTGTGACCGCTATTACAGGTCCTCCCTGGTCCAGATCTACGAGATT 717

Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GNAGAACTAATGATTGAGACTCGAGGAGATCTACTTCNAGGCTGCTTCAGGCTCTG 777

Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCATGACAGCCTGTTCGAGCTGTCTAGGCCCTCATCAAGAACCGG 837

Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCTGCGCGCTCTGGACCTGTCTCCGGGGCTGTGTCTCCACATCTCTCACAT 897

Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTTCCTGCACATCTTTGGACCTGTCTGCGCGGCTCTCTCTCTC 957

Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
Db 958 TACCGCACCATCAAGATTGGGCATCGGCACATTCGAGACTTGGCGGTGTCTGGAA 1017

Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1018 ACGCGCGCCATCTCCAGCCGACGATGACATCTTCGTGGACCGCGGTGTCTGCGCTGCT 1077

Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGGCTCTACTCTGCTTTGATGATCCACTG 1137

Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAACAATCAACACCTGACATGATGATGAGAGAGCCCTGAGGACGCG 1197

Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
Db 1198 ACATGTGTCTGGAGGCGTCTCTTCTGCGAGCCCGCCAGAGACCTTGGGGGAGTCA 1257

Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCGGGAACAGGTGACCGCTGGTGTCTGATGATGAGACCCAGCACCT 1317

Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGGTGGTGTCTCTGATCATCTTCAGGCTCTGGTCTGCTGAGCCCTGCTGGNATT 1377

Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGCC 1392

RESULT 6
US-08-878-989-14
; Sequence 14, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.

```

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; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1435 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PENITUT01
; CLONE: 1452972
; US-08-878-989-14

Alignment Scores:
Pred. No.: 1,03e-120 Length: 1435
Score: 1064.00 Matches: 195
Percent Similarity: 85.95% Conservative: 62
Best Local Similarity: 65.22% Mismatches: 42
Query Match: 68.60% Indels: 0
DB: 2 Gaps: 0

US-10-070-794A-4 (1-305) x US-08-878-989-14 (1-1435)
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Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 248 GTCTTTGATGATCACTATCAAGTTAAAGGCTCTCTTTGCTTTGGTAGCCACGGGTG 307

Qy 41 ArgAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 308 CGAGCAGCGCCACTGTGGGAGAGTAAAGAAACAAGTTTGTAGGAATGCTAACATTA 367

Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluLe 80
Db 368 GATTCATAAATATACATACATGATATAAATCACTATGATGATGATGATGATGATTA 427

Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 428 GAGGAACATAAAATTGAAACATGGGGAGCTTTATTTTACAGAAACATTTTAAGCCTTTA 487

```

101 ValSerIleSerProAenAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
Db GTGAATATATCTCCAGATCAAGCCTCTCGATGCTGTATCTCTTGTATCAAAATAAA 547  
121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db ATCCACAGATTGCCGCTTATTGACCTATCAGTGGGAATGCACCTTATATATCTTACCAC 607  
141 LysArgLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db AAAGAATCTCAAGTCTCTCCAGCTTTATGCTGATATGCAAGACCTGCTTCATG 667  
161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180  
Db AAGCAGAACCTGGATGAGCTTGGAAATAGGAACGTACCACCAATTCGCTTCATATCCA 727  
181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200  
Db GACACTCCCATCATCAAGCCCTTGAACATATTTGTGGAAGACCAATATCAGCTCTGCCT 787  
201 ValValAsnGluCysGlyGlnValValClyLeuTyrSerArgPheAspValIleHisLeu 220  
Db GTTGTGGATGAGTCAGGAAGTTGTAGATATTTATCCAAATTTGATGTAATTAATCTT 847  
221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
Db GCTGCTGAGAAACATACATAAATAGCTAGATATCAGGTGACCCAGGCTTCAGCACCGT 907  
241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260  
Db TCACAGTATTTGAGGTGTTGTGAAGTGCATTAAGCTGGAAATACCTGGAGACCATCGT 967  
261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
Db GACAGATAGTAAGCTGAGGTCCATCGCTGGTGGTGAATGAAGCAGATAGTATT 1027  
281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299  
Db GTGGTATTATTTCCCTGTCGACATTTCTGCAAGCCCTGATCTCTCACACACGAGGT 1084

## RESULT 7

US-09-272-796-14  
; Sequence 14, Application US/09272796  
; Patent No. 6207148

## GENERAL INFORMATION:

; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; TITLE OF INVENTION: KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/272,796  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/878,989

; FILING DATE: INFORMATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0321 US  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1435 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PENITUT01  
; CLONE: 1452972  
; US-09-272-796-14

Alignment Scores:  
Pred. No.: 1.03e-120 Length: 1435  
Score: 1064.00 Matches: 195  
Percent Similarity: 85.95% Conservative: 62  
Best Local Similarity: 65.22% Mismatches: 42  
Query Match: 68.60% Indels: 0  
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-272-796-14 (1-1435)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20  
Db 188 ATGCGATTTCATGAGGTCCACAGTGTATGACATCGTTCCACAGTTCAAGCTTGT 247  
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyVal 40  
Db 248 GTCTTTGATACACTACATTTACAAGTTAAAAGGCTCTCTTGGTTGGTAGCAACGGTGC 307  
Qy 41 ArgAlaAlaProLeuTyrAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60  
Db 308 CGAGCAGCGGCACCTGTGGGAGAGTAAATAAGTTTGTAGGAATGCTTAACAATTACA 367  
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
Db 368 GATTTCATAAATATACATAGATACATATAAATCACCCTATGCTACAGATTATGAATTA 427  
Qy 81 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db 428 GAGGAACATAAAATGAAACATGAGGGAGCTTTATTTACAAGAAACATTTAAGCCTTTA 487  
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
Db 488 GTGAATATATCTCCAGATGCAAGCCTCTTCGATCTGTATATCTCTTGATCAAAATAAA 547  
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db 548 ATCCACAGATTGCCGCTTATTGACCTATCAGTGGGAATGCACCTTATATCTTACCAC 607  
Qy 141 LysArgLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db 608 AAAGAATCTCAAGTCTCTCCAGCTTTTATGCTGATATGCTCAAGACCTGCTTCATG 667  
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180  
Db 668 AAGCAGAACCTGGATGAGCTTGGAAATAGGAACGTACCACCAATTCGCTTCATATCCA 727  
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200  
Db 728 GACACTCCCATCATCAAGCCCTTGAACATATTTGTGGAAGACCAATATCAGCTCTGCCT 787  
Qy 201 ValValAsnGluCysGlyGlnValValClyLeuTyrSerArgPheAspValIleHisLeu 220

Db 788 GTTGTGATGAGTCAGGAAAGTTGTAGATATTATTATCCAAATTTTGATGTAATTAATCTT 847  
Qy 221 AlalaGlnGlnThrTyAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
Db 848 GCTGCTGAGAAAACATCAATAACCTAGATATACGGTGACCGCCCTTCAGCACCGT 907  
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValle 260  
Db 908 TCACAGTATTGTAAGGTGTTGTGAAGTGCATAAGCTGGAAATPACTGGAGACCATCGTG 967  
Qy 261 AspArgileAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
Db 968 GACAGATAGTAAGAGCTGAGCTCATCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1027  
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299  
Db 1028 GTGGGTATTATTTCCCTGTGGACATTCTGCAAGCCCTGATCCTCACACCAGCAGGT 1084

RESULT 8  
US-09-949-016-2390  
; Sequence 2390, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2390  
; LENGTH: 1506  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-2390

Alignment Scores:  
Pred. No.: 1,11e-120 Length: 1506  
Score: 1064.00 Matches: 195  
Percent Similarity: 85.95% Conservative: 62  
Best Local Similarity: 65.22% Mismatches: 42  
Query Match: 68.60% Indels: 0  
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-949-016-2390 (1-1506)

Qy 1 MetArgPheMetGlnGluHisThrCysTyAspAlaMetAlaThrSerSerLysLeuVal 20  
Db 318 ATGGCAATTCATGAGCTCACACAGTGTATGACATCGTTCCCAACAGTTCAAAGCTGTT 377  
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPheAlaLeuAlaAsnGlyVal 40  
Db 378 GTCTTTGATACATACATCAAGTAAAGGCCCTTCCTTTGTTGGTACCAACGGTGTG 437  
Qy 41 ArgAlaAlaProLeuTtpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
Db 438 CGAGCAGCCCACTGTGGAGAGTAAACAAAGTTTGTAGGAATGCTAACCAATTACA 497  
Qy 61 AspPheLeuLeuValLeuHisArgTyTrArgSerProLeuValGlnIleTyGluile 80  
Db 498 GATTTCATAAATATACATACATAGATCTATATAATCACCTATGTTACAGATTATGAATTA 557  
Qy 81 GluGlnHisLysIleGluThrTtpArgGluIleTyLeuGlnGlyCysPheLysProLeu 100  
Db 558 GAGGAACATAAAATTTGAACATGAGGAGGAGCTTTATTTTACAAAGAAACATTTTAAACCTTTTA 617

Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyThrLeuIleLysAsnArg 120  
Db 618 GTGAATATATCTCCAGATCAAGCCTCTTCGATGCTGTATCTCTTGATCAAAATAAA 677  
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db 678 ATCCACAGATTGCGGTTATTTGACCTTATCAGTGGGAAATGCATTTATATATCTTACCAC 737  
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db 738 AAAAGAATCTCAAGTCTCCAGCTTTTATGCTGATATGCCAAAGCCTGCTTCATG 797  
Qy 161 TyArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180  
Db 798 AAGCAGAACCTGGATGAGCTTGAATAGGAACCTGACCAACATTTGCTTCATATCCA 857  
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
Db 858 GACACTCCCATCATCAAGCCTTGACATATTTGTGGAAGACGAATATCAGCTCTGCT 917  
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTySerArgPheAspValIleHisLeu 220  
Db 918 GTTGTGATGAGTCAGGAAAGTTGTAGATATTATTTCAAATTTGATGTAATTAATCTT 977  
Qy 221 AlalaGlnGlnThrTyAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
Db 978 GCTGCTGAGAAAACATCAATAACCTAGATATCAGGTGACCCAGGCCCTTCAGCACCGT 1037  
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValle 260  
Db 1038 TCACAGTATTGTAAGGTGTTGTGAAGTGCATAAGCTGGAATATCTGGAACCATCGTG 1097  
Qy 261 AspArgileAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
Db 1098 GACAGATAGTAAGAGCTGAGTCCATCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 1157  
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299  
Db 1158 GTGGGTATTATTTCCCTGTGGACATTCTGCAAGCCCTGATCCTCACACCAGCAGGT 1214

RESULT 9  
US-09-949-016-5010  
; Sequence 5010, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5010  
; LENGTH: 1500  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5010

Alignment Scores:  
Pred. No.: 6.52e-114 Length: 1500  
Score: 1009.00 Matches: 192  
Percent Similarity: 82.99% Conservative: 52  
Best Local Similarity: 65.31% Mismatches: 50  
Query Match: 65.05% Indels: 0  
DB: 3 Gaps: 0

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US-10-070-794A-4 (1-305) x US-09-949-016-5010 (1-1500)
Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
Db 110 TTCTGAAGTCTCATCGCTGCTATGACCTGATCCCAAGCTCCAAATGGTTGTATTT 169
Qy 23 AspThrMetLeuGluIleLysLeuAlaPheAlaLeuValAlaAsnGlyValArgAla 42
Db 170 GATACGCTCCCTGCGAGGTGAAGAAGCTTTTTCCTTGGTGACTAAACGGGTGACGAGCT 229
Qy 43 AlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 230 GCCCTTTATGGGATAGTAAGACAAAGTTTGTGGGCATGCTGACCATCACTGATTC 289
Qy 63 IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGln 82
Db 290 ATCAATATCTCCACCGCTACTATAAATCAAGCTTGGTACAGATCTATGAGCTAGAAGAA 349
Qy 83 HisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSer 102
Db 350 CACAAGATAGAAACTTGGAGAGAGGTGATCTCCAGGACTCTTTAAACCGCTTGTCTGC 409
Qy 103 IleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHis 122
Db 410 ATTTCTCTATGCCAGCTTGTTCATGCTCTCTTCATTAATTCGGAACAAGATCCAC 469
Qy 123 ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArg 142
Db 470 AGGCTGCCAGTATTATGCCAGATATCAGCAATATCTTGTATCATCTCTCACCAAGCGC 529
Qy 143 LeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg 162
Db 530 ATTTGGAAGTTCCTCAAAATGTTTATCATCTGAGTTCCTCCAGCCAGAGTTTCATGTCCAAG 589
Qy 163 ThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAla 182
Db 590 TCTCTGGAGAGCTACAGATTGGCACCTATGCCAATATGCTATGTTGGCATACCACC 649
Qy 183 ProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProValVal 202
Db 650 CCGCTCTATGTGGCTCTCGGATTTTGTACAGCATCGAGTCTCAGCCCTGCCAGTGTG 709
Qy 203 AsnGluCysGlyGlnValValClyLeuTyrSerArgPheAspValIleHisLysAla 222
Db 710 GATGAGAAGGGCGGTGTGGTGACATCTACTCCAAAGTTTGAATGTTATCAATCTGGCAGCA 769
Qy 223 GlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242
Db 770 GAAAGAGCTTACAACAACCTAGATGATCTGTGACTAAAGCTTGCACATCGATCAGAT 829
Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 262
Db 830 TACTTTGAGGTGTCTCAAGTCTACCTGATGAGACTCTGGAGACCATCATCAACAGG 889
Qy 263 IleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeuGly 282
Db 890 CTAGTGAAGCAGAGGTTTCAACGACTTGTGTGGTGGATGAATAATGATGTGTGTCAGGGA 949
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 950 ATTGATCACTGTCTGACATCTCTGAGGCCCTTGGTGTCTCACA 991

RESULT 10
US-09-016-434-1113
; Sequence 1113, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice An-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1578 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1335855
; US-09-016-434-1113

Alignment Scores:
Pred. No.: 7,07e-114 Length: 1578
Score: 1009.00 Matches: 192
Percent Similarity: 82.99% Conservative: 52
Best Local Similarity: 65.31% Mismatches: 50
Query Match: 65.05% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-016-434-1113 (1-1578)
Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
Db 188 TTCTGAAGTCTCATCGCTGCTATGACCTGATCCCAAGCTCCAAATGGTTGTATTT 247
Qy 23 AspThrMetLeuGluIleLysLysLeuAlaPheAlaLeuValAlaAsnGlyValArgAla 42
Db 248 GATACGCTCCCTGCGAGGTGAAGAAGCTTTTTCCTTGGTGACTAAACGGGTGACGAGCT 307
Qy 43 AlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 308 GCCCTTTATGGGATAGTAAGACAAAGTTTTCCTTGGGCATGCTGACCATCACTGATTC 367
Qy 63 IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGln 82
Db 368 ATCAATATCTTCGACCGCTACTATAAATCAAGCTTGGTACAGATCTATGAGCTAGAAGAA 427
Qy 83 HisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSer 102
Db 428 CACAAGATAGAAACTTGGAGAGAGGTGATCTCTCAGGACTCTCTTTAAACCGCTTGTCTGC 487
Qy 103 IleSerProAsnAspSerLeuPheGluAlaValTyrThrIleLysAsnArgIleHis 122
Db 488 ATTTCTCTAATGCCAGCTTGTTCATGCTCTCTTCATTAATTCGGAACAAGATCCAC 547
Qy 123 ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArg 142
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Db 1027 ATTGTATCACTGTCTGACATCTCTGCAGGCCCTGTGTCTCACA 1068

RESULT 12

US-09-949-016-16752  
 ; Sequence 16752, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 16752  
 ; LENGTH: 20347  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-949-016-16752

Alignment Scores:  
 Pred. No.: 4.89e-46 Length: 20347  
 Score: 472.50 Matches: 197  
 Percent Similarity: 25.49% Conservative: 50  
 Best Local Similarity: 20.33% Mismatches: 47  
 Query Match: 30.46% Indels: 680  
 DB: 3 Gaps: 11

US-10-070-794A-4 (1-305) x US-09-949-016-16752 (1-20347)

Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22  
 Db 14940 TTCATGAAGTCTCATCGTGTGATGACCTGATCCCAAGCTCCAAATTTGGTATTT 14999  
 Qy 23 AspThr 24  
 Db 15000 GATACGTCCTGCAGGTGGGTGAATCTCTTTTCCCTTCCCTTTGGAGCCTGTGGTT 15059  
 Qy 24 24  
 Db 15060 TAATACCTCTCATCTCATCTCAAGGGTAATATCTTATCTTCTGTGAAGTTAGT 15119  
 Qy 24 24  
 Db 15120 CTCATGTTTATCCCAACATGCCAAACACTGTCTTTTTTACAGTCTGCCCTGTGGA 15179  
 Qy 25 Met-LeuGluIleLysLysAlaPhePheAlaLeuVa 36  
 Db 15180 TTGCGCTTATGATTAATTAATCTGTGCTACAGGTGAAGAAGCTTTTTTGTCTTGGT 15239  
 Qy 36 lalaAsnGlyValArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheVal 54  
 Db 15240 GACTAACGGTGTACGAGCTGCCCTTTATGGATAGTAAGAAGCAAGTTTTGTGGGTAA 15299  
 Qy 54 54  
 Db 15300 GCMAAAGTTTCTGGAACAATAATATTATGGCATCTTGTGCTGGGAGGAGACAGCTTC 15359  
 Qy 55 GlyMetLeuThrIleThrAspPheIleL 64  
 Db 15360 AGGAGTGTCTGAGGCTCTGTCTTCTCTAGGCATGCTGACCATCACTGATTCATCA 15419  
 Qy 64 euValLeuHisArgTyrTyrArgSerProLeu 74  
 Db 15420 ATATCTGCACCGCTACTATAAATCAGC-CTTGGTAAGGAACCTTAAACCAATGACCAA 15478

Qy 74 74  
 Db 15479 ATCACTTTCCCTGCCCTAAATCCCTCATTTCTCATTTCTTTTCTCCNAGCAAGCCAGAG 15538  
 Qy 75 ValGlnI 77  
 Db 15539 GGCTTAAGGAAGCAGAGAGATCAGGTCTCAAAATTCGTGTCTTCTGCTTTTCAGGTACAGA 15598  
 Qy 77 leTyrGluIleGluGlnHisIleGluThrTrpArg 89  
 Db 15599 TCTATGAGCTAGAAGAACAACAAGATAGAAAATTGGAG-AGGTATGTAGAGAAATTTGGGTT 15657  
 Qy 89 89  
 Db 15658 ATAAAAGGATAAAGGATGGCGGTTTCTGGGAAACACATTTTCCATGGTGGTATTTTGTG 15717  
 Qy 90 GluIleTyrLeuGlnGlyCysPheLysProValSerI 103  
 Db 15718 ACCATCCCTTTTCCCTTCAGAGGTGTATCTCCAGGACTCTTTAAACCCGTTGTCTGCA 15777  
 Qy 103 leSerProAsn 106  
 Db 15778 TTTCTCTTAATGCCAGGTGAGTTCCAGTTACCCATCTGTCCAAAAGCGGAAGAGATTTT 15837  
 Qy 106 106  
 Db 15838 GTCATCAGCCTAGTAATGCCCTAGACACCAGGAAGGGGAAGAGAGAAAGACA 15897  
 Qy 106 106  
 Db 15898 CACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC 15957  
 Qy 106 106  
 Db 15958 CTCATTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 16017  
 Qy 106 106  
 Db 16018 CTTCCCTAACCTCAGTTTCCCTGTGTGAGCAATACACTGTATGAGCCTGTTTAAATCAC 16077  
 Qy 107 AspSerLeuPheGluIle 113  
 Db 16078 CCCAGCCCCAGCAGTGTGAACTTTATTATCTCCACCTCTCACAGCTTGTTCATGCTG 16137  
 Qy 113 alTyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuAspProValSerGlyA 133  
 Db 16138 TCTCTTCAATTAATTCGGAACAAGATCCACAGGCTGCCAGTTCAGTTCAGTTCAGTTCAG 16197  
 Qy 133 snValLeuHisIleLeuThrHisArgLeuLysPheLeuHisIlePhe 150  
 Db 16198 ATACTTTGTACATCTCACCCCAAGCGCATTCCTGAAGTTCTCAAAATTTGTTTGAAGTG 16257  
 Qy 150 150  
 Db 16258 CTCCTCAGCCCGTCTCTTTTCTCTTTTCTCTTTTCTCTTTTCTCTTTTCTCTTTTCTCT 16317  
 Qy 150 150  
 Db 16318 GAGACAGAGGTCTCACTGTGTGTCTCAGGCTAGTGTCAAACTCCTGAGCTCAAGTGATC 16377  
 Qy 150 150  
 Db 16378 CTCCGGCTCAGCCTCCAAAGTCTAGGATTACAGGTGTGAGCCATGTCATCCAGCCCC 16437  
 Qy 150 150  
 Db 16438 ACTTCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 16497  
 Qy 150 150  
 Db 16498 CGTGAGAGCGCTATCATGCTCACTGACGCTCCAACTCTTGGTCTCAGGTGACCCC 16557  
 Qy 150 150



Db 16558 CGACCTCAACCCCGAGAGAGCTGGGACTACACGTGTGTATCCACACACCTGGCTAATTT 16617  
 Qy 150 ----- 150  
 Db 16618 TTTGGTATTTTATAGAGATAGGTTTGGCATGTTGGCCAGGCTGGTCTCGAAGCTCT 16677  
 Qy 150 ----- 150  
 Db 16678 GGGCTCAAGCAATATGTCCTCCCTCAGCCTCCCAAGTGTGGGATTATAGGCATAAGCCG 16737  
 Qy 150 ----- 150  
 Db 16738 GCGCACCCAGCCCTTATTTCTAATATATCTGGTTGGAGGGGTATCCAAAGGGTGGCTTTG 16797  
 Qy 151 -----ProArgPro 158  
 Db 16798 GGTGCTTGAAGTTAAGCTGATGGTTCTTCTCAGATCAGTCTAGTCTCCCAAG-CCAG 16856  
 Qy 158 erPheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValV 178  
 Db 16857 AGTTTCATGTCAGAGCTCTCGAAGAGCTACAGATTGGCAGCTATGCCAATATTGCTATGG 16916  
 Qy 178 alLeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerA 198  
 Db 16917 TTGCACCTACACCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAG 16976  
 Qy 198 laLeuProValValAsnGluCys----- 205  
 Db 16977 CCCTGCCAGTGTGGATGAGAA-GGGTGAGAGATTGGGCAGAGGAGGAGGGAAGAT 17035  
 Qy 205 ----- 205  
 Db 17036 CCAGGCAAGTCAGGGTGGCTCTGGGAAGATCTGCTTTCCCTCAGCTTAGCCAGAGGGT 17095  
 Qy 205 ----- 205  
 Db 17096 GATTCTATAGTAGGGGAGGCTTTAGATCCAGATCCTCTTACTAGCTGCCTCTGTCTC 17155  
 Qy 206 -----GlyGlnValValGlyLeuTyrSerArgPheAspValIle----- 218  
 Db 17156 CCCTAGGCGGTGTGGTGCACATCTACTCCAAAGTTTGATTTATCGTAGTGATTTGGAG 17215  
 Qy 218 ----- 218  
 Db 17216 GGTCTGGAGGTAGGAAAGTGGTGGGGGGGGGCACTGTTAAATATGAGAGGAGGAAG 17275  
 Qy 218 ----- 218  
 Db 17276 GAGTCTCTCTGTGATCTAAGGGCTTTAGAAAGCTTCCAGGCTTTCAAACTATTGAAA 17335  
 Qy 218 ----- 218  
 Db 17336 AGGAATTGAATGATGGTGTGGCTGTGGCTGACAAATGGCCCTGAATCCCTCTGTGTA 17395  
 Qy 218 ----- 218  
 Db 17396 GGTGGATGGGTTTCCAGGGTTGGAGGCTGCTCTCTTGGCTTCCCTGCAAGCTCCTTCTC 17455  
 Qy 219 -----HisLeuAlaGlnGlnThrIleAsnHisLeuAspMetSerValGlyC 235  
 Db 17456 TGTCTCCCAAGATCTGGCAGCAGAAAGACCTACACACCTAGATGTATCTGTGACTA 17515  
 Qy 235 luAlaLeuArgGlnArgThrLeuCysLeuGlyValLeuSerCysGlnProHisGluS 255  
 Db 17516 AAGCTTGGCAACATCATGATCATATTCTTGGGGTGTCTCAAGTGTCTACCTGCATGAGA 17575  
 Qy 255 erLeuGlyGluValIleAspArgIleAla-----ArgGlu----- 266  
 Db 17576 CTCTGGAGACCATCATCAACAGGCTAGT-GGAAGCAGAGGTAGGGAGCCAGCAACCCCTA 17634  
 Qy 266 ----- 266

Db 17635 AAGGAGCTGAGGGGAGCAGCGCTTGAGAGTGGGGTTTGGCAAGAGAGTAGGGGCGAGAGGG 17694  
 Qy 267 -----GlnValH 269  
 Db 17695 GCTTCCCTCAGGCGCAGCACTAAACATTTCCCTTTCTCCCTTGTGCTCTGTGCCAGGTT 17754  
 Qy 269 isArgLeuValLeuValAspGluThrGlnHisLeuLeuGlyValValSerLeuSerAspI 289  
 Db 17755 ACCGACTTGTAGTGGTGAATGAATAATGATGTGGTCAAGGGAATTGTATCACTGTCTGACA 17814  
 Qy 289 leLeuGlnAlaLeuValLeuSer 296  
 Db 17815 TCCTGCAGGCCCTGGTGTCTCA 17837  
 RESULT 13  
 US-09-513-999C-1659  
 ; Sequence 1659, Application US/09513999C  
 ; Patent No. 6783961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Duclert, A.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; Patent No. 6783961  
 ; FILE REFERENCES: 59.US2.REG  
 ; CURRENT APPLICATION NUMBER: US/09/513,999C  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/122,487  
 ; PRIOR FILING DATE: 1999-02-26  
 ; NUMBER OF SEQ ID NOS: 36681  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 1659  
 ; LENGTH: 350  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 48..350  
 ; US-09-513-999C-1659  
 Alignment Scores:  
 Pred. No.: 3,94e-28 Length: 350  
 Score: 304.00 Matches: 56  
 Percent Similarity: 90.00% Conservative: 7  
 Best Local Similarity: 80.00% Mismatches: 7  
 Query Match: 19.60% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-070-794A-4 (1-305) x US-09-513-999C-1659 (1-350)  
 Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22  
 Db 141 TTCATGAAGTCTCATCGCTGCTATGACCTGATCCCAAGCTCCCAATTTGGTTGATTT 200  
 Qy 23 AspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAenGlyValArgAla 42  
 Db 201 GATACGCTCCCTGCAGGTGAAGAAAGCTTTTGTGCTGACTAACCGGTGACGAGCT 260  
 Qy 43 AlaProLeuThrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62  
 Db 261 GCCCTTTTATGGATAGTAAAGCAAGAAAGTTTGTGGCATGTGCTGACCATGATTTTC 320  
 Qy 63 IleLeuValLeuHisArgTyrTyrArgSer 72  
 Db 321 ATCAATATCTGCACCGCTACTATAATCA 350  
 RESULT 14  
 US-09-248-796A-4769  
 ; Sequence 4769, Application US/09248796A  
 ; Patent No. 6747137  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keith Weinstein et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA, ALBICAN

```

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 4769
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Candida albicans
; US-09-248-796A-4769

Alignment Scores:
Pred. No.: 3,02e-21 Length: 762
Score: 252.50 Matches: 62
Percent Similarity: 50.91% Conservative: 50
Best Local Similarity: 28.18% Mismatches: 73
Query Match: 16.28% Indels: 35
DB: 3 Gaps: 6

US-10-070-794A-4 (1-305) x US-09-248-796A-4769 (1-762)

Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
Db 115 TTTTACAAACCAAACTCTTACGATGCTCTACCTGTGAGTTATAGATTAAATGTTTG 174
Qy 23 AspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAenGlyValArgAla 42
Db 175 GATACTTCATTGTTAGTGAAGAAAGTCATTAAATATTTTATTACAAATAATATAGTTTCA 234
Qy 43 AlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 235 GCACCGTTATGATACCAACATCCAGATTCGCTGGATTGTTAAATCATCATCGGATTT 294
Qy 63 IleLeuValLeuHisArgTyrTyrArgSerPro-----HisLysIleGluThrTrp 73
Db 295 ATCAATGTGATACATACTATTACATTCGCCAGAAAGTTTGAAGTATGATCAACTA 354
Qy 74 ---LeuValGlnIleTyrGluIleGluGln-----HisLysIleGluThrTrp 88
Db 355 ACATTGGGTGGATTAAGAGAATTAAGAAAGCCATAGGTGATGATCAATCGAACA--- 411
Qy 89 ArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIleSerProAsnAspSer 108
Db 412 -----GCATCAATACACCCATTCAAGTCA 435
Qy 109 LeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuAsp 128
Db 436 TTATATGAAGCATGTGTCAAGATGTTGGAATCAAAAGCTAGAGAATCCCATTAATGAT 495
Qy 129 ProValSerGlyAsn-----ValLeuHisIleLeuThrHisLysArgLeuLeu 144
Db 496 GAAGATGAAAAAATAAAGCGTAATGTCGTAGTGTGTTAATCAATACAGAAATTTTG 555
Qy 145 LysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArgThrIle 164
Db 556 AAAATTGGTGGCTTGG-----AATTGTAAGAAAGCAAAATGTTATTGAAACCCCTC 606
Qy 165 GlnAspLeu---GlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAlaPro 183
Db 607 AAGAAATTTGAGTGGGTGGGTGATGTGAAAGATTGCTCTACATGTTACTATGACACACCT 666
Qy 184 IleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProValValAsn 203
Db 667 GTCATAGAAGTCATTCAATTTAATGAGAAATTCCTGCTCTTCAATACCAATATGTCAC 726

RESULT 15
US-09-016-434-194
; Sequence 194, Application US/09016434
; Patent No. 6500938

; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PENITUT01
; CLONE: 1452972
; US-09-016-434-194

Alignment Scores:
Pred. No.: 1.96e-20 Length: 269
Score: 240.00 Matches: 47
Percent Similarity: 77.27% Conservative: 21
Best Local Similarity: 53.41% Mismatches: 20
Query Match: 15.47% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-016-434-194 (1-269)

Qy 176 AlaValValLeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArg 195
Db 1 GCCTTCATACATCAGACACTCCCATCATCAAGCCITGAACATATTTTGGAAAGCA 60
Qy 196 ValSerAlaLeuProValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPhe 215
Db 61 ATATCAGCTCTGCTGTTGTGATGAGTCAGAGAAAGTTGTAGATATTTATTCCTCAATTT 120
Qy 216 AspValIleHisLeuAlaAlaGlnGlnThrTyrAnHisLeuAspMetSerValGlyGlu 235
Db 121 GATGTAATTAATCTTGCTGCTGAGAAACATACATAACCTAGATATCCTGCTGACCCAG 180
Qy 236 AlaLeuArgGlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSer 255
Db 181 GCCCTTCAGCACCGTTCACAGTATTTTGAAGTGTGTGGAAGTGCATAAAGTGGAAATA 240
Qy 256 LeuGlyGluValIleAspArgIle 263
Db 241 CTGGAGACCATCGTGGACAGAATA 264
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Search completed: January 26, 2006, 03:32:42  
Job time : 178.061 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 26, 2006, 01:18:45 ; Search time 656.008 Seconds  
(without alignments)  
3844.711 Million cell updates/sec

Title: US-10-070-794a-4

Perfect score: 1551

Sequence: 1 MRFQHECTCDMATSSKLV.....LSIDLQVLVSPAGIDALGA 305

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Ygapop 10.0	Ygapext 0.5	
Zgapop 6.0	Zgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA Main -OPMT=fastap -SUFFIX=p2n.rnpbm  
-MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1  
-MATRIX=biosum62 -TRANS=human40.cdi -LIST=45 -MODE=LOCAL -OUTFMT=ptc -NORM=ext  
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext  
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10070794 @CEN 1.1 2064 @runat\_24012006.164417.8900 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA Main:

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10:	/cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1551	100.0	1470	9	US-10-503-175-1
2	1551	100.0	1647	3	US-09-826-581-5
3	1551	100.0	1647	7	US-10-705-137-5
4	1551	100.0	2781	7	US-10-473-670-30
5	1525	98.3	2290	9	US-10-756-149-1235
6	1507	97.2	1873	3	US-09-950-022-1
7	1507	97.2	1873	3	US-09-950-022-3

8	1507	97.2	1873	3	US-09-950-022-5	Sequence 5, Appli
9	1507	97.2	1873	10	US-11-075-134-1	Sequence 1, Appli
10	1507	97.2	1873	10	US-11-075-134-3	Sequence 3, Appli
11	1507	97.2	1873	10	US-11-075-134-5	Sequence 5, Appli
12	1506	97.1	1873	3	US-09-950-022-7	Sequence 7, Appli
13	1506	97.1	1873	10	US-11-075-134-7	Sequence 7, Appli
14	1503	96.9	1873	3	US-09-950-022-9	Sequence 9, Appli
15	1503	96.9	1873	10	US-11-075-134-9	Sequence 9, Appli
16	1479	95.4	1518	9	US-10-503-175-3	Sequence 3, Appli
17	1064	68.6	1167	9	US-10-466-162-11	Sequence 11, Appli
18	1064	68.6	1435	3	US-09-769-970-14	Sequence 14, Appli
19	1064	68.6	2223	3	US-10-466-162-13	Sequence 13, Appli
20	1009	65.1	1578	6	US-10-305-720-1113	Sequence 1113, Ap
21	1009	65.1	1578	9	US-10-505-680-407	Sequence 407, App
22	1009	65.1	1578	9	US-10-466-162-15	Sequence 15, Appli
23	1009	65.1	1691	3	US-09-925-297-2	Sequence 2, Appli
24	862.5	55.6	1467	9	US-10-450-763-20069	Sequence 20069, A
25	851.5	54.9	3261	10	US-11-097-143-25526	Sequence 25526, A
26	758	48.9	547	7	US-10-276-774-261	Sequence 261, App
27	747.5	48.2	11527	5	US-10-108-605-70	Sequence 70, Appli
28	747.5	48.2	39651	10	US-11-097-143-25525	Sequence 25525, A
29	687	44.3	2303	9	US-10-450-763-20071	Sequence 20071, A
30	640.5	41.3	1722	3	US-09-826-581-3	Sequence 3, Appli
31	640.5	41.3	1722	7	US-10-705-137-3	Sequence 3, Appli
32	621	40.0	9100	9	US-10-503-175-5	Sequence 5, Appli
33	621	40.0	26000	9	US-10-503-039-1	Sequence 1, Appli
34	501	32.3	602	5	US-10-106-698-2295	Sequence 2295, Ap
35	408	26.3	765	6	US-10-264-237-248	Sequence 248, App
36	357	23.0	1533	7	US-10-425-114-8857	Sequence 8857, Ap
37	357	23.0	2339	8	US-10-425-115-2938	Sequence 2938, Ap
38	352.5	22.7	1507	7	US-10-425-114-29527	Sequence 29527, A
39	352.5	22.7	3077	7	US-10-424-599-44858	Sequence 44858, A
40	352	22.7	1014	3	US-09-826-581-4	Sequence 4, Appli
41	352	22.7	1014	7	US-10-705-137-4	Sequence 4, Appli
42	350.5	22.6	1387	7	US-10-425-114-33827	Sequence 33827, A
43	348	22.4	2315	7	US-10-424-599-79689	Sequence 79689, A
44	347.5	22.4	1844	7	US-10-425-114-1948	Sequence 1948, Ap
45	347.5	22.4	2416	8	US-10-425-115-90096	Sequence 90096, A

#### ALIGNMENTS

RESULT 1  
US-10-503-175-1  
; Sequence 1, Application US/10503175  
; Publication No. US20050172348A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersson, Leif  
; APPLICANT: Marklund, Stefan  
; TITLE OF INVENTION: Transgenic animals expressing prkag3  
; FILE REFERENCE: 11145-020U51  
; CURRENT APPLICATION NUMBER: US/10/503,175  
; CURRENT FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: PCT/IB03/00912  
; PRIOR FILING DATE: 2003-01-31  
; PRIOR APPLICATION NUMBER: US 60/353,430  
; PRIOR FILING DATE: 2002-02-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1470  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1470)  
; OTHER INFORMATION:  
US-10-503-175-1

Alignment Scores:  
Pred. No.: 5.59e-192 Length: 1470  
Score: 1551.00 Matches: 305  
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-070-794A-4 (1-305) x US-10-503-175-1 (1-1470)

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Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 613 ATCTTCGACACCATGCTGGAGATCAAGAGCCCTCTTTGCTCTGGTGGCCAAACGGTGTG 672
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 673 CGGCGACGCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCACT 732
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 733 GACTTCATCTCTGGTGTGCTGCTACGCTACTACAGGTCCCCCTGCTGCTCCAGATCTATGAGATT 792
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 793 GAACACATAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTCAAGCTCTG 852
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 853 GTCTCCATCTCTCTAATGATAGCTGCTTTGAAGCTGTCTACACCCCTCATCAAGAACCGG 912
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 913 ATCCATCGCTGCTGCTGCTTTCTTGACCGGTGTGAGGCAACGCTACTCCATCTCCACAC 972
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 973 AAACGCTTGCTCAAGTCTCTGCACATCTTTGGTTCCTGCTGCCCGGCCCTCTCTCTC 1032
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 1033 TACCGCATATCAAGATTTCGGCATCGGCACATTCGAGACTTTGGCTGTGGTCTGGAG 1092
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
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Qy 201 ValValAsnGluCysGlyValValGlyValLeuTyrSerArgPheAspValIleHisLeu 220
Db 1153 GTGGTCAACGAATGTGGTCAGTGTGGGCCCTCTATTCCCGCTTTGATGTGATTCACCTG 1212
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1213 GCTGCCAGCAAACTACACCATCGCATGAGTGTGGGAGAAGCCCTGAGGACAGAG 1272
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlySerLeuGlyGluValIle 260
Db 1273 ACATATGCTGGAGGAGTCTCTTCTCCAGCCCCACGAGAGCTTGGGGGAAGTGTATC 1332
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1333 GACAGATTGCTCGGAGACAGGTACACAGGCTGGTGTAGTGGACGAGACCCAGCATCTC 1392
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1393 TTGGCGGTGTCTCCCTCTCCGACATCTTCCAGGCACCTGCTGAGCCCTGCTGCGCATC 1452
Qy 301 AspAlaLeuGlyAla 305
Db 1453 GATGCCCTCGGGGCC 1467

RESULT 2
US-09-826-581-5
; Sequence 5, Application US/09826581
```

```
Patent No. US20020142310A1
GENERAL INFORMATION:
APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1647
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (20)...(1486)
US-09-826-581-5

Alignment Scores:
Pred. No.: 6,77e-192 Length: 1647
Score: 1551.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-826-581-5 (1-1647)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 572 ATGCGCTTCATGCGAGGAGCACACCTGCTAGCATGCCATGCCAAGCTAGCTCAAGCTAGTC 631
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 632 ATCTTCGACACCATGCTGGAGATCAAGAGCCCTCTTTGCTCTGGTGGCCAAACGGTGTG 691
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 692 CGGCGACGCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCACT 751
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 752 GACTTCATCTCTGCTGCTGCTACTACAGGTCCCCCTGCTGCTGCTGCTGCTGCTGCTGCT 811
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 812 GAACACATAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTCAAGCTCTG 871
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 872 GTCTCCATCTCTCTAATGATAGCTGCTTTGAAGCTGTCTACACCCCTCATCAAGAACCGG 931
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 932 ATCCATCGCTGCTGCTGCTTGTGGTTCCTGTCACATCTTTGGTTCCTGCTGCCCGGCCCTCTCTC 1051
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 992 AAACGCTTGCTCAAGTCTCTGTCACATCTTTGGTTCCTGCTGCCCGGCCCTCTCTCTC 1051
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 1052 TACCGCATATCAAGATTTCGGCATCGGCACATTCGAGACTTGGCTGTGGTGTGGAG 1111
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1112 ACAGCACCATCTCTGACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
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Db 1172 GTGTCAACGAATGTGTGAGTCTTATTCCTGCTTGTGATGATTCACCTG 1231  
 Qy 221 AlaAlaGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
 Db 1232 GCTGCCAGCAAACTACACCACTGACATGATGCTGGAGAGCCCTGAGGAGAGG 1291  
 Qy 241 ThrLeuGlnGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260  
 Db 1292 ACATATGTCTGGAGGAGTCTTTCCTGTCAGCCCAAGAGCTTGGGGGAGTGTATC 1351  
 Qy 261 AspArgIleAlaArgGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
 Db 1352 GACAGGATGCTCGGAGCAGGTACACAGGCTGTGTGTAGTGACGAGAGCCAGCATCTC 1411  
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
 Db 1412 TTGGCGGTGTCTCCCTCTCCGACATCTTCAGGCACTGTGTCTCAGCCCTGTGTGCATC 1471  
 Qy 301 AspAlaLeuGlyAla 305  
 Db 1472 GATGCCCTCGGGGCC 1486

RESULT 3

US-10-705-137-5  
 ; Sequence 5, Application US/10705137  
 ; Publication No. US20040121385A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Leif  
 ; APPLICANT: Luthman, L. Holger  
 ; APPLICANT: Marklund, Stefan  
 ; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT  
 ; FILE REFERENCE: 11145-007002  
 ; CURRENT APPLICATION NUMBER: US/10705,137  
 ; CURRENT FILING DATE: 2003-11-10  
 ; PRIOR APPLICATION NUMBER: US 09/826,581  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/195,665  
 ; PRIOR FILING DATE: 2000-04-07  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FAST-SEQ for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 1647  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (20)...(1486)  
 US-10-705-137-5

Alignment Scores:  
 Pred. No.: 6.77e-192 Length: 1647  
 Score: 1551.00 Matches: 305  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0

US-10-070-794A-4 (1-305) x US-10-705-137-5 (1-1647)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20  
 Db 572 ATGGCTTTCATGCGAGGAGCACACCTGTACGATGCCCACTAGTCCCAAGCTAGTC 631  
 Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
 Db 632 ATCTTCGACACCATGCTGGAGATCAAGAGGCTTCTTCTCTGTGGTGGCAACGCTGTG 691  
 Qy 41 ArgAlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
 Db 692 CGGGCAGCCCTCTATGGGACAGCAGACAGCTTTGTGGGATGCTGACATCACT 751  
 Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80

Db 752 GACTTCATCTCTGTGTGTCATCTACTACAGTCCCTCCCTGTGTCAGATCTATGAGATT 811  
 Qy 81 GluGlnHisLysIleGluThrTyrAlaGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
 Db 812 GAACAACATAGATTGAGACCTGGAGGAGATCTACTCTGCAAGGCTGCTTCAGACCTCTG 871  
 Qy 101 ValSerIleSerProLeuAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
 Db 872 GTCTCCATCTCTCTAATGATAGCTGTGTTGAAGCTGTCTACACCTCTCATCAAGACCGG 931  
 Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
 Db 932 ATCCATCGCTGCTGCTGTCTTGACCCGGGTGTCAGGCAACGTACTCCACATCTCTCACAC 991  
 Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
 Db 992 AAACGGCTGCTCAAGTCTCTGTCACATCTTTGTGACCGGGTGTCTGCTGCTGCTCTCTC 1051  
 Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180  
 Db 1052 TACCGCACTATCCAGATTGGGCACTCGGCACATTCGAGACTTGGCTGTGTGCTGGAG 1111  
 Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
 Db 1112 ACAGCACCCATCTGACTGCACTGGACATCTTTGTGACCGGGTGTGTCTGCACTGCTCT 1171  
 Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
 Db 1172 GTGTCAACGAATGTGTGAGTGTGGGCTCTATTCCTGCTTGTGATGATTCACCTG 1231  
 Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
 Db 1232 GCTGCCAGCAAACTACACCACTGGACATGAGTGTGGAGAGCCCTGAGGACAGG 1291  
 Qy 241 ThrLeuGlnGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260  
 Db 1292 ACATATGTCTGGAGGAGTCTTTCCTGTCAGCCCAAGAGCTTGGGGGAGTGTATC 1351  
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
 Db 1352 GACAGGATGCTCGGAGCAGGTGTACAGGCTGTGTGTAGTGACGAGACCCAGCATCTC 1411  
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
 Db 1412 TTGGCGGTGTCTCCCTCTCCGACATCTTCAGGCACTGTGTCTCAGCCCTGTGTGCATC 1471  
 Qy 301 AspAlaLeuGlyAla 305  
 Db 1472 GATGCCCTCGGGGCC 1486

RESULT 4

US-10-473-670-30  
 ; Sequence 30, Application US/10473670  
 ; Publication No. US20040110180A1  
 ; GENERAL INFORMATION:

; APPLICANT: RECIPON, Shirley A.; BURRILL, John D.;  
 ; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;  
 ; APPLICANT: TANG, Y. Tom; THORNTON, Michael;  
 ; APPLICANT: BOROMSKY, Mark L.; BAUGHN, Mariah R.;  
 ; APPLICANT: BURFORD, Neil; LEE, Soo Yeun;  
 ; APPLICANT: GANDHI, Ameena R.; SWARNAKAR, Anita;  
 ; APPLICANT: YAO, Monique G.; RAMKUMAR, Jayalaxmi;  
 ; APPLICANT: CHAWLA, Narinder K.; LU, Dyung Aina M.;  
 ; APPLICANT: ARVIZU, Chandra S.; ISON, Craig H.;  
 ; APPLICANT: DING, Li; LU, Yan;  
 ; APPLICANT: GURURAJAN, Rajagopal; WALSH, Roderick T.;  
 ; APPLICANT: GANDHI, Ameena R.; SWARNAKAR, Anita;  
 ; APPLICANT: FORSYTHE, Ian J.; YUE, Henry;  
 ; APPLICANT: AU-YOUNG, Janice K.; ELLIOTT, Vicki S.;  
 ; APPLICANT: LEE, Sally  
 ; TITLE OF INVENTION: KINASES AND PHOSPHATASES  
 ; FILE REFERENCE: PI-0398 USN

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; CURRENT APPLICATION NUMBER: US/10/473,670
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/10818
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/282,119
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/283,588
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,759
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/285,589
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/287,037
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/287,036
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/288,608
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/288,712
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/289,909
; PRIOR FILING DATE: 2001-05-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7474666CB1
US-10-473-670-30

Alignment Scores:
Pred. No.: 1,65e-191 Length: 2781
Score: 1553.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-070-794A-4 (1-305) x US-10-473-670-30 (1-2781)
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerIysLeuVal 20
Db 573 ATGGCTTCATCGAGGACACACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTC 632
Qy 21 IlePheAspThrMetLeuGluIleIysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 633 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCCTTTGCTGTGGTGGCCAAAGGTGTG 692
Qy 41 ArgAlaAlaProLeuTrpAspSerIysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 693 CGGGCAGGCCCTCTATGGACGACGACGAAGACGAGCTTTGTGGGATGCTGCACCATCACT 752
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 753 GACTTCATCCTGGTGTGCTGCTACTACAGTCCCGCTGGTCCAGATCTATGAGATT 812
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheIysProLeu 100
Db 813 GAACAACATAAGATTGAGACCTGGAGGAGGATCTACCTGCAAGGCTGCTTCAAGCCTCTG 872
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 873 GTCTCCATCTCTCTTAATGATAGCTGTTGAGCTGTCTACACCTCATCAAGAACCGG 932
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 933 ATCCATCGCCTGCTGCTTCTTACCCGGTGTGAGCAACGCTACTCCATCTCCTCACAC 992
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160

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Db 993 AAACGGCTGCTCAAGTTCCTGTCACATCTTGGTTCCTGCTGCCCGCCCTCTCTCTC 1052
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
Db 1053 TACCGCACTATCCAAGATTGGGCGATCGGCACATTCGAGACTTGGCTGTGGTGGAG 1112
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1113 ACAGCACCCCATCTGACTGACCTGGACATCTTTGTGACCGGTGTGTCTGCACTGCT 1172
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1173 GTGGTCAACGAATGTGGTCAAGTCTGGGCTCTATTCCCGCTTTGATGTGATTCACCTG 1232
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1233 GCTGCCCGACCAACCTACAAACCACTGGACATGATGATGTGGGAAGCCCTGAGGACAGG 1292
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
Db 1293 ACATATGTCTGGAGGAGTCTTCTCTGCGAGCCCGACGAGCTTGGGGGAAGTGTATC 1352
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1353 GACAGGATTGCTCGGAGCAGGTACACAGGCTGGTGTCTAGTGACGAGACCCAGCATCTC 1412
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1413 TTGGGCGTGGTCTCTCCCTCTCCGACATCTTTCAGGCACTGGTGTGCTCAGCCCTGTGGCATC 1472
Qy 301 AspAlaLeuGlyAla 305
Db 1473 GATGCCCTCGGGGCC 1487

RESULT 5
US-10-756-149-1235
; Sequence 1235, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1235
; LENGTH: 2290
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-1235

Alignment Scores:
Pred. No.: 3,05e-188 Length: 2290
Score: 1525.00 Matches: 299
Percent Similarity: 99.34% Conservative: 3
Best Local Similarity: 98.36% Mismatches: 2
Query Match: 98.32% Indels: 0
DB: 9 Gaps: 0

US-10-070-794A-4 (1-305) x US-10-756-149-1235 (1-2290)
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerIysLeuVal 20
Db 574 ATGGCTTCATCGAGGACACACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTC 633
Qy 21 IlePheAspThrMetLeuGluIleIysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 634 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCCTTTGCTGTGGTGGCCAAAGGTGTG 693

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QY 41 ArgAlaAlaProLeuThrAspSerIysLysGlnSerPheValGlyMetLeuThrIleThr 60  
Db 694 CGGCAGCCCCCTCATGGGACAGAAAGCAGAGCTTTGTGGGATGCTGACCATCACT 753  
QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
Db 754 GACTTCATCTCTGGTGTGCTGCTGCTATCAGAGTCCCTCCCTGGTCCAGATCTATGAGATT 813  
QY 81 GluGlnHisIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db 814 GAACAACATAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTG 873  
QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
Db 874 GTCTCCATCTCTCTAATAGTAGCTGTTTGAAGCTGTCTACACCTCATCAAGACCGG 933  
QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db 934 ATCCATGCGCTGCTGCTTGTGACCGGTGTACAGGACGACTTCCATCCTCCACAC 993  
QY 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db 994 AAACGCTGCTCAAGTTCCTGTCACATCTTTGGTTCCTGCTGCCCGGCTCTCTCTC 1053  
QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180  
Db 1054 TACCGCATATCAAGATTGGGCATCGGCATCGGCATCTCGAGACTTGGCTGTGGTCTGGAG 1113  
QY 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
Db 1114 ACAGCCCATCTCTGACTGCACTGGACATCTTTGTGACCGGCTGTGTCTGCACTGCCT 1173  
QY 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
Db 1174 GTGGTCAACGAATGTGTGCTGAGTCTGGGCTCTATTCCCGCTTTGATGTATCACTG 1233  
QY 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
Db 1234 GCTGCCAGCAAACTCAACACCTGACATGATGTGGAGAGGCTTGGAGAGG 1293  
QY 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260  
Db 1294 ACATATGTCTGGAGGAGTCTCTTCTGTCAGCCCCACAGAGCTTGGGGAGTGTATC 1353  
QY 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
Db 1354 GACAGGATGCTCGGAGCAGGTACACAGGCTGTGTGTGAGCAGACCCAGCATCTC 1413  
QY 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
Db 1414 TTGGCGTGTCTCTCCCTCTCCGACATCTTTCAGGCACTGTGTGCTCAGCCCTGTGGCATC 1473  
QY 301 AspAlaLeuGly 304  
Db 1474 GATCCCTCGGGG 1485

## RESULT 6

US-09-950-022-1  
; Sequence 1, Application US/09950022  
; Publication No. US20030017470A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Novel PKA3G Alleles and Use fo the Same as Genetic Markers for  
; FILE OF INVENTION: Reproductive and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950,022  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239

; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1873

; TYPE: DNA  
; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1392)  
US-09-950-022-1

## Alignment Scores:

Pred. No.:	4,98e-186	Length:	1873
Score:	1507.00	Matches:	296
Percent Similarity:	98.36%	Conservative:	4
Best Local Similarity:	97.05%	Mismatches:	5
Query Match:	97.16%	Indels:	0
DB:	3	Gaps:	0

US-10-070-794A-4 (1-305) x US-09-950-022-1 (1-1873)

QY 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20  
Db 478 ATGCACCTTCATGCAGGAGCACACTGCTACGATGCCATGCCGACGACTCCAAACTGGTC 537  
QY 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
Db 538 ATCTTCGACACCACTGCTGGAGATCAAGAAGGCCCTTCTTTCCTGCTGGTGGCAACGGCGTC 597  
QY 41 ArgAlaAlaProLeuThrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
Db 598 CGAGCGGACCTTTGTGGGACACAGAACAGAGCTTCGTGGGAGTGTGACCATCACA 657  
QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
Db 658 GACTTCATCTTGTGTGTCACCGCTATTACAGGTCCCTCCCTGCTCCAGATCTACGAGATT 717  
QY 81 GluGlnHisIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db 718 GAAGAACAATAAGATTGAGACCTCGAGGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777  
QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
Db 778 GTCTCCATCTCTCCCAATGACACCTTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837  
QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db 838 ATCCACCGCTGCGGTCCTGGACCTGCTCCGGGCTGTGCTCCACATCTCCACAT 897  
QY 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db 898 AAGCGCTTCTCAAGTTCCTGACATCTTTGGCACCTTGTGGCACCTGCTGCGCGCTCTCTCTC 957  
QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180  
Db 958 TACCGCACCATCCAGATTTGGGACATCCGACATTCGAGACTTGGCGGTGGTCTGGAA 1017  
QY 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
Db 1018 ACGCGCCCATCTGACCGCCTGACATCTTGTGACCGGCTGTGTCTGCGCTGCT 1077  
QY 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
Db 1078 GTGGTCAACGAACCTGACAGGAGTAGTGGGCTCTACTCTCGCTTTGATGTGATCCACTG 1137  
QY 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
Db 1138 GCTGCCCAACAACATACACACCTGGACATGAATGTGGGAGAACCTCTGAGGACGG 1197  
QY 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260

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Db 1198 AACTGTGTCTGGAGCGGTCCTTCTGTCAGCGCCACAGACCTTGGGGAGTCATT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCCGGGAACAGGTGCACCGCTGTGTGTCTGTGGATGAGACCCAGACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGTGTGTCTCTGACATCTTTCAGGCTCTGGTGTCTGAGCCCTGCTGGAAATT 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 7
US-09-950-022-3
; Sequence 3, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use to the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-3

Alignment Scores:
Pred. No.: 4, 98e-186 Length: 1873
Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservative: 4
Best Local Similarity: 97.05% Mismatches: 5
Query Match: 97.16% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022-3 (1-1873)
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerIysLeuVal 20
Db 478 ATGCACCTTCATGCAGGAGCACACCTGTCTAGCATGCGATGCGGACCGACCTCCAAACTGGTCTC 537
Qy 21 IlePheAspThrMetLeuGluIleIysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATCTGTGAGATCAAGAGGCTCTTCTTGCCCTGTGGCCCAACGGCGTCTC 597
Qy 41 ArgAlaAlaProLeuTyrAspSerIysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGACACCTTGTGGAGCAGCAGACGAGCTTCGTGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTTGGTGTGTCACCGCTATTACAGGTCCCCCTGCTCCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheIysProLeu 100
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Db 718 GAAGAACATAAGATTGAGACCTTGAGCGAGATCTACTTCAAGGCTGCTTCAAGGCTCTGTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCCTGTTCGAAGCTGTGTACGCCCTCATCAAGAACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACGCGCTGCGGTCTCTGGACCTGTCTCCGGGGCTGTGTCTCCACATCTCTCACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGCTTCTCAAGTTCCTGTCACATCTTTTGGCACCTGTCTGCCCGCGCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 958 TACCGCACCATCCAAGATTTGGGCATCGGCACATTCGAGACTTGGCGCTGGTCTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1018 ACGCGCGCCATCTCTGACCGCACCTGGACATCTTCTGTGACCGCGGTGTCTGTGGCTGCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAACCTGACAGGTAGTGGGCTCTACTCTCGCTTGTGATGTATCCACTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAACATCAACACCATCTGGACATGAATGTGGGAAGCCCTTGAGGACGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1198 ACCTGTGTCTGGAAGCGTCCTTCTCTGACGCCCCACGAGACTTGGGGGAAGTCAATT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCCGGGAACAGGTGCACCGCTGTGTCTGTGGATGAGACCCAGACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGTGTGTCTCTCTGACATCTTTCAGGCTCTGGTGTCTGAGCCCTGCTGGAAATT 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 8
US-09-950-022-5
; Sequence 5, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use to the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
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FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1392)  
US-09-950-022-5

## Alignment Scores:

Pred. No.: 4, 98e-186 Length: 1873  
Score: 1507.00 Matches: 296  
Percent Similarity: 98.36% Conservative: 4  
Best Local Similarity: 97.05% Mismatches: 5  
Query Match: 97.16% Indels: 0  
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022-5 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20  
Db 478 ATGCACCTTCATGTCAGGAGCACACCTGTACATGCCATGGGACACGCTCCAACTGGTC 537  
Qy 21 IlePheAspThrMetLeuGluHisLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGGCCCTGGTGGCAACGGGCTC 597  
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
Db 598 CGAGCGCACCTTTGTGGGACAGCAAGACGAGCTTCGTGGGGATGCTGACCATCACA 657  
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
Db 658 GACTTCATCTGTGGTGCACCGCTATTACAGGTCCCTGGTCCAGATCTACGAGATT 717  
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db 718 GAAGACATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777  
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
Db 778 GTCTCCATCTCTCCATGACAGGCTGTTCGAGCTGTCTACGCCCTCATCAAGAACCGG 837  
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db 838 ATCCACCGCTGCGGCTGTGGACCTGTCTCCGGGCTGTGCTCCACATCTCCACAT 897  
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db 898 AAGCGGCTTCTCAAGTTCCTGCACATCTTTGGCACCTGTCTGCCCGGCTCTCTCTC 957  
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180  
Db 958 TACCGCACCATCCAAAGATTTGGGCATCGGCACATTCGAGACTTGGCGGTGGTGGAA 1017  
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
Db 1018 ACGGGCGCATCTGACCGCATCTGGACATCTTGTGGACCGGCTGTCTGCGCTGCT 1077  
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
Db 1078 GTGTCACCAACCACTGACAGGATGTGGGCTCTACTCTCGCTTGTATGTATCCACCTG 1137  
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
Db 1138 GCTGCCCAACAAACATACACACCTGGACATGAATGTGGGAAAGCCCTTGAGGACGG 1197  
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260  
Db 1198 ACATGTGTCTGGNAGCGCTCTTCTCTGCAGCCCCACAGACCTTGGGGGAAGTCATT 1257  
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
Db 1258 GACCGGATTGTCGGGAACAGGTGCACCGCTGTGTGCTGTGTGATGAGACCCAGACCTT 1317  
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300

Db 1318 CTGGGCGTGTGTCCCTCTCTGACATCCTTCAGGCTCTGTGTGCTCAGCCCTGTGGAATT 1377  
Qy 301 AspAlaLeuGlyAla 305  
Db 1378 GATGCCCTCGGGGCC 1392

## RESULT 9

US-11-075-134-1  
; Sequence 1, Application US/11075134  
; Publication No. US20050208551A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/11/075,134  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: US/09/950,022  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 1873  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1392)  
; OTHER INFORMATION:  
US-11-075-134-1

Alignment Scores:  
Pred. No.: 4, 98e-186 Length: 1873  
Score: 1507.00 Matches: 296  
Percent Similarity: 98.36% Conservative: 4  
Best Local Similarity: 97.05% Mismatches: 5  
Query Match: 97.16% Indels: 0  
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-11-075-134-1 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20  
Db 478 ATGCACCTTCATGTCAGGAGCACACCTGTACATGCCATGGGACACGCTCCAACTGGTC 537  
Qy 21 IlePheAspThrMetLeuGluHisLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGGCCCTGGTGGCAACGGGCTC 597  
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
Db 598 CGAGCGCACCTTTGTGGGACAGCAAGACGAGCTTCGTGGGGATGCTGACCATCACA 657  
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
Db 658 GACTTCATCTGTGTGCTGCACCGCTATTACAGTCCCTGGTCCAGATCTACGAGATT 717  
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db 718 GAAGACATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777  
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120

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778 GTCTCCATCTCTCCCATGACAGCCTGTTGAGAGCTGTCTACGCCCTCATCAAGAACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCTGCGGCTCTGGACCTGTCTCCGGGCTGTGCTCCACATCTCCACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTCTCTGACATCTTTGGACCTGTGCTGCGCCGCGCTCTCTCCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 958 TACCGCACCATCCAAAGATTGGGCAATGGGCATTCGCACATTCGAGACTTGGCGGTGCTGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1018 ACGCGGCCATCTCTGCGCACCTGGACATCTTCTGTCGACCGCGCTGTGCTCTGCGCTGCCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValIleGlyThrPheArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGGCTCTACTCTGCTTTGATGTGATCCACCTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAAACATACACCACTGGACATGATGTGGAGAGCCCTGAGGCAGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyGlnValValIleGlyThrPheArgPheAspValIleHisLeu 260
Db 1198 ACCTGTGCTGGAAGGCGTCTTCTTCCAGCCGCCACGAGACTTGGGGGAAGTCATT 1257
Qy 261 AspArgIleAlaArgGlnGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATGTCCCGGAAACAGGTGACCGCTGGTGTCTGAGATGAGACCAACACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGGTGGTGTCTCTCTGACATCTTTCAGGCTCTGGTGTCTCAGCCCTGCTGGAATT 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGCC 1392

RESULT 10
US-11-075-134-3
; Sequence 3, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothechild, Max
; APPLICANT: Ciohanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668U3
; CURRENT APPLICATION NUMBER: US/11/075,134
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-11-075-134-3
Alignment Scores:
Pred. No.: 4,98e-186 Length: 1873
Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservative: 4
Best Local Similarity: 97.05% Mismatches: 5
Query Match: 97.16% Indels: 0
DB: 10 Gaps: 0
US-10-070-794A-4 (1-305) x US-11-075-134-3 (1-1873)
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 478 ATGCACCTTATGAGGAGGACACCTGCTACGATGCCATGGCAGCTCCAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAGAGGCCCTTCTTGGCCCTGGTGGCCAAAGCGGTC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGCACCTTGTGGGACAGCAAGACAGAGCTTCGTGGGATGTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTTGTGGTGTGACCGCTATTACAGGTCCCTCTTCAAGGCTGCTTCAAGGCTCTG 777
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAGAACATAGATTGAGACTTGAGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAGAGCTGTCTACGCCCTCATCAAGAACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCTGCGGCTCTGGACCTGTCTCCGGGCTGTGCTCCACATCTCCACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTCTCTGACATCTTTGGACCCCTGTGCTGCCGCGCTCTCTCCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgPheAspValIleHisLeu 180
Db 958 TACCGCACCATCCAAAGATTGGGCAATGGGCATTCGCACATTCGAGACTTGGCGGTGCTGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1018 ACGCGGCCATCTCTGACCGCACTGGACATCTTCTGTCGACCGCGCTGTGCTGCTGCTGCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValIleGlyThrPheArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGGCTCTACTCTGCTTTGATGTGATCCACCTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAAACATACACCACTGGACATGATGTGGAGAGCCCTGAGGCAGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyGlnValValIleGlyThrPheArgPheAspValIleHisLeu 260
Db 1198 ACCTGTGCTGGAAGGCGTCTTCTTCCAGCCGCCACGAGACTTGGGGGAAGTCATT 1257
Qy 261 AspArgIleAlaArgGlnGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATGTCCCGGAAACAGGTGACCGCTGGTGTCTGAGATGAGACCAACACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGGTGGTGTCTCTCTGACATCTTCTCAGGCTCTGGTGTCTCAGCCCTGCTGGAATT 1377

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Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 11
US-11-075-134-5
; Sequence 5, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2001-01-08
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-11-075-134-5

Alignment Scores:
Pred. No.: 4.98e-186 Length: 1873
Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservative: 4
Best Local Similarity: 97.05% Mismatches: 5
Query Match: 97.16% Indels: 0
DB: 10 Gaps: 0

US-10-070-794A-4 (1-305) x US-11-075-134-5 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 478 ATGCACCTTCATGAGGAGCACACTGCTAGTGCCATGCGGACGAGCTCCAAACTGGTC 537

Qy 21 IlePheAspThrMetLeuGluIleLysLeuAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGSCCTTCTTCCCTGGTGGCCAAACGGCGTC 597

Qy 41 ArgAlaAlaProLeuThrAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGGATGCTGACCATCACA 657

Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTGTGGCTGACCGCTATTACAGGTCCCTCCCTGTCAGATCTACGAGATT 717

Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGAACAATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777

Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837
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Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCCTGCGGTCCTGGACCCCTGTCTCCGGGGCTGTGTCTCCACATCTCCACACAT 897

Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTTCTTCGCACATCTTTGGCACCTGTGTGCCCGGCCCTCTCTCTC 957

Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 958 TACCGCACCATCCAGATTGGGCATCGGCACATTCGAGACTTGGCGGTGGTCTGGAA 1017

Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1018 ACGCGGCCCATCTGACCGCACTGGACATCTTCGTGGACCGCGTGTGTCTGCGCTGCT 1077

Qy 201 ValValAsnGlnCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAAACTGGACAGGTAGTGGGCTCTTACTCTCGCTTTGTATGTATCCACTG 1137

Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAACATACAAACCTGACATGATGTGGAGAACCCCTGAGGACGCGG 1197

Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
Db 1198 ACATGTGTCTGGAGGCGTCTTCTCTGCGACCCACGAGACTTGGGGGAAGTCACT 1257

Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCGGGGAACAGGTGCACCGCTGTGTCTCGTGGATGAGACCCAGCACCTT 1317

Qy 281 LeuGlyValValSerLeuSerAspIleLeuGluAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGGTGTGTGTCCTCTCTGACATCTTCTGAGCTCTGTGGTCTGAGCCCTGCTGGAATT 1377

Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 12
US-09-950-022-7
; Sequence 7, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2001-01-08
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-7

Alignment Scores:
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Pred. No.: 6.74e-186 Length: 1873
Score: 1506.00 Matches: 295
Percent Similarity: 98.36% Conservatives: 5
Best Local Similarity: 96.72% Mismatches: 5
Query Match: 97.10% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022-7 (1-1873)

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Db 478 ATGCACCTTCATGCGAGGACACACCTGCTAGCATGCCATGCCAGCAGCTCCAAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluLeuLysAlaPhePheAlaAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAGGCTTCTTTGCCCTGGTGGCCACGCGATC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGCACCTTTGGGACAGCAAGACAGAGCTTCGTGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluLe 80
Db 658 GACTTCATCTTGGTGTGTCACCGCTATTACAGGTCCCGCTGCTCCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGACATATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCATGACAGCTGTTGAAAGCTGTCTAGCGCCTCATCAAGAACGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCCTGCGGCTCTGTCGCGGCTGTCGCTCCACATCTCTCACACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTCTCTGCACATCTTTGGCACCTGCTGCGCCGCGCTCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 958 TACGCGACCATCCAGATTGGGCATCGGCATATCCGAGACTTGGCGGTGGTGTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgA-gValSerAlaLeuPro 200
Db 1018 ACGCGCCCATCTTGACCGCACTGGACATCTTCGTGGACCGCGCTGTGCTGCGCTGCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
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Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1198 ACATGTGCTTGGAAAGGCTCTCTTCTCCGACGCCCCACGAGACCTTGGGGAGAGTCATT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
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Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGGCGGTGGTGTCTCTGACATCTCTTACAGGCTCTGGTCTCAGCCCTGCTGGAATT 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392
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RESULT 13
US-11-075-134-7
; Sequence 7, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
; US-11-075-134-7

Alignment Scores:
Pred. No.: 6.74e-186 Length: 1873
Score: 1506.00 Matches: 295
Percent Similarity: 98.36% Conservatives: 5
Best Local Similarity: 96.72% Mismatches: 5
Query Match: 97.10% Indels: 0
DB: 10 Gaps: 0

US-10-070-794A-4 (1-305) x US-11-075-134-7 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
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Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAGGCTTCTTTGCCCTGGTGGCCACGCGATC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGCACCTTTGGGACAGCAAGACAGAGCTTCGTGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTTGGTGTGTCACCGCTATTACAGGTCCCGCTGCTCCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGACATATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCATGACAGCTGTTGAAAGCTGTCTAGCGCCTCATCAAGAACGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCCTGCGGCTCTGTCGCGGCTGTCGCTCCACATCTCTCACACAT 897
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Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
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Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180  
Db 958 TACCGCACCATCCAAAGATTGGGCATTCGGACATTCGAGACTTGGCGGTGTCTGGAA 1017  
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200  
Db 1018 ACGCGGCCCATCTCTGACCGCATCTGACATCTTCTGTGGACCGCGTGTCTGCGCTGCT 1077  
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
Db 1078 GTGGTCAACGAACCTGGACAGGTAGTGGCGCTCTACTCTCGCTTTGATGTGATCCACTG 1137  
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240  
Db 1138 GCTGCCCAACAAACATACACCATCTGACATGATGATGAGAGAGCCCTTGAGGACCGG 1197  
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260  
Db 1198 ACCTGTGTCTGGAAGCGCTCTTCTCTGCCAGCCACGAGACCTTTGGGGAAGTCATT 1257  
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspArgValSerAlaLeuPro 280  
Db 1258 GACCGGATGTTCGGGAACAGGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317  
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
Db 1318 CTGGCGGTGTGTCTCTCTGACATCTTCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1377  
Qy 301 AspAlaLeuGlyAla 305  
Db 1378 GATGCCCTCGGGGCC 1392

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; Sequence 9, Application US/09950022  
; Publication No. US20030017470A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for  
; TITLE OF INVENTION: Reproductive and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950,022  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1873  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1392)  
US-09-950-022-9

Alignment Scores:  
Pred. No.: 1.67e-185 Length: 1873  
Score: 1503.00 Matches: 295  
Percent Similarity: 98.36% Conservative: 5  
Best Local Similarity: 96.72% Mismatches: 5  
Query Match: 96.91% Indels: 0

DB: 3 Gaps: 0  
US-10-070-794A-4 (1-305) x US-09-950-022-9 (1-1873)  
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20  
Db 478 ATGCACCTTATGACGAGACACCTCTGCTACGATGCCATGGACACCTCAAACTGGTC 537  
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40  
Db 538 ATCTTCGACACCATCTGCGGATCAAGAGCCCTCTTTGCCCTGGTGGCAACGCGGTC 597  
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60  
Db 598 CAAGCGCACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGGATGCTGACCATCACA 657  
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80  
Db 658 GACTTCATCTTGTGTGCTGCCACCGCTATTACAGGTGCCCTCTGGTCCAGATCTACGAGATT 717  
Qy 81 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100  
Db 718 GAAGAACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777  
Qy 101 ValSerIleSerProLeuAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCCAAAGCTGTCTACGCGCTCTCATCAAGACCGG 837  
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140  
Db 838 ATCCACCGCTGCTGGGCTCTGGACCTGTCTCCGGGGCTGTGTCTCCACATCTCTCACACAT 897  
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db 898 AAGCGGCTTCTCAAGTCTCTGACATCTTTGGCACCTGTGTCGCCCGCCCTCTCTCTC 957  
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180  
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Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
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Db 1378 GATGCCCTCGGGGCC 1392

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; Sequence 9, Application US/11075134  
; Publication No. US20050208551A1  
; GENERAL INFORMATION:

APPLICANT: Rothschild, Max  
APPLICANT: Ciobanu, Dan  
APPLICANT: Malek, Massoud  
APPLICANT: Plastow, Graham  
TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for  
TITLE OF INVENTION: Reproductive  
TITLE OF INVENTION: and Meat Quality Traits  
FILE REFERENCE: P046680S3  
CURRENT APPLICATION NUMBER: US/11/075,134  
CURRENT FILING DATE: 2005-03-08  
PRIORITY FILING DATE: US/09/950,022  
PRIORITY FILING DATE: 2001-09-10  
PRIORITY FILING DATE: 2000-09-08  
PRIORITY FILING DATE: 2001-01-08  
PRIORITY FILING DATE: 2001-06-18  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 1873  
TYPE: DNA  
ORGANISM: Sus scrofa  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1392)  
OTHER INFORMATION:  
US-11-075-134-9

Alignment Scores:  
Pred. No.: 1.67e-185 Length: 1873  
Score: 1503.00 Matches: 295  
Percent Similarity: 98.36% Conservative: 5  
Best Local Similarity: 96.72% Mismatches: 5  
Query Match: 96.91% Indels: 0  
DB: 10 Gaps: 0

US-10-070-794A-4 (1-305) x US-11-075-134-9 (1-1873)

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Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAAGGCCTTCTTTGGCCCTGGTGGCCAAAGCGCGTC 597  
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Db 718 GAAGAAACATAAGATTGAGACCTGGAGGGAGATCTACCTTCAAGGCTGCTTCAAGCGCTCTG 777  
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120  
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Db 838 ATCCACCGCTCCCGGTCTGGACCTGTCTCCGGGGTGTGCTCCACATCTCCACAT 897  
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160  
Db 898 AAGCGGCTTCTCAAGTTCCTGACATCTTTGGACCTGTGTCGCCCGGCTCCTTCCTC 957  
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180

Db 958 TACCGCACCATCCAGATTTCGGCATCGGCACATTCGAGACTTGGCGGTGCTGGAA 1017  
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200  
Db 1018 ACGCGGCCCATCTCTGACCGCATCGACATCTTCGTGGACCGGCTGTGTCTGCGCTGCCT 1077  
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220  
Db 1078 GTGGTCAACGAAACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGATCCACTG 1137  
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Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280  
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Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300  
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Qy 301 AspAlaLeuGlyAla 305  
Db 1378 GATGCCCTCGGGCC 1392

Search completed: January 26, 2006, 07:59:22

Job time : 671.008 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:15:19 ; Search time 13.485 Seconds  
(without alignments)  
229.213 Million cell updates/sec

Title: US-10-070-794A-4  
Perfect score: 1551  
Sequence: 1 MRFQHTCYDAMATSSKLV.....LSDILQALVLSGIDALGA 305

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 70609 seqs, 10134256 residues

Total number of hits satisfying chosen parameters: 70609

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	111	7.2	494	7	US-11-156-084-34
4	107.5	6.9	498	6	US-10-467-657-5006
5	102	6.6	461	7	US-11-156-084-35
6	100.5	6.5	495	7	US-11-156-084-36
7	99	6.4	330	7	US-11-156-084-230
8	89.5	5.8	488	6	US-10-793-626-2308
9	87	5.6	1251	7	US-11-043-889-22
10	86.5	5.6	506	7	US-11-055-822-946
11	85.5	5.5	158	7	US-11-055-822-948
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13	80.5	5.2	319	6	US-10-873-528-64
14	79	5.1	564	7	US-11-082-389-78
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17	77	5.0	274	6	US-10-467-657-2140
18	77	5.0	323	7	US-11-156-084-336
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23	76	4.9	450	7	US-11-074-176-212
24	76	4.9	469	6	US-10-467-657-6280
25	76	4.9	737	6	US-10-055-877-156

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45	74	4.8	368	6	US-10-793-626-742	Sequence 742, App

ALIGNMENTS

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; Publication No. US20060010515A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology LLC  
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to  
; FILE REFERENCE: (38-21)  
; CURRENT APPLICATION NUMBER: US/11/156,084  
; CURRENT FILING DATE: 2005-06-17  
; NUMBER OF SEQ ID NOS: 364  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-11-156-084-26

Query Match 7.2%; Score 111; DB 7; Length 466;  
Best Local Similarity 23.2%; Pred. No. 0.0031;  
Matches 68; Conservative 45; Mismatches 90; Indels 90; Gaps 16;

QY	69	YRSPVLQIYEIQHKIETWREIYLOGCFKPLVISPNDSLFEAV	-----YTLIKN 119
DB	120	YTIQAVVSKFLDDAAEDT-----ECCADVASVVDQDMVSVFGRDDLHSHGYELKE 173	
QY	120	RIHRLPVLDPVSNVHLTHKLLKFLHFGSLRPPSELY--RTQDLG-IGTFR-DL 175	
DB	174	-----LDPVAANRHPNNHRKINQYLSLHSGRGLPSKLYQCKTAENGCINASRPDY 226	
QY	176	AVV--LETAPILTALDIFVDRVSALPVNVEGQVVGLY-----S 213	
DB	227	CLICMDAETA-----VLDRVQVQVDAMVDAGLDEVYDIYKPGADYTRGLRQSIGVREFE 282	
QY	214	RPDVIHLAAQQTNYHL-----DMSVGEALRQRTLCLEGLVSCOPHES-----LGEVIDRI 263	
DB	283	DFLKIHL-SETCAGHLTSLSDNDKVMKENLRK-----ILNFKDDKLRLMLEAIDRV 334	
QY	264	-----AREQVHRLV-----DETQHLGVVSLSDILOALVLSA 298	
DB	335	KLNTRLLRRQRKRVRSLRTVFGWNIHYIDATYILS--KSEESMNAQVVKPA 385	

RESULT 2  
US-11-156-084-33  
; Sequence 33, Application US/11156084  
; Publication No. US20060010515A1







```
US-11-055-822-948
; Sequence 948, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 948
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-948

Query Match          5.5%; Score 85.5; DB 7; Length 158;
Best Local Similarity 24.1%; Pred. No. 0.2;
Matches 34; Conservative 29; Mismatches 57; Indels 21; Gaps 5;

QY 153 LLPRPSLYTIDGLGIGTFRDLAVLETPILTALDIFVDRVSALPVVNECGVVGL- 211
Db 29 LLPDASDVVPSEVDTSTQLTRNRL-----NTPILSA-----AMDTVTTEARMAIGMA 75
QY 212 -YSRFDVIH--LAAQQTYNHLDMSVGBALRQTLICLEGVLSQPHESLGEVIDRIAREQV 268
Db 76 RHGGIGVLRHNLISQEAQENVEL-----VKESBSGWTDPTCTPDMISIQEVDLCAFRRI 131
QY 269 HRLVLVDETOHLGVSLSDI 289
Db 132 SGLFVVVDEAGKLVGICTNRDM 152

RESULT 12
US-10-467-657-8240
; Sequence 8240, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8240
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8240

Query Match          5.5%; Score 85.5; DB 6; Length 554;
Best Local Similarity 25.5%; Pred. No. 1.2;
Matches 47; Conservative 26; Mismatches 62; Indels 49; Gaps 11;

QY 2 RFMQEHTCYDAMATSSKLVIKKAFFALVANGVRAAPLWDSKKQSFVGMILTID 61
Db 251 RYAIRFQCYRRRLCNKKISVFQIPE-TLAFFSIVETPI-----DPLRQT---VRIAD 300
QY 62 -----FILVLH---RYRSPVLQIYEIEQ-----HKIETWREIYLOGCCKP 99
Db 301 HKTVRLHPGHPHILIKHITARVRCNPVALFAEVFNLLVIRDIPVPRQIYLHLITP 360
QY 100 ---LVISPNDSLFEAVYTLIKNRIHRLP-----VLDPVSGNVLHILTHKRLKFL 147
Db 361 EAMLINIFED---FPAP-RRIKRTVRLNPNPISCRFIIFPVSRSAVHIY-RKRTIVPI 415
QY 148 HIFG 151
Db 416 QIFG 419

RESULT 13
US-10-873-528-64
; Sequence 64, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129W0
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-64

Query Match          5.2%; Score 80.5; DB 6; Length 319;
Best Local Similarity 21.4%; Pred. No. 1.7;
Matches 34; Conservative 28; Mismatches 50; Indels 47; Gaps 5;

QY 101 VSISPNDLSFE-----AVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLKFLHIFGSLP 155
Db 20 IBITPNSANTEIAPPDGIQOVLSNLLKL-VDPNV--NALLTANYIRILSWAVIFGIAMR 76
QY 156 RPS-----FLYRTIQLGIGTFRDLAVLE----- 180
Db 77 EAKNSQELTKTIADVTSKIVEMIINLAPFGILGVFKTISDKGVGLANYIGILLVLT 136
QY 181 ----TAPILTALDIFVDRVSALPVVNECGVVGLYSRF 215
Db 137 TMLFVAPVNVNPLIAFFFMRRNPYPVLVWNCIRVSGVTAF 175
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RESULT 14  
 US-11-082-389-78  
 ; Sequence 78, Application US/11082389  
 ; Publication No. US20050244935A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pompejus, Markus  
 ; APPLICANT: Kroger, Burkhard  
 ; APPLICANT: Schroder, Hartwig  
 ; APPLICANT: Zelder, Oskar  
 ; APPLICANT: Haberhauer, Gregor  
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 ; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
 ; TITLE OF INVENTION: TRANSPORT  
 ; FILE REFERENCE: BGI-131CPCN  
 ; CURRENT APPLICATION NUMBER: US/11/082,389  
 ; CURRENT FILING DATE: 2005-03-16  
 ; PRIOR APPLICATION NUMBER: US 09/603024  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: US 60/141031  
 ; PRIOR FILING DATE: 1999-06-25  
 ; PRIOR APPLICATION NUMBER: US 60/143262  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: US 60/151281  
 ; PRIOR FILING DATE: 1999-08-27  
 ; PRIOR APPLICATION NUMBER: DE 19930487.4  
 ; PRIOR FILING DATE: 1999-07-01  
 ; PRIOR APPLICATION NUMBER: DE 19930489.0  
 ; PRIOR FILING DATE: 1999-07-01  
 ; PRIOR APPLICATION NUMBER: DE 19931549.3  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931550.7  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19932134.5  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19941379.7  
 ; PRIOR FILING DATE: 1999-08-31  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 446  
 ; SEQ ID NO 78  
 ; LENGTH: 564  
 ; TYPE: PRT  
 ; ORGANISM: Corynebacterium glutamicum  
 US-11-082-389-78

Query Match 5.1%; Score 79; DB 7; Length 564;  
 Best Local Similarity 23.9%; Pred. No. 5.1;  
 Matches 48; Conservative 31; Mismatches 54; Indels 68; Gaps 11;  
 Qy 142 RLKFLHIF-----GSLLP-----PSFLYRTIQLG--IGTFRDL 175  
 Db 306 RLRSFVHLRLSMSYFRTMSGRINTRMTTIDNLSFLQSLAQTVVSGTLIGVVTML 365  
 Qy 176 A-----VVLETAPILTALDIFVDRVSALPVVNECGQVVGLYSRFDVHLAAQOTYN 227  
 Db 366 AITDAQLALVALSVVPIIIVTL-IFRAIS-----SR---LYTASREQAS 406  
 Qy 228 HLDMSVGLRALRQRTLCLGVLSQPHESLGEVIDRIA--REQVHRLVLVDETQ---HLLG 282  
 Db 407 QVNAVPHES-----IAGLRTAQMHRMEDQVFDNYAGEAEFRRLRVKVSQTATAYPPG 459  
 Qy 283 VVLSLDILQALVLSPADIDAL 303  
 Db 460 LGALSEIAQALVL-----GFGAL 477

RESULT 15  
 US-10-485-517-272  
 ; Sequence 272, Application US/10485517  
 ; Publication No. US20050256299A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Sheffield  
 ; APPLICANT: Biosynexus Incorporated

; APPLICANT: Foster, Simon  
 ; APPLICANT: Mond, James  
 ; TITLE OF INVENTION: Antigenic Polypeptides  
 ; FILE REFERENCE: F100629WO  
 ; CURRENT APPLICATION NUMBER: US/10/485,517  
 ; CURRENT FILING DATE: 2004-02-02  
 ; PRIOR APPLICATION NUMBER: GB 0118825.9  
 ; PRIOR FILING DATE: 2001-08-02  
 ; PRIOR APPLICATION NUMBER: GB 0200349.9  
 ; PRIOR FILING DATE: 2002-01-09  
 ; NUMBER OF SEQ ID NOS: 424  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 272  
 ; LENGTH: 449  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus aureus  
 US-10-485-517-272

Query Match 5.0%; Score 77.5; DB 6; Length 449;  
 Best Local Similarity 18.8%; Pred. No. 5.2;  
 Matches 46; Conservative 46; Mismatches 82; Indels 71; Gaps 9;  
 Qy 79 EIEQHKIETWREIYLQCPK-----PLVSI SPNDSLFEAVVTLKNRIHRL 124  
 Db 198 EINQTEL-----AYMQNIFSDERHAKDIMVPRQTOMITLNEPFPNVDLLETIKHQFTRY 252  
 Qy 125 PVLDPVSGNVHLTHKRLKLLKELHIFGSLLPSPFLYRTIQLDGLGTF-RDLAVVLETP 183  
 Db 253 PITD--DGDKDHKGFINVKEFLTEYAS-----GKTIK---IANYIHELPMISETTR 299  
 Qy 184 ILTALDIFVDRVSALPVVNECGQVVGLYSRFDVHLAAQOTVYHLDMSVGEALRQRTL 243  
 Db 300 ISDALIRMQREHVHMSLIIDYGGTAGILTMEDIL----- 334  
 Qy 244 LEGVLSQPHESLGEVIDRIAQVHRLVLVD-ETQHLLGVVSLSDILQALVL---SPAG 299  
 Db 335 -----EEIVGEIRDEFDDDEVNDIVKIDNKTFQVNGRVLDDLTTEFGIEFDDSD 385  
 Qy 300 IDALG 304  
 Db 386 IDTIG 390

Search completed: January 24, 2006, 22:31:43  
 Job time : 14.485 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:04:33 ; Search time 25.3836 Seconds  
(without alignments)  
993.400 Million cell updates/sec

Title: US-10-070-794A-4  
Perfect score: 1551  
Sequence: 1 MRFMQBHTCYDAMATSSKLV.....LSDIQLQVLSPAGIDALGA 305

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
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4: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1507	97.2	464	2	US-09-950-022A-4
3	1507	97.2	464	2	US-09-950-022A-6
4	1506	97.1	464	2	US-09-950-022A-8
5	1503	96.9	464	2	US-09-950-022A-10
6	1064	68.6	328	1	US-08-878-989-7
7	1064	68.6	328	2	US-09-272-796-7
8	1064	68.6	413	2	US-09-949-016-8261
9	1009	65.1	331	1	US-08-878-989-21
10	1009	65.1	331	2	US-09-101-146-64
11	1009	65.1	331	2	US-09-272-796-21
12	1009	65.1	331	2	US-09-538-092-1211
13	1009	65.1	336	2	US-09-949-016-10881
14	1007	64.9	330	2	US-09-359-161-6
15	457	29.5	322	2	US-09-359-161-7
16	457	29.5	322	2	US-09-538-092-297
17	304	19.6	101	2	US-09-513-999C-5736
18	252.5	16.3	254	2	US-09-248-796A-18872
19	214	13.8	379	2	US-09-359-161-5
20	196.5	12.7	629	2	US-09-248-796A-14535
21	190	12.3	373	2	US-09-359-161-3
22	104.5	6.7	375	2	US-09-328-352-6078
23	99.5	6.4	490	2	US-09-252-991A-30355
24	98.5	6.4	375	2	US-09-634-238-260
25	97.5	6.3	510	2	US-09-489-039A-11778
26	97	6.3	622	2	US-09-605-703B-2098
27	96.5	6.2	481	2	US-09-252-991A-31708

ALIGNMENTS

RESULT 1

US-09-950-022A-2  
; Sequence 2, Application US/09950022A  
; Patent No. 6919177  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950, 022A  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; TYPE: PRT  
; LENGTH: 464  
; ORGANISM: Sus scrofa  
US-09-950-022A-2

Query Match	97.2%	Score 1507;	DB 2;	Length 464;
Best Local Similarity	97.0%	Pred. No. 1.1e-166;		
Matches 296;	Conservative 4;	Mismatches 5;	Indels 0;	Gaps 0;
Qy	1	MRFQEHCTCDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT	60	
Db	160	MRFQEHCTCDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT	219	
Qy	61	DFILVLRHYRSPVLQIYEIEQHKIETWREIYLGQCFKPLVISPNDLSFEAVYTLIKNR	120	
Db	220	DFILVLRHYRSPVLQIYEIEEHKIETWREIYLGQCFKPLVISPNDLSFEAVYTLIKNR	279	
Qy	121	IHRLPVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE	180	
Db	280	IHRLPVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE	339	
Qy	181	TAPILTALDIFVDRRVSALPVNCCQVGLYSRFDVIHLAAQOQTYNHLDMVSCEALRQR	240	
Db	340	TAPILTALDIFVDRRVSALPVNCCQVGLYSRFDVIHLAAQOQTYNHLDMNVGEALRQR	399	
Qy	241	TLCLEGLVSCOPHESICEVIDRIAREQVHRLVLVDETHQLLGVVLSLSDILQALVLPAGI	300	

Db 400 TLLCEGLVSCQPHETLGEVIDRIVREQVHRLVLDVDETHQLLGVVSLDILQALVLSPAGI 459  
Qy 301 DALGA 305  
Db 460 DALGA 464

RESULT 2  
US-09-950-022A-4  
; Sequence 4, Application US/09950022A  
; Patent No. 6919177  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950,022A  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-09-950-022A-4

Query Match 97.2%; Score 1507; DB 2; Length 464;  
Best Local Similarity 97.0%; Pred. No. 1.le-166;  
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 MRFQEHCTCYDAMATSSKLVIFDTMLTKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60  
Db 160 MHFQEHCTCYDAMATSSKLVIFDTMLTKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 219  
Qy 61 DFILVLRHYRSPVQIYEIEBQHKIETWREIYLGCCFKPLVSI SPNDSLFEAVVTLIKNR 120  
Db 220 DFILVLRHYRSPVQIYEIEBQHKIETWREIYLGCCFKPLVSI SPNDSLFEAVVTLIKNR 279  
Qy 121 IHRPLVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTTQDLGIGTFRDLAVVLE 180  
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTTQDLGIGTFRDLAVVLE 339  
Qy 181 TAPILTALDIFDVRVSALPVVNECGVGLYSRFDVIHLAAQOTYNNHLDMSVGEALRQR 240  
Db 340 TAPILTALDIFDVRVSALPVVNETGVVGLYSRFDVIHLAAQOTYNNHLDMSVGEALRQR 399  
Qy 241 TLLCEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHQLLGVVSLDILQALVLSPAGI 300  
Db 400 TLLCEGLVSCQPHETLGEVIDRIAREQVHRLVLDVDETHQLLGVVSLDILQALVLSPAGI 459  
Qy 301 DALGA 305  
Db 460 DALGA 464

RESULT 3  
US-09-950-022A-6  
; Sequence 6, Application US/09950022A  
; Patent No. 6919177  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan

; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950,022A  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-09-950-022A-6

Query Match 97.2%; Score 1507; DB 2; Length 464;  
Best Local Similarity 97.0%; Pred. No. 1.le-166;  
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 MRFQEHCTCYDAMATSSKLVIFDTMLTKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60  
Db 160 MHFQEHCTCYDAMATSSKLVIFDTMLTKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 219  
Qy 61 DFILVLRHYRSPVQIYEIEBQHKIETWREIYLGCCFKPLVSI SPNDSLFEAVVTLIKNR 120  
Db 220 DFILVLRHYRSPVQIYEIEBQHKIETWREIYLGCCFKPLVSI SPNDSLFEAVVTLIKNR 279  
Qy 121 IHRPLVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTTQDLGIGTFRDLAVVLE 180  
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTTQDLGIGTFRDLAVVLE 339  
Qy 181 TAPILTALDIFDVRVSALPVVNECGVGLYSRFDVIHLAAQOTYNNHLDMSVGEALRQR 240  
Db 340 TAPILTALDIFDVRVSALPVVNETGVVGLYSRFDVIHLAAQOTYNNHLDMSVGEALRQR 399  
Qy 241 TLLCEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHQLLGVVSLDILQALVLSPAGI 300  
Db 400 TLLCEGLVSCQPHETLGEVIDRIAREQVHRLVLDVDETHQLLGVVSLDILQALVLSPAGI 459  
Qy 301 DALGA 305  
Db 460 DALGA 464

RESULT 4  
US-09-950-022A-8  
; Sequence 8, Application US/09950022A  
; Patent No. 6919177  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max  
; APPLICANT: Ciobanu, Dan  
; APPLICANT: Malek, Massoud  
; APPLICANT: Plastow, Graham  
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark  
; TITLE OF INVENTION: Reproductive  
; TITLE OF INVENTION: and Meat Quality Traits  
; FILE REFERENCE: P04668US3  
; CURRENT APPLICATION NUMBER: US/09/950,022A  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231045  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/260,239  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/299,111  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 21





Query Match 68.6%; Score 1064; DB 1; Length 328;  
Best Local Similarity 65.2%; Pred. No. 3e-115;  
Matches 195; Conservative 62; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MRFMOEHTCYDAMATSSKLVIFDTMLKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
Db 21 MRFMRSHKCYDIVPTSSKLVVFDITLQVKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 80

Qy 61 DFILVLRHYRSPVQIYEIEQHKTWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 120  
Db 81 DFILVLRHYRSPVQIYEIEQHKTWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 140

Qy 121 IHRPLVLDPVSGNVLHILTKRLKFLHIFGSLPRPSFLYRTQDGLGIGTFRDLAVLE 180  
Db 141 IHRPLVLDPVSGNVLHILTKRLKFLHIFGSLPRPSFLYRTQDGLGIGTFRDLAVLE 200

Qy 241 TLCLEGVLSGOPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDIILQALVLS 299  
Db 261 SQYFEGVVKCNKLEILEITIVDRIVRAEVHRLVNVVNEADSIIVGIIISLSDIILQALVLS 319

RESULT 7  
US-09-272-796-7  
; Sequence 7, Application US/09272796  
; Patent No. 6207148  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; TITLE OF INVENTION: KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/272,796  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/878,989  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0321 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 328 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PENITUT01  
; CLONE: 1452972  
US-09-272-796-7

Query Match 68.6%; Score 1064; DB 2; Length 328;  
Best Local Similarity 65.2%; Pred. No. 3e-115;  
Matches 195; Conservative 62; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MRFMOEHTCYDAMATSSKLVIFDTMLKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
Db 21 MRFMRSHKCYDIVPTSSKLVVFDITLQVKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 80

Qy 61 DFILVLRHYRSPVQIYEIEQHKTWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 120  
Db 81 DFILVLRHYRSPVQIYEIEQHKTWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 140

Qy 121 IHRPLVLDPVSGNVLHILTKRLKFLHIFGSLPRPSFLYRTQDGLGIGTFRDLAVLE 180  
Db 141 IHRPLVLDPVSGNVLHILTKRLKFLHIFGSLPRPSFLYRTQDGLGIGTFRDLAVLE 200

Qy 181 TAPILTALDIFVDRRVSALPVNCGOVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR 240  
Db 201 DTPILKALNIFVERRISALPVNCGOVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR 260

Qy 241 TLCLEGVLSGOPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDIILQALVLS 299  
Db 261 SQYFEGVVKCNKLEILEITIVDRIVRAEVHRLVNVVNEADSIIVGIIISLSDIILQALVLS 319

RESULT 8  
US-09-949-016-8261  
; Sequence 8261, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8261  
; LENGTH: 413  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8261

Query Match 68.6%; Score 1064; DB 2; Length 413;  
Best Local Similarity 65.2%; Pred. No. 4.3e-115;  
Matches 195; Conservative 62; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MRFMOEHTCYDAMATSSKLVIFDTMLKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
Db 106 MRFMRSHKCYDIVPTSSKLVVFDITLQVKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 165

Qy 61 DFILVLRHYRSPVQIYEIEQHKTWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 120  
Db 166 DFILVLRHYRSPVQIYEIEQHKTWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 225

Qy 121 IHRPLVLDPVSGNVLHILTKRLKFLHIFGSLPRPSFLYRTQDGLGIGTFRDLAVLE 180  
Db 226 IHRPLVLDPVSGNVLHILTKRLKFLHIFGSLPRPSFLYRTQDGLGIGTFRDLAVLE 285

Qy 181 TAPILTALDIFVDRRVSALPVNCGOVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR 240

Db 286 DTPIIKALNIPVERRISALPVDSESGKVDIYKFDVINLAAEKTNNLDITVTQALQHR 345  
Qy 241 TLCLEGLVSCOPHESLGEVIDRIAREQVHRLVLDVDETHLGGVLSLSDIILQALVLS 299  
Db 346 SQYEGGVKNCKLEILETIVDRIVRAEVRHLVVVNEADSVIGIISLSDIILQALVLS 404

## RESULT 9

US-08-878-989-21  
; Sequence 21, Application US/08878989  
; Patent No. 5885803  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/878,989  
; FILING DATE:  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0321 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:

INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 331 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1335856  
US-08-878-989-21

Query Match 65.1%; Score 1009; DB 1; Length 331;  
Best Local Similarity 65.3%; Pred. No. 8e-109;  
Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;

Qy 3 FMOEHTCYDAMATSSKLVIFDTWLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIDF 62  
Db 32 FMKSHRCYDLIPTSSKLVVDFDTSLQVKKAFALVTNGVRAAPLWDSKKQSFVGMILTIDF 91  
Qy 63 ILVLRHYRSPVQIYEIOHKIETWREIYLCQCFKPLVSI SPNDSLFAVYTLIKNRH 122  
Db 92 INILHRYKSAVQIYELEBKETWREIYLDQSFPLVCISPNASLFDVAVSLIRNKIH 151

Qy 123 RLPVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETA 182  
Db 152 RLPVIDPESGNTLYILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETA 211  
Qy 183 PILTALDIFVDRVRSALPVVNECGVGVGLYSRSDVIHLAAQQTYNHLDMSVGEALRQRTL 242  
Db 212 PVTVALGIFVQHRVSALPVVDEKRVVDIYKFDVINLAAEKTNNLDVSVTKALQHRSH 271  
Qy 243 CLEGLVSCOPHESLGEVIDRIAREQVHRLVLDVDETHLGGVLSLSDIILQALVLS 296  
Db 272 YFEGVLKCYLHETLEIINRLVEAEVRHLVVVDENDVVKGVLSLSDIILQALVLT 325

## RESULT 10

US-09-101-146-64  
; Sequence 64, Application US/09101146  
; Patent No. 6124125  
; GENERAL INFORMATION:  
; APPLICANT: Dartmouth College, St. Vincents Institute of  
; APPLICANT: Medical Research, Kemp et al.  
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jane Massey Licata, Esq.  
; STREET: 66 E. Main Street  
; CITY: Marlton  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08053

COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: WINDOWS 95  
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/101,146  
; FILING DATE: October 7, 1998  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PN7450  
; FILING DATE: 8 JAN 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane Massey Licata  
; REGISTRATION NUMBER: 32,257  
; REFERENCE/DOCKET NUMBER: DC-0050  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (856) 810-1515  
; TELEFAX: (856) 810-1454  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 331  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-09-101-146-64

Query Match 65.1%; Score 1009; DB 2; Length 331;  
Best Local Similarity 65.3%; Pred. No. 8e-109;  
Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;

Qy 3 FMOEHTCYDAMATSSKLVIFDTWLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIDF 62  
Db 32 FMKSHRCYDLIPTSSKLVVDFDTSLQVKKAFALVTNGVRAAPLWDSKKQSFVGMILTIDF 91  
Qy 63 ILVLRHYRSPVQIYEIOHKIETWREIYLCQCFKPLVSI SPNDSLFAVYTLIKNRH 122  
Db 92 INILHRYKSAVQIYELEBKETWREIYLDQSFPLVCISPNASLFDVAVSLIRNKIH 151  
Qy 123 RLPVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETA 182  
Db 152 RLPVIDPESGNTLYILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETA 211  
Qy 183 PILTALDIFVDRVRSALPVVNECGVGVGLYSRSDVIHLAAQQTYNHLDMSVGEALRQRTL 242

Db 212 PVYVALGIFVQHRVSALPVVDEKGRVVDIYKSPDVINLAAEKTNNLDVSVTKALQHRSH 271

Qy 243 CLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVETQHLGLVSVLSLILQALVLS 296

Db 272 YFEGVLKCYLHETLETTIINRLVEAEVHRLVVVDENDVVKGVISLSLILQALVLT 325

RESULT 11

US-09-272-796-21

Sequence 21, Application US/09272796

Patent No. 6207148

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jennifer L.

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl G.

APPLICANT: Lal, Preeti

APPLICANT: Goli, Surva K.

APPLICANT: Shah, Purvi

TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/272,796

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/878,989

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0321 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 331 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 1335856

US-09-272-796-21

Query Match 65.1%; Score 1009; DB 2; Length 331;

Best Local Similarity 65.3%; Pred. No. 8e-109;

Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;

Qy 3 FMOEHTCYDAMATSSKLVIPTDMLIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDF 62

Db 32 FMKSHRCYDLIPTSSKLVVFDTSQVKKAFALVTVNGVRAAPLWDSKKQSFVGMLTITDF 91

Qy 63 ILVLHRYRSPLVQIYEIQHKIETWREIYLQGCFKPLVSPNDSLFEAVYTLIKNRIH 122

Db 92 INILHRYYSALVQIYELEEHKIETWREIYLDQSFKPLVCISPNASLFDVAVSLIRNKIH 151

Qy 123 RLPVLDPVSGNVHLTHKRLKFLHFGSLPPSPFLYRTIQDLIGTFRDLAVVLETA 182

Db 152 RLPVIDPESGNTLYLTHKRLKFLHFGSLPPSPFLYRTIQDLIGTFRDLAVVLETA 211

Qy 183 PILTALDIFVDRRVVSALPVVNECGVGLYSRDPVHIAAQOYTNHLDMVSGEALRQRTL 242

Db 212 PVYVALGIFVQHRVSALPVVDEKGRVVDIYKSPDVINLAAEKTNNLDVSVTKALQHRSH 271

Qy 243 CLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVETQHLGLVSVLSLILQALVLS 296

Db 272 YFEGVLKCYLHETLETTIINRLVEAEVHRLVVVDENDVVKGVISLSLILQALVLT 325

US-09-272-796-21

Query Match 65.1%; Score 1009; DB 2; Length 331;

Best Local Similarity 65.3%; Pred. No. 8e-109;

Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;

Qy 3 FMOEHTCYDAMATSSKLVIPTDMLIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDF 62

Db 32 FMKSHRCYDLIPTSSKLVVFDTSQVKKAFALVTVNGVRAAPLWDSKKQSFVGMLTITDF 91

Qy 63 ILVLHRYRSPLVQIYEIQHKIETWREIYLQGCFKPLVSPNDSLFEAVYTLIKNRIH 122

Db 92 INILHRYYSALVQIYELEEHKIETWREIYLDQSFKPLVCISPNASLFDVAVSLIRNKIH 151

Qy 123 RLPVLDPVSGNVHLTHKRLKFLHFGSLPPSPFLYRTIQDLIGTFRDLAVVLETA 182

Db 152 RLPVIDPESGNTLYLTHKRLKFLHFGSLPPSPFLYRTIQDLIGTFRDLAVVLETA 211

Qy 183 PILTALDIFVDRRVVSALPVVNECGVGLYSRDPVHIAAQOYTNHLDMVSGEALRQRTL 242

Db 212 PVYVALGIFVQHRVSALPVVDEKGRVVDIYKSPDVINLAAEKTNNLDVSVTKALQHRSH 271

Qy 243 CLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVETQHLGLVSVLSLILQALVLS 296

Db 272 YFEGVLKCYLHETLETTIINRLVEAEVHRLVVVDENDVVKGVISLSLILQALVLT 325

RESULT 12

US-09-538-092-1211

Sequence 1211, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 60/178,965

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CurapatSeqFormatter Version 0.9

SEQ ID NO 1211

LENGTH: 331

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (0)..(0)

OTHER INFORMATION: Polypeptide Accession Number P54619

US-09-538-092-1211

Query Match 65.1%; Score 1009; DB 2; Length 331;

Best Local Similarity 65.3%; Pred. No. 8e-109;

Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;

Qy 3 FMOEHTCYDAMATSSKLVIPTDMLIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDF 62

Db 32 FMKSHRCYDLIPTSSKLVVFDTSQVKKAFALVTVNGVRAAPLWDSKKQSFVGMLTITDF 91

Qy 63 ILVLHRYRSPLVQIYEIQHKIETWREIYLQGCFKPLVSPNDSLFEAVYTLIKNRIH 122

Db 92 INILHRYYSALVQIYELEEHKIETWREIYLDQSFKPLVCISPNASLFDVAVSLIRNKIH 151

Qy 123 RLPVLDPVSGNVHLTHKRLKFLHFGSLPPSPFLYRTIQDLIGTFRDLAVVLETA 182

Db 152 RLPVIDPESGNTLYLTHKRLKFLHFGSLPPSPFLYRTIQDLIGTFRDLAVVLETA 211

Qy 183 PILTALDIFVDRRVVSALPVVNECGVGLYSRDPVHIAAQOYTNHLDMVSGEALRQRTL 242

Db 212 PVYVALGIFVQHRVSALPVVDEKGRVVDIYKSPDVINLAAEKTNNLDVSVTKALQHRSH 271

Qy 243 CLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVETQHLGLVSVLSLILQALVLS 296

Db 272 YFEGVLKCYLHETLETTIINRLVEAEVHRLVVVDENDVVKGVISLSLILQALVLT 325

US-09-538-092-1211

Query Match 65.1%; Score 1009; DB 2; Length 331;

Best Local Similarity 65.3%; Pred. No. 8e-109;

Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;

Qy 3 FMOEHTCYDAMATSSKLVIPTDMLIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDF 62

Db 32 FMKSHRCYDLIPTSSKLVVFDTSQVKKAFALVTVNGVRAAPLWDSKKQSFVGMLTITDF 91

Qy 63 ILVLHRYRSPLVQIYEIQHKIETWREIYLQGCFKPLVSPNDSLFEAVYTLIKNRIH 122

Db 92 INILHRYYSALVQIYELEEHKIETWREIYLDQSFKPLVCISPNASLFDVAVSLIRNKIH 151

Qy 123 RLPVLDPVSGNVHLTHKRLKFLHFGSLPPSPFLYRTIQDLIGTFRDLAVVLETA 182

RESULT 13

US-09-949-016-10881

Sequence 10881, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

QY	3	FMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMMLTITDF	62
QY	3	FMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMMLTITDF	62
Db	31	FKMSHCYDLIPTSSKLVVFDTSLOVKKAPFALVNGVRAAPLWDSKKQSFVGMMLTITDF	90
QY	63	ILVLHRYRSPLOVIEIHOHKIETWREIYLOGCFKPLVSI SPNDLSFEAVVTLIKRIH	122
Db	91	INILHRYKSAVQVIELEHETWREIYLOGCFKPLVSI SPNDLSFEAVVTLIKRIH	150
QY	123	RPLVDPVSGNVLHILTHKRLKFLHIFGSLLPSPFLYRTIQDIGITFRDLAVVLETA	182
Db	151	RLPVIDPESGNTLYLTHKRLKFLHIFGSLLPSPFLYRTIQDIGITFRDLAVVLETA	210
QY	183	PILTALDIFVDRVSALPVNCEGVVGLYSRPFVHILAAQOTYNNHLDMSVGEALRQRTL	242
Db	211	PVTVALGIFVQHRVSALPVNCEGVVGLYSRPFVHILAAQOTYNNHLDMSVGEALRQRTL	270
QY	243	CLEGVLSQCPHESLGEVDRVIAEQVHRLVLDVDETHLLGVVSLDIILQALVLS	296
Db	271	YFEGVLKCYLHETLEINRLVEAEVHRLVLDVDETHLLGVVSLDIILQALVLS	324
RESULT 15			
US-09-359-161-7			
; Sequence 7, Application US/09359161A			
; Patent No. 6342656			
; GENERAL INFORMATION:			
; APPLICANT: Bradford, Kent J.			
; APPLICANT: Dahal, Peetambar			
; APPLICANT: Yang, Hong			
; APPLICANT: Cooley, Michael			
; APPLICANT: Downie, Bruce			
; APPLICANT: Gee, Oliver			
; APPLICANT: The Regents of the University of California			
; TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses			
; FILE REFERENCE: 023070-095900US			
; CURRENT APPLICATION NUMBER: US/09/359,161A			
; CURRENT FILING DATE: 1999-07-21			
; NUMBER OF SEQ ID NOS: 7			
; SOFTWARE: Patent In Ver. 2.1			
; SEQ ID NO 7			
; LENGTH: 322			
; TYPE: PRT			
; ORGANISM: Saccharomyces cerevisiae			
; FEATURE:			
; OTHER INFORMATION: yeast sucrose nonfermenting protein kinase 1			
; OTHER INFORMATION: kinase subunit (SNF1)			
US-09-359-161-7			
Query Match 29.5%; Score 457; DB 2; Length 322;			
Best Local Similarity 34.2%; Pred. No. 1.8e-44;			
Matches 106; Conservative 66; Mismatches 108; Indels 30; Gaps 6			
QY	2	RFQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMMLTITD	61
Db	24	KFLNSKTSYDVLVPSYRLVLDTSLLVKSLLNVLQNSIVSAPLWDSKTSFAGLLTITD	83
QY	62	FILVLHRYRSPLOVIEIHOHKIETWREIYLOGCFKPLVSI SPNDLSF	110
Db	84	FINVIQYFSPN-----DKFELVDKLDG-LKDIERALGVLDQDTSIHPSRPLF	133
QY	111	EAVYTLIKRIHRLPVLDPVSGN-----VLHILTHKRLKFLHIFGSLLPSPFLYRTIQ	165
Db	134	EACLMKLSRSGRIPLIDQDETHREIVSVLTQVRLKVF-----ALMCRTHFLKPIG	189
QY	166	DLGIGITFRDLAVVLETAIPALTALDIFVDRVSALPVNCEGVVGLYSRPFVHILAAQOT	225
Db	190	DLNIIQDNMKSQMTTVIDVQLMTOGRVSSPIIDENGLYNNVYAYDVLGILKGI	249
QY	226	YNHLDMSVGEALRQRTLCLEGVLSQCPHESLGEVDRVIAEQVHRLVLDVDETHLLGVVSL	285
Db	250	YNDLSLSVGEALMRSDDFEGYVTTCTKNDKLSITMDNIRKARVHRFFVDVGVRLVGLT	309
US-09-359-161-6			
Query Match 64.9%; Score 1007; DB 2; Length 330;			
Best Local Similarity 65.3%; Pred. No. 1.4e-108;			
Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;			
US-09-359-161-6			
Query Match 65.1%; Score 1009; DB 2; Length 336;			
Best Local Similarity 65.3%; Pred. No. 8.2e-109;			
Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;			
US-09-949-016-10881			
Query Match 65.1%; Score 1009; DB 2; Length 336;			
Best Local Similarity 65.3%; Pred. No. 8.2e-109;			
Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;			
US-09-949-016-10881			
QY	3	FMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMMLTITDF	62
Db	37	FKMSHCYDLIPTSSKLVVFDTSLOVKKAPFALVNGVRAAPLWDSKKQSFVGMMLTITDF	96
QY	63	ILVLHRYRSPLOVIEIHOHKI	

Qy 286 LSDILQALVL 295  
| | | | : : |  
Db 310 LSDILKYILL 319

Search completed: January 24, 2006, 22:16:24  
Job time : 26.3836 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:01:17 ; Search time 90.0325 Seconds  
(without alignments)  
2390.094 Million cell updates/sec

Title: US-10-070-794a-4  
Perfect score: 1551  
Sequence: 1 MRFMQHCTCDMATSSKLV.....LSDILQALVLSAGIDALGA 305

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_05\_80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1551	100.0	464	1 AAKG3_HUMAN	Q9ug19 homo sapien
2	1551	100.0	489	2 Q4QG8_HUMAN	Q4qg98 homo sapien
3	1551	100.0	489	2 Q4V779_HUMAN	Q4v779 homo sapien
4	1507	97.2	464	2 Q532T5_PIG	Q532t5 sus scrofa
5	1507	97.2	514	1 AAKG3_PIG	Q9mvp4 sus scrofa
6	1489	96.0	464	2 Q8C341_MOUSE	Q8c341 mus musculus
7	1489	96.0	489	2 Q8BGW7_MOUSE	Q8bgw7 m amp-activ
8	1478.5	95.3	465	2 Q4G3U3_BOVIN	Q4g3u3 bos taurus
9	1478.5	95.3	490	2 Q8WVK8_MOUSE	Q8wvk8 mus musculus
10	1408	90.8	447	2 Q6TEH8_HORSE	Q6teh8 equus caball
11	1376	88.7	440	2 Q6U7S1_HORSE	Q6u7s1 equus caball
12	1250	80.6	363	2 Q4JK38_CHICK	Q4jk38 gallus gall
13	1250	80.6	382	2 Q4JK39_CHICK	Q4jk39 gallus gall
14	1195	77.0	337	2 Q7ZYL2_XENILA	Q7zyl2 xenopus lae
15	1068	68.9	326	2 Q6V7V4_RAT	Q6v7v4 rattus norv
16	1068	68.9	326	2 Q6V7V5_MOUSE	Q6v7v5 mus musculus
17	1068	68.9	443	2 Q4QRB9_RAT	Q4qrb9 rattus norv
18	1067	68.8	443	2 Q8B1Q9_MOUSE	Q8b1q9 mus musculus
19	1067	68.8	566	2 Q91WG5_MOUSE	Q91wg5 mus musculus
20	1064	68.6	328	2 Q5Y3O7_HUMAN	Q5y3o7 homo sapien
21	1064	68.6	525	2 Q6NUI0_HUMAN	Q6nu10 homo sapien
22	1064	68.6	569	1 AAKG2_HUMAN	Q9ug10 homo sapien
23	1063	68.5	328	2 Q5ZK07_CHICK	Q5zk07 gallus gall
24	1058	68.2	558	2 Q6PA60_XENILA	Q6pa60 xenopus lae
25	1056.5	68.1	343	2 Q4RVG2_TETNG	Q4rvg2 tetraodon n
26	1054	68.0	524	2 Q5R4S0_PONPY	Q5r4s0 pongo pygma
27	1036	66.8	297	2 Q4RTT1_TETNG	Q4rtt1 tetraodon n
28	1026	66.2	330	2 Q6PCS7_BRARE	Q6pcs7 brachydania
29	1015	65.4	323	2 Q4RXW4_TETNG	Q4rxw4 tetraodon n
30	1010	65.1	330	2 Q5PRE8_MOUSE	Q5pre8 mus musculus
31	1009	65.1	330	2 Q6X275_PIG	Q6x275 sus scrofa

32	1009	65.1	331	1 AAKG1_HUMAN	P54619 homo sapien
33	1008	65.0	333	2 Q4S1Z9_TETNG	Q4s1z9 tetraodon n
34	1007	64.9	330	1 AAKG1_RAT	P80385 rattus norv
35	1007	64.9	330	2 Q4QW6_RAT	Q4qw6 rattus norv
36	1005	64.8	330	1 AAKG1_BOVIN	P58108 bos taurus
37	1003	64.7	239	2 Q4RSP4_MACPA	Q4rsp4 macaca fasc
38	994.5	64.1	340	2 Q8N7V9_HUMAN	Q8n7v9 homo sapien
39	991	63.9	334	2 Q6GN94_XENILA	Q6gn94 xenopus lae
40	990	63.8	287	2 Q6U7I6_RAT	Q6u7i6 rattus norv
41	989	63.8	330	1 AAKG1_MOUSE	Q54950 mus musculus
42	946	61.0	329	2 Q4RY44_TETNG	Q4ry44 tetraodon n
43	899	58.0	267	2 Q8EM63_MOUSE	Q8em63 mus musculus
44	857	55.3	598	2 Q7PXX4_ANOGA	Q7pxx4 anopheles g
45	854	55.1	594	2 Q5BU45_AEDAE	Q5bu45 aedes aegy

## ALIGNMENTS

### RESULT 1

ID	AAKG3_HUMAN	STANDARD;	PRT;	464 AA.
AC	Q9UG19; Q9NEL1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain) (AMPK gamma3).			
DE	Name=PRKAG3; Synonyms=AMPKG3;			
OS	Homo sapiens (Human).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=20164049; PubMed=10698692; DOI=10.1042/0264-6021:3460659;			
RA	Cheung P.C.F., Salt I.P., Davies S.P., Hardie D.G., Carling D.;			
RT	"Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding.";			
RL	Biochem. J. 346:659-669(2000).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Skeletal muscle;			
RX	MEDLINE=20280150; PubMed=10818001; DOI=10.1126/science.288.5469.1248;			
RA	Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M.,			
RA	Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H.,			
RA	Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,			
RA	Andersson L.;			
RT	"A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle.";			
RL	Science 288:1248-1251(2000).			
CC	-!- FUNCTION: AMPK is responsible for the regulation of fatty acid synthesis by phosphorylation of acetyl-CoA carboxylase. Also regulates cholesterol synthesis via phosphorylation and inactivation of hydroxymethylglutaryl-CoA reductase and hormone-sensitive lipase. This is a regulatory subunit. It may play a role in the regulation of energy metabolism in skeletal muscle.			
CC	-!- SUBUNIT: Heterotrimer of an alpha catalytic subunit, a beta and a gamma non-catalytic regulatory subunits.			
CC	-!- TISSUE SPECIFICITY: Skeletal muscle, with weak expression in heart and pancreas.			
CC	-!- SIMILARITY: Belongs to the 5'-AMP-activated protein kinase gamma subunit family.			
CC	-!- SIMILARITY: Contains 4 CBS domains.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	EMBL; AJ249977; CAB65117.1; ALT_INIT; mRNA.			

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DR EMBL; AF214519; AAF73987.1; -; mRNA.
DR Ensembl; ENSG00000115592; Homo sapiens.
DR HGNC; HGNC:9387; PRKAG3.
DR MIM; 604976; -.
DR GO; GO:0004679; F:AMP-activated protein kinase activity; TAS.
DR GO; GO:0007243; P:protein kinase cascade; TAS.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 4.
DR CBS domain; Fatty acid biosynthesis; Lipid synthesis; Repeat.
FT DOMAIN 147 201 CBS 1.
FT DOMAIN 228 282 CBS 2.
FT DOMAIN 303 356 CBS 3.
FT DOMAIN 375 428 CBS 4.
FT CONFLICT 58 58 T -> A (in Ref. 1).
FT CONFLICT 163 164 MQ -> IE (in Ref. 1).
FT CONFLICT 398 398 Q -> K (in Ref. 1).
FT CONFLICT 461 464 ALGA -> PSGPEKI (in Ref. 1).
SQ SEQUENCE 464 AA; 51514 MW; 53985C2C77003A63 CRC64;

Query Match 100.0%; Score 1551; DB 1; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRFQEHCTCDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 160 MRFQEHCTCDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT 219

Qy 61 DFILVLRHYRSPVLQIYEIOHQKIETWREIYLGCFKPLVISPNDLSFEAVYTLIKNR 120
Db 220 DFILVLRHYRSPVLQIYEIOHQKIETWREIYLGCFKPLVISPNDLSFEAVYTLIKNR 279

Qy 121 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLLPRESFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLLPRESFLYRTIQDLGIGTFRDLAVVLE 339

Qy 181 TAPILTALDIFVDRRVSAFPVNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRRVSAFPVNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 399

Qy 241 TLCLEGVLSQPHSEGLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDILQALVLSAGI 300
Db 400 TLCLEGVLSQPHSEGLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDILQALVLSAGI 459

Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 2
Q4QQG8 HUMAN PRELIMINARY; PRT; 489 AA.
AC Q4QQG8
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE AMP-activated protein kinase, non-catalytic gamma-3 subunit.
GN Name=PRKAG3;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC098306; AAH98306.1; -; mRNA.
DR EMBL; BC098255; AAH98255.1; -; mRNA.
KW Kinase.
SQ SEQUENCE 489 AA; 54232 MW; A67D9DEAB76BF0C9 CRC64;

Query Match 100.0%; Score 1551; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRFQEHCTCDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 185 MRFQEHCTCDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT 244

Qy 61 DFILVLRHYRSPVLQIYEIOHQKIETWREIYLGCFKPLVISPNDLSFEAVYTLIKNR 120
Db 245 DFILVLRHYRSPVLQIYEIOHQKIETWREIYLGCFKPLVISPNDLSFEAVYTLIKNR 304

Qy 121 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLLPRESFLYRTIQDLGIGTFRDLAVVLE 180
Db 305 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLLPRESFLYRTIQDLGIGTFRDLAVVLE 364

Qy 181 TAPILTALDIFVDRRVSAFPVNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 240
Db 365 TAPILTALDIFVDRRVSAFPVNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424

Qy 241 TLCLEGVLSQPHSEGLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDILQALVLSAGI 300
Db 425 TLCLEGVLSQPHSEGLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDILQALVLSAGI 484

Qy 301 DALGA 305
Db 485 DALGA 489

RESULT 3
Q4V779 HUMAN PRELIMINARY; PRT; 489 AA.
AC Q4V779
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE AMP-activated protein kinase, non-catalytic gamma-3 subunit.
GN Name=PRKAG3;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J.J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schumacher J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalious D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=PCR rescued clones;  
RG NIH MGC Project;  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC098102; AAH98102.1; -; mRNA.  
DR EMBL; BC098277; AAH98277.1; -; mRNA.  
KW Kinase.  
SQ SEQUENCE 489 AA; 54258 MW; 0E93E2B5117B328D CRC64;  
Query Match 100.0%; Score 1551; DB 2; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRFMQHCTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60  
DB 185 MRFMQHCTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 244  
QY 61 DFTLVLRHYRSPVQIYEIOHKIETWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 120  
DB 245 DFTLVLRHYRSPVQIYEIOHKIETWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 304  
QY 121 IHRPLVLPDVPVSGNVHLTHKRLKFLHFGSLPRPSFLYRTIQDLGIGTFRDLAVLVE 180  
DB 305 IHRPLVLPDVPVSGNVHLTHKRLKFLHFGSLPRPSFLYRTIQDLGIGTFRDLAVLVE 364  
QY 181 TAPILTALDIFVDRRVSALPVVNECCQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 240  
DB 365 TAPILTALDIFVDRRVSALPVVNECCQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424  
QY 241 TLCLEGLVSCOPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLDILQALVLSPAGI 300  
DB 425 TLCLEGLVSCOPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLDILQALVLSPAGI 484  
QY 301 DALGA 305  
DB 485 DALGA 489  
RESULT 4  
ID Q53ZT5\_PIG PRELIMINARY; PRT; 464 AA.  
AC Q53ZT5;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DE AMP-activated protein kinase gamma subunit.  
GN Name=PRKAG3;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RX PubMed=14970697; DOI=10.1159/000075743;  
RA Amarger V., Erlendsson R., Fieberg G., Jeon J.T., Andersson L.;  
RT "Comparative sequence analysis of the PRKAG3 region between human and  
RL pig: evolution of repetitive sequences and potential new exons.";  
RL Cytogenet. Genome Res. 102:163-172(2003).  
DR EMBL; AV264345; AAP12533.1; -; mRNA.  
KW Kinase.  
SQ SEQUENCE 464 AA; 51308 MW; 17638CB12A2BA9DF CRC64;  
Query Match 97.2%; Score 1507; DB 2; Length 464;  
Best Local Similarity 97.0%; Pred. No. 5.3e-115;  
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MRFMQHCTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60  
DB 160 MRFMQHCTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 219  
QY 61 DFTLVLRHYRSPVQIYEIOHKIETWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 120  
DB 220 DFTLVLRHYRSPVQIYEIOHKIETWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 279  
QY 121 IHRPLVLPDVPVSGNVHLTHKRLKFLHFGSLPRPSFLYRTIQDLGIGTFRDLAVLVE 180  
DB 280 IHRPLVLPDVPVSGNVHLTHKRLKFLHFGSLPRPSFLYRTIQDLGIGTFRDLAVLVE 339  
QY 181 TAPILTALDIFVDRRVSALPVVNECCQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 240  
DB 340 TAPILTALDIFVDRRVSALPVVNECCQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 399  
QY 241 TLCLEGLVSCOPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLDILQALVLSPAGI 300  
DB 400 TLCLEGLVSCOPHETLGEVIDRIVRQVHRLVLDVDETHLLGVVSLDILQALVLSPAGI 459  
QY 301 DALGA 305  
DB 460 DALGA 464  
RESULT 5  
AAKG3\_PIG STANDARD; PRT; 514 AA.  
AC Q9WYP4; Q6WZ89;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)  
DE (AMPK gamma3).  
GN Name=PRKAG3;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANT RN(-) GLN-250.  
RC TISSUE=Skeletal muscle;  
RX MEDLINE=20280150; PubMed=10818001; DOI=10.1126/science.288.5469.1248;  
RA Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M.,  
RA Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H.,  
RA Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,  
RA Andersson L.;  
RT "A mutation in PRKAG3 associated with excess glycogen content in pig  
RL skeletal muscle.";  
RL Science 288:1248-1251(2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).  
RC TISSUE=Skeletal muscle;  
RA Milan D., Jeon J.T., Looft C., Amarger V., Robic A.,  
RA Rogel-Gaillard C., Paul S., Gellin J., Lundstrom K., Reinsch N.,  
RA Kalm E., Le Roy P., Chardon P., Andersson L.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).

```

RX PubMed=14970697; DOI=10.1159/000075743;
RA Anarger V., Erlandson R., Pielberg G., Jeon J.T., Andersson L.;
RT "Comparative sequence analysis of the PRKAG3 region between human and
RT pig: evolution of repetitive sequences and potential new exons.";
RL Cytogenet. Genome Res. 102:163-172(2003).
CC -1- FUNCTION: AMPK is responsible for the regulation of fatty acid
CC synthesis by phosphorylation of acetyl-CoA carboxylase. Also
CC regulates cholesterol synthesis via phosphorylation and
CC inactivation of hydroxymethylglutaryl-CoA reductase and hormone-
CC sensitive lipase. This is a regulatory subunit. It may play a role
CC in the regulation of energy metabolism in skeletal muscle.
CC -1- SUBUNIT: Heterotrimer of an alpha catalytic subunit, a beta and a
CC gamma non-catalytic regulatory subunits.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=2;
CC IsoId=Q9MYP4-1; Sequence=Displayed;
CC Name=1;
CC IsoId=Q9MYP4-2; Sequence=VSP_008059;
CC -1- TISSUE SPECIFICITY: Muscle.
CC -1- DISEASE: Defects in PRKAG3 are the cause of the RN- phenotype
CC which is associated with excess glycogen content (about 70%) in
CC skeletal muscle. This mutation originated in the Hampshire breed
CC pigs and has beneficial effects on meat content but detrimental
CC effects on processing yield. Thus, this mutation is of
CC considerable economic significance in the pig breeding industry.
CC -1- SIMILARITY: Belongs to the 5'-AMP-activated protein kinase gamma
CC subunit family.
CC -1- SIMILARITY: Contains 4 CBS domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF214520; AAF73988.2; -; mRNA.
CC EMBL; AF214521; AAF73989.1; -; Genomic DNA.
CC EMBL; AY263454; AAP14907.1; -; Genomic DNA.
CC InterPro; IPR000644; CBS.
CC Pfam; PF00571; CBS; 2.
CC Alternative splicing; CBS domain; Disease mutation;
CC Fatty acid biosynthesis; Lipid synthesis; Repeat.
CC FT DOMAIN 222 276 CBS 1.
CC FT DOMAIN 303 357 CBS 2.
CC FT DOMAIN 378 431 CBS 3.
CC FT DOMAIN 450 503 CBS 4.
CC FT VARSPLIC 1 50 Missing (in isoform 1).
CC FT VARIANT 250 250 R -> Q (in RN-).
CC FT CONFLICT 418 418 V -> E (in Ref. 3).
CC FT CONFLICT 441 441 N -> S (in Ref. 3).
CC SEQUENCE 514 AA; 56790 MW; 8CE025FBBF93E4AE CRC64;

Query Match 97.2%; Score 1507; DB 1; Length 514;
Best Local Similarity 97.0%; Pred. No. 6e-115;
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRFQHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 210 MHFQHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 269

Qy 61 DFILVLHRYRSPVQVIEIEHOKIETWREIYLOGCFKPLVSI SPNDSLFAVYTLIKNR 120
Db 270 DFILVLHRYRSPVQVIEIEHOKIETWREIYLOGCFKPLVSI SPNDSLFAVYTLIKNR 329

Qy 121 IHRPLVLPDPSGNVLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLE 180
Db 330 IHRPLVLPDPSGNVLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLE 389

Qy 181 TAPILTALDIFVDRVSALPVVNECGVVGYSRFDVIHLAAQQTYNHLDMSVGEALRQR 240
Db 390 TAPILTALDIFVDRVSALPVVNECGVVGYSRFDVIHLAAQQTYNHLDMSVGEALRQR 449

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Qy 241 TLCLGVLSCOPHESLGEVIDRIAREQVHRLVLVDVETQHLGVVSLSDILQALVLSPAGI 300
Db 450 TLCLGVLSCOPHETIGELVIDRIVREQVHRLVLVDVETQHLGVVSLSDILQALVLSPAGI 509

Qy 301 DALGA 305
Db 510 DALGA 514

RESULT 6
Q8CJ41_MOUSE PRELIMINARY; PRT; 464 AA.
AC Q8CJ41_MOUSE PRELIMINARY; PRT; 464 AA.
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)
DE 01-JUN-2003 (TREMBLrel. 24, last annotation update)
DE AMP-activated protein kinase gamma 3 subunit short form.
GN Name=Prkag3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Skeletal muscle;
RX PubMed=14512293; DOI=10.1152/ajpcell.00319.2003;
RA Yu H., Fujii N., Hirshman M.F., Pomerleau L.J., Goodyear L.J.;
RT "Cloning and characterization of mouse 5'-AMP-activated protein kinase
RT gamma3 subunit".
RL Am. J. Physiol. Cell Physiol. 286:C283-C292(2004).
DR EMBL; AF525501; AAM47138.1; -; mRNA.
DR MGI; MGI:1891343; Prkag3.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 4.
KW Kinase.
SQ SEQUENCE 464 AA; 51116 MW; CEC324A5855C3F2E CRC64;

Query Match 96.0%; Score 1489; DB 2; Length 464;
Best Local Similarity 96.1%; Pred. No. 1.6e-113;
Matches 293; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MRFQHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 160 MHFQHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 219

Qy 61 DFILVLHRYRSPVQVIEIEHOKIETWREIYLOGCFKPLVSI SPNDSLFAVYTLIKNR 120
Db 220 DFILVLHRYRSPVQVIEIEHOKIETWREIYLOGCFKPLVSI SPNDSLFAVYTLIKNR 279

Qy 121 IHRPLVLPDPSGNVLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLPDPSGNVLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLE 339

Qy 181 TAPILTALDIFVDRVSALPVVNECGVVGYSRFDVIHLAAQQTYNHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRVSALPVVNECGVVGYSRFDVIHLAAQQTYNHLDMSVGEALRQR 399

Qy 241 TLCLGVLSCOPHESLGEVIDRIAREQVHRLVLVDVETQHLGVVSLSDILQALVLSPAGI 300
Db 400 TLCLGVLSCOPHESLGEVIDRIAREQVHRLVLVDVETQHLGVVSLSDILQALVLSPAGI 459

Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 7
Q8BGW7_MOUSE

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ID AC QBGM7\_MOUSE PRELIMINARY; PRT; 489 AA.  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE AMP-activated protein kinase gamma 3 subunit long form (Mus musculus  
 DE adult male bone cDNA, RIKEN full-length enriched library,  
 DE clone:9830136C07 product:5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-3  
 DE SUBUNIT (AMPK GAMMA-3 CHAIN) (AMPK GAMMA3) homolog).  
 GN Name=Prkg3;  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALB/c; TISSUE=Muscle;  
 RX PubMed=14512293; DOI=10.1152/ajpcell.00319.2003;  
 RA Yu H., Fujii N., Hirshman M.F., Pomerleau J.M., Goodyear L.J.;  
 RT "Cloning and characterization of mouse 5'-AMP-activated protein kinase  
 gamma3 subunit".  
 RL Am. J. Physiol. Cell Physiol. 286:C283-C292(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning".  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection".  
 RL Nature 409:685-690(2001).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Clothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Glessi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,  
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs".  
 RL Nature 420:563-573(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=20493374; PubMed=11076861; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes".  
 RL Genome Res. 10:1617-1630(2000).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kusunagi T., Tashiro H., Itoh M.,  
 RA Suni N., Ishii Y., Nakamura S., Hatama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multiplexed capillary sequencer".  
 RL Genome Res. 10:1757-1771(2000).  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF525500; AAN47137.1; -; mRNA.  
 DR EMBL; AK036585; BAC29492.1; -; mRNA.  
 DR Ensembl; ENSMUSG0000006542; Mus musculus.  
 DR MGI; MGI:1891343; Prkg3.  
 DR GO; GO:0016301; P-kinase activity; IEA.  
 DR GO; GO:0006633; P-fatty acid biosynthesis; IEA.  
 DR InterPro; IPR000644; CBS.  
 DR Pfam; PF00571; CBS; 2.  
 DR SMART; SM00116; CBS; 4.  
 KW Kinase.  
 SQ SEQUENCE 489 AA; 53848 MW; 85C9F71D8BDBDA5D CRC64;  
 Query Match 36.0%; Score 1489; DB 2; Length 489;  
 Best Local Similarity 96.1%; Pred. No. 1.7e-113;  
 Matches 293; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 MRPMQSHCTCDAMATSSKLIVFDITMLEIKKAFPAALVANGRAAPLWDSKKQSFVGLMTIT 60  
 DB 185 MRPMQSHCTCDAMATSSKLIVFDITMLEIKKAFPAALVANGRAAPLWDSKKQSFVGLMTIT 244  
 QY 61 DFTLVLRHYRSPVQIYRIEQHKIETWREIYLGQCFKPLVSPNDLSLPEAVYTLIKNR 120

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Db      245 DFILVLRHRYRSPVQIYEIEEHKIEIETWRIYLGCCFKPLVSPNDLSLFEAVYALIKNR 304
Qy      121 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPLPRPSFLYRTIQDGLIGTFRDLAVL 180
Db      305 IHRPLVLDPVSGTVLYILTHKRLKFLHIFGALLPRPSFLCRTIQDGLIGTFRDLAVL 364
Qy      181 TAPILTALDIFVDRVSALPVNCEGQVGLYSRFDVHILAAQOTYNHLDMSVGEALRQ 240
Db      365 TAPVLTALDIFVDRVSALPVNCEGQVGLYSRFDVHILAAQOTYNHLDMSVGEALRQ 424
Qy      241 TLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSAGI 300
Db      425 TLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSAGI 484
Qy      301 DALGA 305
Db      485 DALSA 489

RESULT 8
Q4G3U3_BOVIN
ID Q4G3U3_BOVIN PRELIMINARY; PRT; 465 AA.
AC Q4G3U3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE AMP-activated protein kinase gamma subunit.
GN Name=PRKAG3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Steleal muscle;
RA Yu S.L., Kim J.E., Jung K.C., Lee J.H., Choi I.H., Yoon D.H.,
RT "Cloning and characterization of bovine AMP-activated protein kinase
gamma subunit (PRKAG3) gene."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY692035; AAV67666.1; -; Genomic_DNA.
KW Kinase.
SQ SEQUENCE 465 AA; 51523 MW; 35C8BC32C901D565 CRC64;

Query Match 95.3%; Score 1478.5; DB 2; Length 465;
Best Local Similarity 95.4%; Pred. No. 1.2e-112;
Matches 292; Conservative 8; Mismatches 5; Indels 1; Gaps 1;

Qy      1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db      160 MHFQEHCTCYDAMATSSKLVIFDTMLQIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 219
Qy      61 DFILVLRHRYRSPVQIYEIEEHKIEIETWRIYLGCCFKPLVSPNDLSLFEAVYALIKNR 120
Db      220 DFILVLRHRYRSPVQIYEIEEHKIEIETWRIYLGCCFKPLVSPNDLSLFEAVYALIKNR 279
Qy      121 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPLPRPSFLYRTIQDGLIGTFRDLAVL 179
Db      280 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPLPRPSFLYRTIQDGLIGTFRDLAVL 339
Qy      180 ETAPILTALDIFVDRVSALPVNCEGQVGLYSRFDVHILAAQOTYNHLDMSVGEALRQ 239
Db      340 ETAPILTALDIFVDRVSALPVNCEGQVGLYSRFDVHILAAQOTYNHLDMSVGEALRQ 399
Qy      240 TLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSAGI 299
Db      400 TLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSAGI 459
Qy      300 IDALGA 305
Db      460 IDALSA 465

```

## RESULT 9

```

Q80WK8_MOUSE
ID Q80WK8_MOUSE PRELIMINARY; PRT; 490 AA.
AC Q80WK8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE AMP-activated protein kinase gamma subunit.
GN Name=Prkag3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=14970697; DOI=10.1159/000075743;
RA Amarger V., Erlandsson R., Pielberg G., Jeon J.T., Andersson L.;
RT "Comparative sequence analysis of the PRKAG3 region between human and
p1g: evolution of repetitive sequences and potential new exons.";
RL Cytogenet. Genome Res. 102:163-172(2003).
DR EMBL; AY263402; AAP22981.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 4.
KW Kinase.
SQ SEQUENCE 490 AA; 53948 MW; DBFEF917B67D4CD5 CRC64;

Query Match 95.3%; Score 1478.5; DB 2; Length 490;
Best Local Similarity 95.8%; Pred. No. 1.2e-112;
Matches 293; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Qy      1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db      185 MHFQEHCTCYDAMATSSKLVIFDTMLEIKKAFAMVANGVRAAPLWDSKKQSFVGMLTIT 244
Qy      61 DFILVLRHRYRSPVQIYEIEEHKIEIETWRIYLGCCFKPLVSPNDLSLFEAVYALIKNR 120
Db      245 DFILVLRHRYRSPVQIYEIEEHKIEIETWRIYLGCCFKPLVSPNDLSLFEAVYALIKNR 304
Qy      121 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPLPRPSFLYRTIQDGLIGTFRDLAVL 180
Db      305 IHRPLVLDPVSGTVLYILTHKRLKFLHIFGALLPRPSFLCRTIQDGLIGTFRDLAVL 364
Qy      181 TAPILTALDIFVDRVSALPVNCEG-QVVGLYSRFDVHILAAQOTYNHLDMSVGEALRQ 239
Db      365 TAPVLTALDIFVDRVSALPVNCEGQVVGLYSRFDVHILAAQOTYNHLDMSVGEALRQ 424
Qy      240 TLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSAGI 299
Db      425 TLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSAGI 484
Qy      300 IDALGA 305
Db      485 IDALSA 490

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## RESULT 10

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Q6TEH8_HORSE
ID Q6TEH8_HORSE PRELIMINARY; PRT; 447 AA.
AC Q6TEH8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AMP-activated protein kinase gamma subunit 3 (Fragment).
GN Name=prkag3;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.

```

NCBI\_TaxID=9796;  
 [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RX PubMed=14970705; DOI=10.1159/000075751;  
 RA Park H.B., Marklund S., Jeon J.T., Mickelson J.R., Valberg S.J.,  
 RA Sandberg K., Andersson L.;  
 RA "Molecular characterization and mutational screening of the PRKAG3  
 RT gene in the horse";  
 RL Cytogenet. Genome Res. 102:211-216(2003).  
 DR EMBL; AY423273; AAR03832.1; -; Genomic DNA.  
 DR EMBL; AY423271; AAR03832.1; JOINED; Genomic DNA.  
 DR EMBL; AY423272; AAR03832.1; JOINED; Genomic DNA.  
 DR GO; GO:0016301; P:kinase activity; IEA.  
 DR InterPro; IPR000644; CBS.  
 DR Pfam; PF00571; CBS; 2.  
 DR SMART; SM00116; CBS; 4.  
 KW Kinase.  
 FT NON\_TER 447 447  
 FT SEQUENCE 447 AA; 49219 MW; 3BB4E70BA6F93C3E CRC64;  
 Query Match 90.8%; Score 1408; DB 2; Length 447;  
 Best Local Similarity 95.8%; Pred. No. 6.7e-107;  
 Matches 276; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 MRFMOEHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
 DB 160 MHFMOEHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 219  
 QY 61 DFILVLHRYRSPVLQVYEIEHQKIEWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 120  
 DB 220 DFILVLHRYRSPVLQVYEIEHQKIEWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 279  
 QY 121 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
 DB 280 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPPRPSFLYRTIQDLGIGTFRDLAVVLE 339  
 QY 181 TAPILTALDIFVDRRVSALPVNVEGQVGLYSRFDVIHLAAQOQTYNHLDMVSVEALRQR 240  
 DB 340 TAPILTALDIFVDRRVSALPVNVEGQVGLYSRFDVIHLAAQOQTYNHLDMVSVEALRQR 399  
 QY 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLL 281  
 DB 400 TVCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLL 440  
 RESULT 11  
 Q6U7S1\_HORSE PRELIMINARY; PRT; 440 AA.  
 AC Q6U7S1\_HORSE  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE AMP-activated protein kinase gamma subunit 3 (Fragment).  
 GN Name=Prkag3;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.  
 OC NCBI\_TaxID=9796;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE  
 RX PubMed=14970705; DOI=10.1159/000075751;  
 RA Park H.B., Marklund S., Jeon J.T., Mickelson J.R., Valberg S.J.,  
 RA Sandberg K., Andersson L.;  
 RA "Molecular characterization and mutational screening of the PRKAG3  
 RT gene in the horse";  
 RL Cytogenet. Genome Res. 102:211-216(2003).  
 DR EMBL; AY376689; AAR03583.1; -; mRNA.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR InterPro; IPR000644; CBS.  
 DR Pfam; PF00571; CBS; 2.  
 DR SMART; SM00116; CBS; 3.  
 KW Kinase.  
 FT NON\_TER 440 440

NCBI\_TaxID=9796;  
 [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RX PubMed=14970705; DOI=10.1159/000075751;  
 RA Park H.B., Marklund S., Jeon J.T., Mickelson J.R., Valberg S.J.,  
 RA Sandberg K., Andersson L.;  
 RA "Molecular characterization and mutational screening of the PRKAG3  
 RT gene in the horse";  
 RL Cytogenet. Genome Res. 102:211-216(2003).  
 DR EMBL; AY423273; AAR03832.1; -; Genomic DNA.  
 DR EMBL; AY423271; AAR03832.1; JOINED; Genomic DNA.  
 DR EMBL; AY423272; AAR03832.1; JOINED; Genomic DNA.  
 DR GO; GO:0016301; P:kinase activity; IEA.  
 DR InterPro; IPR000644; CBS.  
 DR Pfam; PF00571; CBS; 2.  
 DR SMART; SM00116; CBS; 4.  
 KW Kinase.  
 FT NON\_TER 447 447  
 FT SEQUENCE 447 AA; 49219 MW; 3BB4E70BA6F93C3E CRC64;  
 Query Match 90.8%; Score 1408; DB 2; Length 447;  
 Best Local Similarity 95.8%; Pred. No. 6.7e-107;  
 Matches 276; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 MRFMOEHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
 DB 160 MHFMOEHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 219  
 QY 61 DFILVLHRYRSPVLQVYEIEHQKIEWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 120  
 DB 220 DFILVLHRYRSPVLQVYEIEHQKIEWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 279  
 QY 121 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
 DB 280 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPPRPSFLYRTIQDLGIGTFRDLAVVLE 339  
 QY 181 TAPILTALDIFVDRRVSALPVNVEGQVGLYSRFDVIHLAAQOQTYNHLDMVSVEALRQR 240  
 DB 340 TAPILTALDIFVDRRVSALPVNVEGQVGLYSRFDVIHLAAQOQTYNHLDMVSVEALRQR 399  
 QY 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLL 281  
 DB 400 TVCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLL 440  
 RESULT 12  
 Q4JK38\_CHICK PRELIMINARY; PRT; 363 AA.  
 AC Q4JK38\_CHICK  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE 5'-AMP-activated protein kinase gamma-3 non-catalytic subunit short  
 DE form-PRKAG3;  
 GN Name=PRKAG3;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE  
 RC TISSUE=Skeletal muscle;  
 RA Proszkowiec-Weglarz M., Richards M.P., Poch S.M.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; DQ079815; AAY86042.1; -; mRNA.  
 KW Kinase.  
 QY SEQUENCE 363 AA; 41151 MW; 06FCD94FCC3AEDC CRC64;  
 Query Match 80.6%; Score 1250; DB 2; Length 363;  
 Best Local Similarity 77.4%; Pred. No. 4.7e-94;  
 Matches 236; Conservative 39; Mismatches 30; Indels 0; Gaps 0;  
 QY 1 MRFMOEHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60  
 DB 59 MHFMRSHCCYDAVPTSCKLWVDTTLEIKKAFVALVANGVRAAPLWDSKKQSFVGMLTIT 118  
 QY 61 DFILVLHRYRSPVLQVYEIEHQKIEWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 120  
 DB 119 DFILVLHRYRSPVLQVYEIEHQKIEWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 178  
 QY 121 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPPRPSFLYRTIQDLGIGTFRDLAVVLE 180  
 DB 179 IHRPLVLPDPSGVNVLHILTHKRLKFLHIFGSLPPRPSFLYRTIQDLGIGTFRDLAVVLE 238  
 QY 181 TAPILTALDIFVDRRVSALPVNVEGQVGLYSRFDVIHLAAQOQTYNHLDMVSVEALRQR 240  
 DB 239 NAFVYAALEIFVDRRVSALPVNNAAGQVGLYSRFDVIHLAAQOQTYNHLDMVSVEALRQR 298  
 QY 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDI 300

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Db 299 TVCLEGVLTCPHETMEDIIDRITTEQVHRLVLDENYPRGIVSLSDILQALVLTGAGI 358
Qy 301 DALGA 305
   ||| :
Db 359 DALNS 363

RESULT 13
Q4JK39 CHICK
ID Q4JK39 CHICK PRELIMINARY; PRT; 382 AA.
AC Q4JK39;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 5'-AMP-activated protein kinase gamma-3 non-catalytic subunit long
DE form.
GN Name=PKAG3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal muscle;
RA Proszkowiec-Weglarz M., Richards M.P., Poch S.M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ079814; AAY86041.1; -; mRNA.
KW Kinase.
SQ SEQUENCE 382 AA; 42960 MW; 70988BFF1A2C77A59 CRC64;

Query Match 80.6%; Score 1250; DB 2; Length 382;
Best Local Similarity 77.4%; Pred. No. 5e-94;
Matches 236; Conservative 39; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MRFQHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMILTIT 60
Db 78 MHRSHCCYDAVPTSCKLVVFDITLTKKAFALVANGVRAAPLWDSKKQSFVGMILTIT 137

Qy 61 DFILVLRHYRSPVQIYEIEBQHKIETWREIYLGQCFKPLVSIISPNDLSLFEAVYTLIKNR 120
Db 138 DFINILHRYRSPVQIYEIEVEEHKIEIWRVYLGQSFKPLVSIISPNDLSLFEAVYSLIKHK 197

Qy 121 IHRPLVLPDPSGVNLHILTHKRLKFLHI FGSLLPRPSFLYRTTQDILGIGTFRDLAVYLE 180
Db 198 IHRPLVPIEPISGVNLHILTHKRLKFLHI FGSLLPRPSFLYRTTQDILGIGTFRDVAVYPE 257

Qy 181 TAPILTALDIFVDRVSALPVNCGVGVLYSRFDVTHLAAQQTYNHLDMSVGEALRQR 240
Db 258 NAPVYAALEIFVDRVSALPVNAGQVGVLYSRFDVTHLAAQQTYNHLDISVREALRQR 317

Qy 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETQHLGLGVSLSDILQALVLSGAGI 300
Db 318 TVCLEGVLTCPHETMEDIIDRITTEQVHRLVLDENYPRGIVSLSDILQALVLTGAGI 377

Qy 301 DALGA 305
   ||| :
Db 378 DALNS 382

RESULT 14
Q7ZYL2 XENLA
ID Q7ZYL2 XENLA PRELIMINARY; PRT; 337 AA.
AC Q7ZYL2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prkag3-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043738; AAH43738.1; -; mRNA.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 4.
SQ SEQUENCE 337 AA; 38325 MW; BPF4AE102D6F1DC4 CRC64;

Query Match 77.0%; Score 1195; DB 2; Length 337;
Best Local Similarity 75.4%; Pred. No. 1.4e-89;
Matches 227; Conservative 39; Mismatches 35; Indels 0; Gaps 0;

Qy 1 MRFQHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMILTIT 60
Db 33 MEFMKCCYNATPTSCKLVVFDITLTKKAFALVANGVRAAPLWDSKKQSFVGMILTIT 92

Qy 61 DFILVLRHYRSPVQIYEIEBQHKIETWREIYLGQCFKPLVSIISPNDLSLFEAVYTLIKNR 120
Db 93 DFINILHRYRSPVQIYEIEVEEHKIEIWRVYLGQSFKPLVSIISPNDLSLFEAVYSLIKNK 152

Qy 121 IHRPLVLPDPSGVNLHILTHKRLKFLHI FGSLLPRPSFLYRTTQDILGIGTFRDLAVYLE 180
Db 153 IHRPLVMDPSGVNLHILTHKRLKFLHI FGSLLPRPSFLYRTTQDILGIGTFRDLAVYQD 212

Qy 181 TAPILTALDIFVDRVSALPVNCGVGVLYSRFDVTHLAAQQTYNHLDMSVGEALRQR 240
Db 213 TSSVYNALEIFVDRVSALPVNCGVGVLYSRFDVTHLAAQQTYNHLDMSVGEALRQR 272

Qy 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETQHLGLGVSLSDILQALVLSGAGI 300
Db 273 SLCEGVLMCPHESLGEVIDRIAREQVHRLVLDVDETQHLGLGVSLSDILQALVLSGAGI 332

Qy 301 D 301
Db 333 D 333
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## RESULT 15

Q6V7V4	RAT
ID	Q6V7V4_RAT PRELIMINARY; PRT; 326 AA.
AC	Q6V7V4;
QC	Q6V7V4;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	AMP-activated protein kinase gamma 2 non-catalytic subunit.
GN	Name=Prkag2;
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
[1]	
RN	NUCLEOTIDE SEQUENCE.
RP	STRAIN=Sprague-Dawley;
RC	Zhou G., Li W., Yu L.;
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBDJ databases.
DR	EMBL; A1348865; AAQ55225.1; -; mRNA.
DR	RGD; 727782; Prkag2.
DR	GO; GO:0016301; F.kinase activity; IEA.
DR	GO; GO:0006633; P.fatty acid biosynthesis; IEA.
DR	InterPro; IPR000644; CBS.
DR	Pfam; PF00571; CBS; 2.
DR	SMART; SM00116; CBS; 4.
KW	Kinase.
SQ	SEQUENCE 326 AA; 37311 MW; 7CAC0EAB955E799E CRC64;

Query Match	58.9%	Score 1068	DB 2	Length 326
Best Local Similarity	65.2%	Pred. No. 3.5e-79		
Matches 195	Conservative 63	Mismatches 41	Indels 0	Gaps 0
QY	1	MRFQSBHTCYDAMATSSKLVIFDTMLEIKKAFPAALVANGVRAAPLMDSKKQSFVGM	IT	60
DB	19	MRFMRSHKCYDVFPTSSKLVFDTTLQVKKAFPAALVANGVRAAPLMDSKKQSFVGM	IT	78
QY	61	DFTLVLHRRYRSPVQIYEIOEHKIEWRIYILQGGCFKPLVSPISPNDSLFEAVVTLL	KNR	120
DB	79	DFNILLHRRYKSPWQIYELEEHKIEWRRLYILQETFKPLVNI <sup>1</sup> SPDASLFDAYSLIK	KNK	138
QY	121	IHRLPVLDPVSGNVLHILTHKRLKLFHIGSLLPRPSFLYRTIQDLGIGTFRDLAV	LVLE	180
DB	139	IHRLPVDPISGNALYILTHKRLKFLQLPMSDMPKPAFMQNLDLGIGTYHNIAR	FIHP	198
QY	181	TAPILTALDIFVDRRV <sup>1</sup> SALPVNNECGOVGLYSRFDVHILAAQTYNHLDM <sup>1</sup> SVGEAL	RQR	240
DB	199	NTPIIKALNIFVERRISALPVDSGKVDIYSKFDVINLAAEKTYNNL <sup>1</sup> DI <sup>1</sup> TVTQALQ	HR	258
QY	241	TLCLEGLVSCQPHESIGEVD <sup>1</sup> RTARQVHRLVLVDETOHLLGVVSLIDILQALV	SPAG	299
DB	259	SQYFEGVW <sup>1</sup> CKSLTLET <sup>1</sup> IVD <sup>1</sup> IRVRAE <sup>1</sup> HLRVVNN <sup>1</sup> ADSIVG <sup>1</sup> ISIDILQAL <sup>1</sup> ILTP	AG	317

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Job time : 93.0325 secs

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